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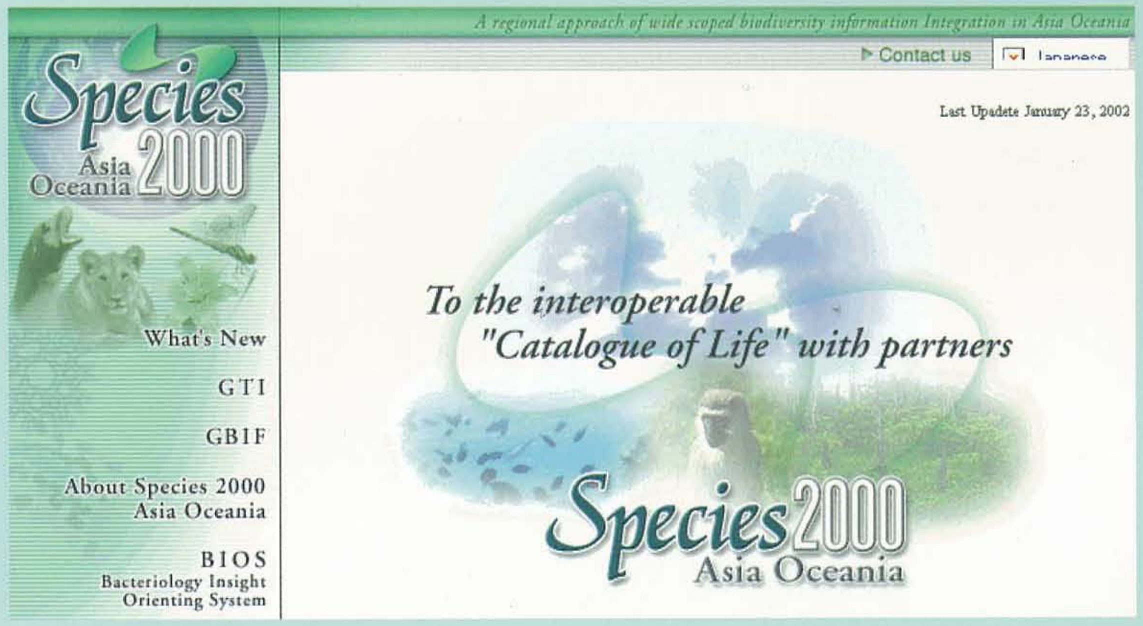

A regional approach of wide scoped biodiversity information Integration in Asia Oceania

Last Upadete January 23, 2002

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Edited by Junko Shimura, Karen L. Wilson and Dennis Gordon

NIES

独立行政法人 国立環境研究所
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Preface

Those of us who work on global biodiversity are in the midst of an upheaval. Society and scientists alike are becoming seriously concerned about the consequences of loss of species. This is not only about the loss of benefits from each individual species, but also about the resilience of the major biomes on earth, and their ability to provide ecological goods and services that we depend on. But in parallel with concern about loosing species there has been a series of shocks to our fundamental assumptions on species numbers: how many species are there? Whole new biota have been discovered or extrapolated – in deep sea vents, deep under the soil, in marine waters, as endosymbionts in every insect - in a continuing story of surprises. As a result estimates of total numbers of species on earth have rocketed and the truth is that no-one presently knows for sure whether conservative estimates of about 13 million are more reliable than extrapolations that can run up to about 100 million.

Set against this turmoil the seemingly modest objective of the Species 2000 organisation becomes ever more urgent as a tool and baseline for biodiversity studies. Its objective is to create a quality index to all species that are presently known, estimated at about 1.75 million, including viruses, micro-organisms, fungi, plants and animals. This is planned as a global programme over a ten year period, the so-called "Catalogue of Life", to be developed by Species 2000 in partnership with Species 2000 Asia Oceania and the North American ITIS organisation, plus other organisations willing to join the enterprise. As this symposium amply illustrates, energetic projects on taxonomic treatments and catalogue compilation are going on all over the world. The challenge is to create an architecture that can both bring these many contributions into a single assembly, and be sufficiently dynamic to respond to the fast-changing picture.

Frank Bisby, Chair of Species 2000

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July 14-16,1999

Species 2000: A Global Architecture for the Catalogue of Life

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Abstract

The Species 2000 Programme is creating a uniform index to the world's known species for use as a practical tool in monitoring biodiversity worldwide. The task is ambitious because of the difficulty both in obtaining coverage of all groups, and in navigating a responsible route through the alternative taxonomic treatments. The organisational architecture adopted is that a central Common Access System (CAS) will access a distributed array of taxonomic databases for different components of the index. These databases are ideally Global Species Databases (GSD's), taxonomic databases that contain a globalised taxonomic treatment of all species within one major taxon. In addition to creating the globalised index, Species 2000 needs to establish links with the regional taxonomic databases, many of which are of high quality and rich in associated species diversity data. This is a novel area of organisation, but present plans are for the links to be of two kinds. First the synonymy of the GSD will allow electronic connections to be maintained with relevant species in the regional databases even where they use different accepted names for the same organisms. Second, and more difficult to organise, there needs to be some flow of information and discussion between the organisers of the global and the regional systems. This is because novelties and taxonomic disparities can be introduced in both. Where possible it is important to work towards consensus, and to eliminate disparities not caused by genuinely different taxonomic views.

Key Words : Species 2000, Catalogue of Life, Global Species Databases, Taxonomy, Taxonomic Databases, Animals, Plants, Fungi, Micro-organisms

Introduction

Species 2000 (http://www.sp2000.org) involves taxonomists throughout the world collating a uniform and validated index to the world's known species. This index will act as an electronic baseline species list for use in inventorying projects and will form a comprehensive worldwide catalogue for checking the status, classification and names of species.

The index is being formed by linking a number of individual taxonomic databases (Fig. 1), to create a virtual "Dynamic Checklist" on the World Wide Web and a standard "Annual Checklist" produced on an annual basis, available on CD-ROM as well as the Internet. Each individual database will have a global coverage of the species in one taxon, that is, it will be a Global Species Database or GSD. When an appropriate species name is entered in the "Species Locator" web page (or chosen from a number of names returned from a search on a partial name) the relevant GSD will deliver a standard set of data about the species.

The GSDs will increasingly contain onward links from species entries to secondary sources of information about those species held in other databases and information repositories (Fig. 1). For users wishing to access the myriad but chaotic biological resources on the Internet, the Species 2000 'Catalogue of Life' can thus also be used to provide an index and biodiversity organising principle. The index will become a gateway to a digital library of biodiversity information on the Internet, using direct species links between the index and other data systems on subjects as varied as specimen data, agriculture, pharmacy, conservation, and trade and importation legislation.

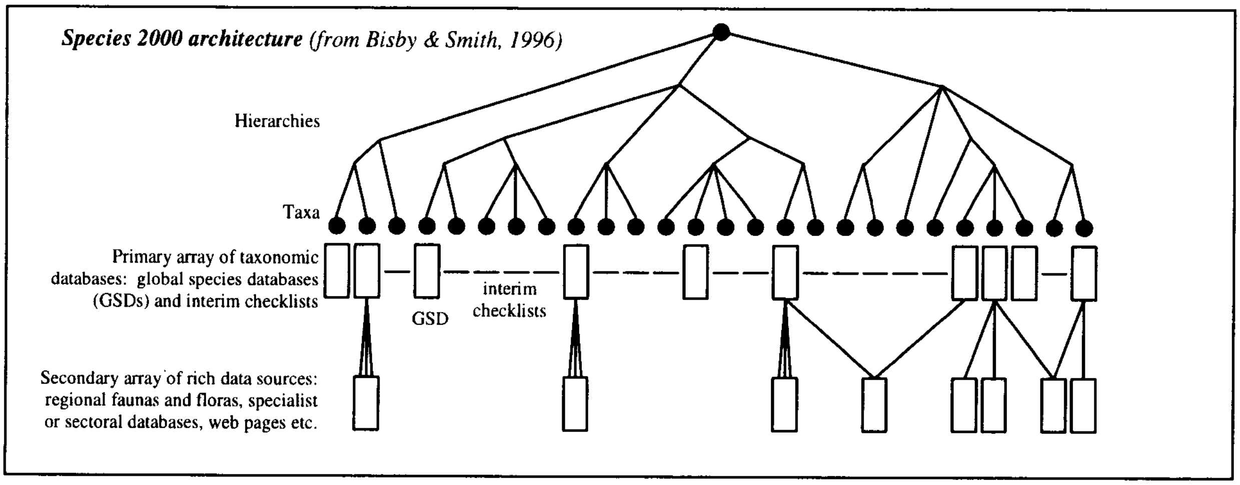


Fig. 1. The Species 2000 index is being formed by linking GSDs, with onward links to other information sources

Prototypes of the Dynamic and Annual Checklists and the Common Access System software are available on the web site (www.sp2000.org). Species in the databases linked to the prototype Dynamic Checklist also demonstrate onward links to other information sources.

Species 2000 held its inaugural meeting in Manila in 1996. The project was established by the international scientific unions IUBS (International Union of Biological Sciences), CODATA (Committee on Data in Science and Technology) and IUMS (International Union of Microbial Sciences). It was subsequently endorsed by UNEP (United Nations Environment Program) and the Clearing House Mechanism of the CBD (Convention on Biological Diversity) and is also recognised at a global scale by OECD (Organisation for Economic Co-operation and Development) (Lovejoy and Lane, 1997) and GEF (Global Environment Facility) (Cresswell and Bridgewater, 1998).

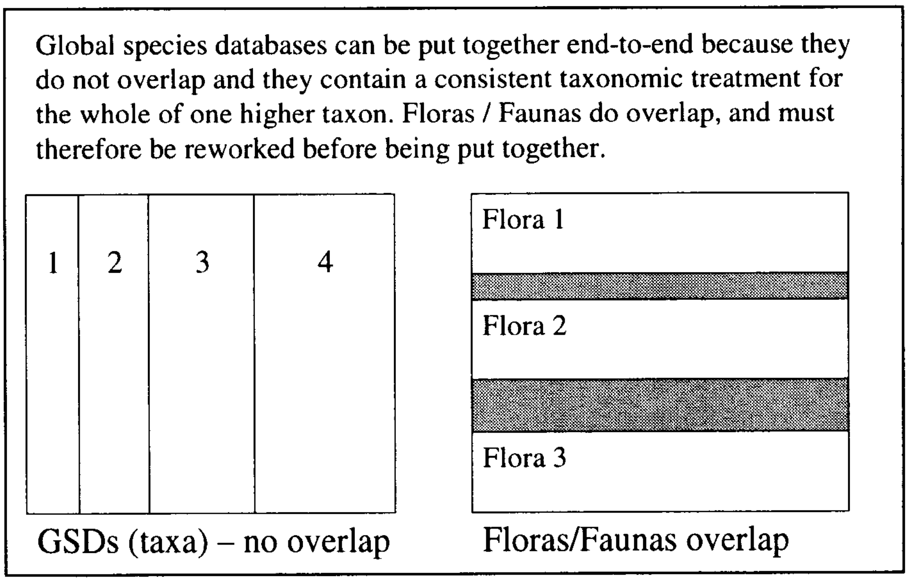
Global Species Databases and Taxonomic Quality

The Species 2000 project has defined a method, which has been widely accepted, for achieving a uniform and validated quality taxonomic checklist of all known species of plants, animals, fungi and micro-organisms. The checklist will be composed from segments held in a set of Global Species Databases (GSDs), where each GSD is an independent taxonomic database containing information about all the species in a defined group of organisms.

Each GSD participating in Species 2000 is or will be created and maintained by the relevant taxonomic experts and includes identifying information about each species (the Species 2000 Standard Data), as follows: accepted (or valid) scientific name; synonyms; name statuses; original, acceptance and synonymic literature citations; common names and their language and place tags; other selected literature citations; position within a genus and higher taxa; scrutinising expert's name; and date of last scrutiny.

The reason for using GSDs to build the index, rather than regional floras and faunas is that the species within floras and faunas overlap (Fig. 2). For example, 65% of the legume species found in the Indian Ocean region are also present in mainland Africa (J. Heald, pers. comm.; data from the ILDIS World Database of Legumes (Bisby *et al.*, 1999)). Therefore when two regional checklists are merged, the species in both lists must be carefully examined to ascertain which species are represented twice, whether the same accepted or valid names have been used, and if they have, whether they refer to the same species concept and so on. This process must then be repeated for each additional checklist until global coverage is achieved.

Whilst this is a valid method for creating a GSD, it requires the involvement of a significant proportion of the taxonomic specialists for the group, to ensure that the final list has a uniform taxonomic treatment, and that species information is not duplicated under different names. It is therefore necessary that the taxonomic experts for a particular group produce their own world list; it would be impossible for Species 2000 to oversee the merging of and resolution of taxonomic conflicts within databases for all taxa. In addition it is essential that the world lists continue to be maintained and updated by taxonomists, another task which would be wholly unsuitable for a central organisation. So, the role of Species 2000 is to locate and bring together GSDs for different taxonomic sectors, and to locate gaps in coverage and stimulate the building of new GSDs to fill those gaps.



Global species databases can be put together end-to-end because they do not overlap and they contain a consistent taxonomic treatment for the whole of one higher taxon. Floras / Faunas do overlap, and must therefore be reworked before being put together.

Fig. 2. Advantages of using GSDs

Users will need reassurance on the taxonomies selected by GSDs. Are the taxonomic views moderated by responsible choice where alternatives exist? How broad is the expert group making these choices? Can alternative classifications and the use of synonyms be adequately cross-referenced to the preferred taxonomy? What are the quality controls?

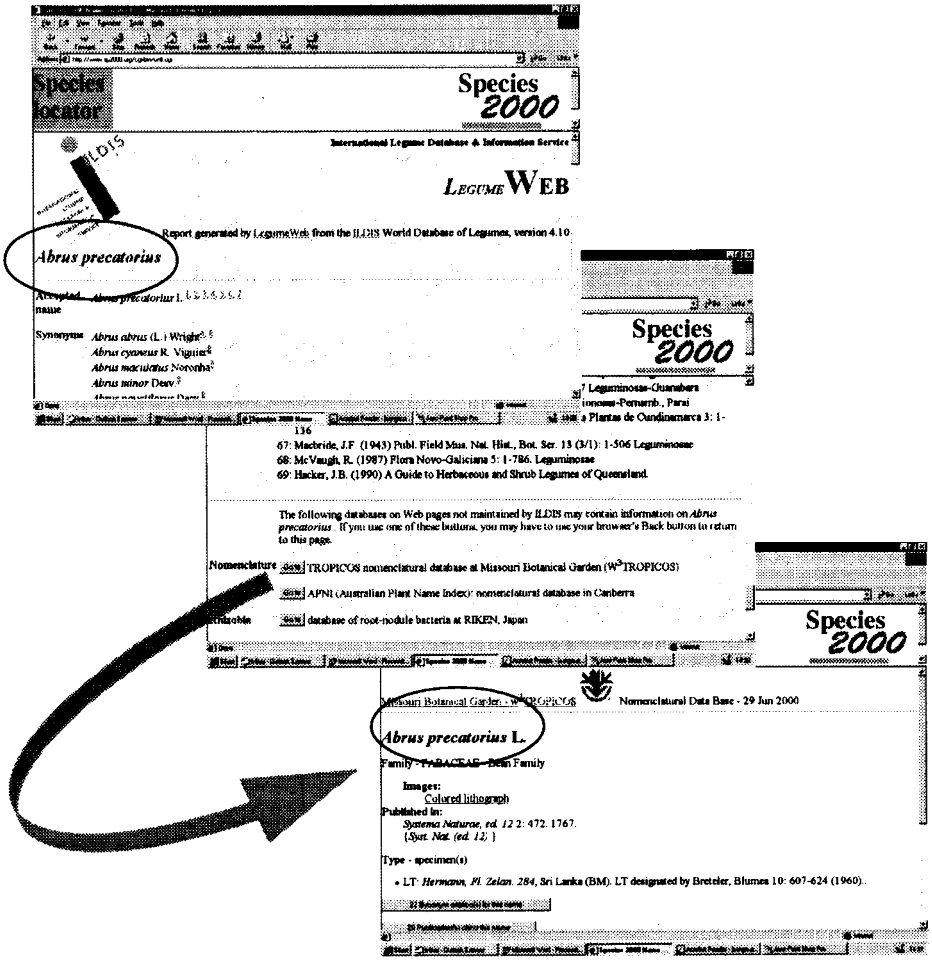
Species 2000 now holds details of over 100 GSDs. A growing number of these have evolved infrastructures by which panels of experts either create or moderate preferred taxonomic views, globalise regional systems, cross-link alternatives and in the best cases enhance the taxonomy through slow-moving changes over a number of years (Zarucchi *et al.*, 1993). These are becoming accepted as useful and reliable resources within both the taxonomic and the user communities. A number of these are leading partners in the Species 2000 project, such as the ILDIS World Database of Legumes (Bisby *et al.*, 1999), FishBase (Froese and Pauly, 2000) and ProkaryoBase (now part of BIOS (Watanabe *et al.*, 2000)), which covers Bacteria and Archaea. We now need to demonstrate that these properties can be homogenised over a community of GSDs, including taxonomic databases with a wide range of sources, motives and origins.

GSDs have an explicit mechanism for seeking at least one responsible / consensus taxonomy, and for applying it consistently. For example ILDIS (Bisby *et al.*, 1999) receives information from 12 regional centres, providing detailed local knowledge about the species present in a particular region, then periodically, the species in a particular tribe are reviewed by one or more taxonomic experts, to check that a consistent taxonomic scheme has been followed for the preferred taxonomy. Species 2000 would ideally like to build the Index of all known species from large GSDs – since the technical and administrative effort in linking the required number of small databases would be huge. However, there is some evidence that there is a practical upper limit for the size of a GSD administered (as is typical) by an academic institution or network. Some of the best GSDs are those with a coverage of 10,000 to 25,000 species – resulting in a project which is large enough to have a significant impact in the taxonomic community, but not so large that the administration and project management becomes unwieldy.

Many users of GSDs are not taxonomists, or even necessarily biologists, and these users tend to prefer to use a single consensus taxonomy. However, it is important that people using alternative taxonomies, or names no longer in frequent use, are also able to locate data. This is achieved through synonymic indexing – whereby users searching on names considered by the GSDs to be synonyms are taken directly to the accepted name and the standard data for that species (which includes the original synonym used in the query).

Onward Links to Additional Species Information

The most important potential use of the Species 2000 'Catalogue of Life' is for it to organise biodiversity information on the Internet. Users will be able navigate directly from a page of information about a species with Species 2000 to information about the same species in other systems. Such "direct species links" are already demonstrated by some of the on-line databases involved in Species 2000 (Fig. 3). For example, once a user has accessed the Species 2000 standard data for a fish species they can go directly to detailed information about the same species in Fishbase (Froese and Pauly 2000), the GSD which provides the standard data for fish. From FishBase they can go directly to information on the same species in GenBank (www.ncbi.nlm.nih.gov/Genbank/index.html). The ILDIS database (Bisby *et al.*, 1999), which provides the standard data for legumes, has direct species links to several additional databases, including TROPICOS at Missouri Botanical Garden (http://mobot.mobot.org/Pick/Search/pick.html), the Flora Europaea (Tutin *et al.*, 1964-93) database at RBG Edinburgh (www.rbge.org.uk/forms/fe.html) and the Australian Plant Name Index (Chapman, 1947-1991) nomenclatural database in Canberra.



Report generated by LegumeWeb from the ILDIS World Database of Legumes, version 4.10

Abrus precatorius

Accepted name *Abrus precatorius* L.

Synonyms *Abrus abrus* (L.) Wright
Abrus cyaneus R. Viguier
Abrus maculatus Noronha
Abrus minor Desv.

7 Leguminosae-Guanabara
Leguminosae-Pernamb., Parai
Plantas de Cundinamarca 3: 1-136

67: Macbride, J.F. (1943) Publ. Field Mus. Nat. Hist., Bot. Ser. 13 (3/1): 1-506 Leguminosae
68: McVaugh, R. (1987) Flora Novo-Galiciana 5: 1-786. Leguminosae
69: Hacker, J.B. (1990) A Guide to Herbaceous and Shrub Legumes of Queensland.

The following databases on Web pages not maintained by ILDIS may contain information on *Abrus precatorius*. If you use one of these buttons, you may have to use your browser's Back button to return to this page.

Nomenclature TROPICOS nomenclatural database at Missouri Botanical Garden (W^3TROPICOS)
APNI (Australian Plant Name Index): nomenclatural database in Canberra
Rhizobia database of root-nodule bacteria at RIKEN, Japan

Missouri Botanical Garden - W^3TROPICOS Nomenclatural Data Base - 29 Jun 2000

***Abrus precatorius* L.**

Family - FABACEAE - Bean Family

Images:
Colored lithograph

Published in:
Systema Naturae, ed. 12 2: 472. 1767.
{*Syst. Nat. (ed. 12)* }

Type - specimen(s)

- LT: *Hermann, Fl. Zelan. 284*, Sri Lanka (BM). LT designated by Breteler, Blumea 10: 607-624 (1960)..

Fig. 3. Direct species links in Species 2000: from ILDIS to TROPICOS

At present most direct species links operate by linking together species with the same accepted / valid name. One of the biggest challenges is to make these links more "taxonomically intelligent" so that the users are led to the correct information even the second information source uses a different accepted name for that species. Similarly if a single species in Species 2000 is represented by two or more species in another system it is important that links are made to both species, and that care is taken to explain that even if a species is known by the same accepted name in the second system, it represents a different (pro-parte) concept of that taxon (Fig. 4).

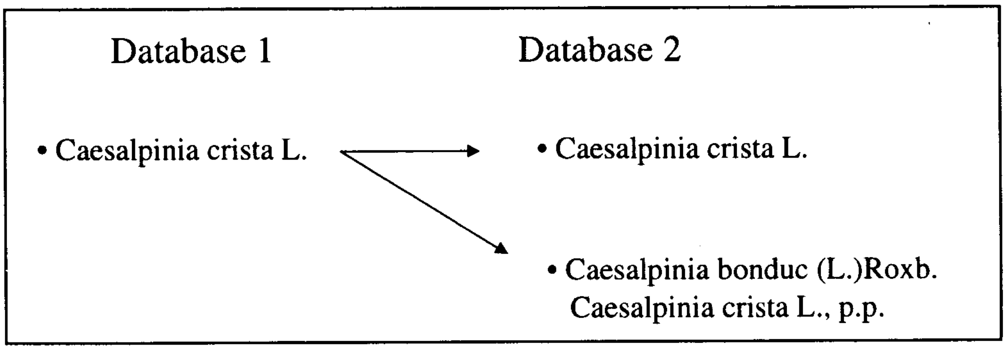


Fig. 4. The same accepted name may represent different species concepts.

Working Towards Consensus

One of the most important areas in which "taxonomically intelligent links" will be needed is in the linkage of regional floras and faunas to Species 2000. Comparison of the taxonomy of regional lists of legume species suggest that taxonomic disparities are common between checklists created in different parts of the world (Bisby and Brandt, unpublished information). There are many reasons for this. In some cases there are genuine differences of opinion. For example taxonomists in Russia prefer to treat species placed in the genus *Trifolium* by the ILDIS World Database of Legumes (Bisby *et al.*, 1999) as three separate genera: *Amoria*, *Chrysaspis* and *Trifolium* (Roskov *et al.*, 1998). However, other differences may be due to historical reasons, ignorance of data recorded in other parts of the world, or compound errors caused by inaccuracies in the names recorded in one publication being duplicated in subsequent works. Comparisons of these systems, whether by manual or electronic means (Jones *et al.*, 2000, Embury *et al.*, 1999) provide the data for discussions which can help to minimise non-essential taxonomic disparities and thus make the first moves towards taxonomic consensus, whilst maintaining important differences of opinion.

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Developing Data and Database Standards in Science: Some Challenges and How CODATA Can Help Meet Them

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Abstract

The triple revolutions caused by advanced computers, advanced informatics and the Internet have changed forever the way scientific and technical data are stored, located and disseminated. There is no turning back. Today almost every scientist uses the Internet to share data, sometimes just with close colleagues, other times through large-scale databases. Standards are clearly going to be required to allow data exchange and data sharing to proceed smoothly and coherently. Some areas of science already have such standards, specifically crystallography, x-ray photoelectron spectroscopy, materials testing (in part) and neutron interactions. In addition, virtually every International Scientific Union has established standard nomenclature for its discipline, though almost never from the perspective of computer database building and dissemination. In this talk I identify the common elements of all scientific data exchange standards, including those related to substance/object description, test and property data, test conditions, and data and database quality. I discuss how data formats should and can be integrated thereby linking different distance scales – atomic to bulk or molecular biology to ecological. Finally I identify opportunities for CODATA to develop specific guidelines for scientific data exchange standards and to provide support for standards development in a few key areas.

Key Words: Standards, Databases, Informatics, Scientific data, Technical data, Database standards

Introduction

Without debate, scientists today have greater access to the results of research than ever before. Not only is the primary and secondary literature almost fully computerized, but also large databases that bring together many disparate measurement results are widely available. As the Internet and WorldWide Web continue to grow, the accessibility of this information will only increase. At the same time, modern computing, networking and information technology make it easier for scientists to collaborate and share data across large geographical distances and among different applications and disciplines. To take full advantage of the potential for wide dissemination and data exchange and sharing, the scientific community must develop a suite of standards, easy to use, yet robust enough to work in a wide variety of situations. In this paper, I will describe the types of standards needed, as well as several approaches to developing these standards. I also describe how CODATA can help the standards development process.

Despite the obvious problems evident when discussing the subject of scientific and technical (S&T) data and database standards, it must be noted that the scientific community is at the beginning of a new era. Computers and computer networks are not going away. Literature and numerical databases will only continue to grow. The role of modeling and simulation, which are strongly dependent on data as input, will only increase as vehicles for scientific discovery. Until fifty years ago, scientific communication made use of natural language, with all its ambiguities, imprecision and multiple representations. The need for precision as demanded by computer technology is a recent phenomena. Heretofore, the human brain was the processor, and through thinking processes that are only now being unraveled, the brain was able to bring precision when needed. However, computer technology requires what natural language does not provide: precision and accuracy in communication. In the world of data sharing and data exchange, standards are the way that this precision and accuracy will be achieved.

The Nature of Quantitative Data

In this paper, I will concentrate on that part of scientific information used to describe substances and systems, their structure and their properties and interactions. Specifically, I will concentrate on data that describe nature, including properties, observations, structure, correlations, heuristic fits, diagrams and associations. Usually these are quantitative, but sometimes qualitative information is all that is measured, reported or available. These data are represented in many ways, almost always using numbers, text, scientific text (e.g., Greek letters, symbols), relationships (e.g., equations), rules, pictures and diagrams (Rumble and Smith 1990). The data result from experiments, measurements, calculations, observations, models and simulations. They are normally reported within scientific reports, the formal primary literature, informal reports, lab notebooks, and deposition databases. With the use of new instruments and computers, scientific data are now often generated and collected on unprecedented scales. Genome sequences, astronomical surveys, chemical substance property calculations, weather observations are but examples.

The Structure of Scientific Disciplines

While scientists often identify themselves with specific narrow scientific disciplines, for the purposes of considering S&T data and database standards, it is useful to look at science and technology in terms of broad disciplines that encompass increasing levels of scale. With the increase in scale, complexity grows in terms of the number of components, size, internal associativity and connectivity, and interactions. Examples include:

- From individual molecules to industrial chemistry;
- From molecular biology to cells to tissues to organs to species to ecosystem to biodiversity;
- From atomic silicon to manufactured silicon material to chip feature to chip to electronic device; and
- From pure phase to microstructure to engineering material to part to manufactured product.

Within each level, a wide variety of data is collected and used. In the future, sharing these data across levels of complexity and scale will become increasingly important. Data generated by and for one level will be valuable to higher levels. Consequently, when developing S&T data and database standards, the movement of data from one level to another must considered. Because each level has usually developed its own specific nomenclature and terminology, reconciliation between two levels is an important task that must be considered from the start.

The Need for Scientific Data and Database Standards

Four primary motivating factors exist for developing standards for collection, reporting, sharing and using scientific data and databases. The first is for *improved data collection.* Standards define what complete data sets are. They facilitate uniformity and make it easier to develop automated data collecting. Standards *promote efficiency in database building and application software development.* The standards represent collective, community-wide solutions to nomenclature and data representational problems. They form the basis for data dictionaries and ease the development of database schemas. *Standards enable data sharing,* *exchange and integration.* They let smaller data sets be combined into meaningful larger data collections. They allow data comparison to be accomplished correctly. Finally, standards *ease data use.* They provide the common connections to applications. They allow knowledge discovery to be based in reality. In a networked environment, they allow data from different sources to be used concurrently with minimal transformation.

There is no doubt that standards for scientific data and databases will foster increased value in all types of data collections, from a small table of properties in an individual research report to the largest collection of high energy physics observations. Later in this paper, we will point out some barriers, including economic, that prevent rapid development of standards. However, it is difficult to imagine a S&T data future without standards.

Basic Principles of Data and Database Standards

The first primary element of data and database standards is *format neutrality.* The standard should not be designed to replace existing or future internal formats. The standard should define a neutral format that only requires database maintainers and application developers to translate into and out of the format. Individual developers of data collections and databases often have specific needs and requirements that dictate their schemas and formats. For certain community data collection efforts, it may be desirable that the initial data collection is done with a standardized format. Or it may be the case that data are collected automatically, such as in the case of high-energy physics experiments. Or instruments that routinely collect measurement results, say powder diffractometers, all use a standard format. However, there is no need for such a requirement, and in many situations, especially when considerable investment has already been made, establishing neutrality leads to easier consensus because existing database formats will not have to be changed.

The second primary aspect of these standards is that they should *define all data elements* using normal data dictionary information plus rules, inheritance and relationships. To accomplish this, a robust information model should be developed, preferably using a modern data modeling language. The standard should also identify the minimum set of data elements that must be included to make a data collection or database meaningful. It should define other data elements in case they are to be used. It should allow for extensions to allow new data elements to be included. Extensions could be included in different ways, through committee action or by self-definition.

The third primary principle of building these standards is to *separate the semantics from syntax.* The semantics, that is, the meaning of the data elements, reflect the major challenge in developing these standards. It is almost impossible to underestimate the difficulties in developing acceptable definitions and resolving nomenclature problems. The challenges are impressive: multiple nomenclature systems developed at different times; different languages and custom; turf issues; and the changing of nomenclature across discipline and sub-discipline boundaries. The syntax of data and database standards will change over time as new computer technology evolves. Further, in many instances, data use will necessitate multiple syntactic standards to fit the needs of different uses. When semantics are separated from syntax, addressing changes in syntactic requirements can be done in a formal and efficient manner.

Today a buzzword often heard in standards development is *ontology*, that is, the collection of related concepts in a given discipline. Interesting work is going on to develop tools that define ontologies, test them for completeness and use the ontologies for practical standards. However, that work should not obscure the very real differences that exist within the semantics of individual S&T disciplines. The problems, however, are not intractable and best handled directly by involving all concerned parties.

It has recently been suggested that instead of demanding uniformity, a better approach to data exchange is through the use of interfaces that allow users to inspect data models on demand and to resolve differences through such interfaces. First, that implies the existence of definitive and formal data models for each and every resource being used, which is not true. In addition, the data models would need to be robust and detailed enough to support resolution of differences. Even if such an approach proves feasible, a small set of uniform data elements will likely be needed to begin a more detailed comparison. For example, in Species 2000, about seven common data elements are being defined, which allow easy access to multiple species inventory resources in their own individual formats.

Content of Data and Database Standards

Most scientific databases contain properties of a substance, system, species or other object. Consequently, the standards concerning the contents of these databases must address three primary aspects: Description of the substance, system, species or object; reporting the properties, measurements, observations, characteristics, calculations and results; and the context in which the properties, etc. are meaningful. There is not sufficient space in this paper to go into detail about these three components, but the following table summarizes some of the major parts of each component:

Computerized description of a substance, system or species

- Define the substance, system, species or object as unique
  - *It is this substance, not that one*
  - Must support different levels of detail, e.g., protein, protease, protease IV, protease IV (acidophilus)
- Allow determination of equivalency
  - *Two systems are same to a specified level*
  - For example, both are ketones, both are ethyl-ketones, etc.
  - Can include association (bonding, joining, etc.), interactions, reactions and interactions
- Several types of information
  - Primary identifiers (names), specifications, characterization and composition, source, processing history, reference test results, association (bonding, joining), material form, supplement information
- Millions of chemicals, species, objects – do not have to include all in standard
- Often have variety of description approaches

Properties, measurements, observations, characteristics, calculations, results

- Can be represented in a variety of ways – text, numbers, equations, coordinate systems, etc.
- Often have complex structure
- Greater dependency on variables than often realized

Conditions (situation) under which the property, observation, etc., is meaningful

- Independent variables of two types
  - Those set at beginning and not changed
  - Those varied throughout data set
- Includes data collection methods, data analysis documentation, other variables
- Variables can be very numerous (hundreds) and complex
- Most researchers do not record every variable
- Must construct definitions of two types

  - Mandatory – without these, data set would be useless
  - Optional – if you record, do it this way
- Lists
  - Controlled vocabulary
  - Suggested vocabulary
  - Free text

Types of Standards and Standards Bodies

Standards are developed in a variety of situations. Industry and engineering make heavy use of formal standards development organizations (SDOs). On the international level, this includes groups such as the International Standards Organization (ISO) and the International Electrotechnical Committee (IEC). Every country has one or more national SDOs. In the United States, hundreds of SDOs are officially recognized, but in other countries, the number is usually one or a very few at most. In recent years, the Internet era has spawned a number of new international SDOs such as the WorldWide Web Consortium (W3C) and Object Management Group (OMG). These at present lack the official standing that ISO and IEC have, but they have been very effective in bringing together the major networking players in order to develop standards quickly and efficiently.

In addition, a number of national and international scientific unions and societies have long developed standards for their disciplines. In many cases the standards deal just with nomenclature and terminology issues and have not addressed the issues associated with computerized data and databases. However, many of these organizations are now beginning to address these issues, and the resulting S&T data and database standards are gaining considerable acceptance.

Examples of some existing S&T data and database related standards are given in the table below.

Field	**Standard Name**	**Organization**	**Reference No.**
Crystallography	CIF, mmCIF	International Union of Crystallography	IUCR
Analytical Chemistry	Mass Spectrometry	American Society for Testing and Materials	ASTM
Nuclear Data	Nuclear Reactions	International Atomic Energy Agency	IAEA-EXFOR IAEA-ENDF
	Nuclear Structure	International Atomic Energy Agency	IAEA-ENSDF
Chemistry	Nomenclature	International Union of Pure and Applied Chemistry	IUPAC
	Nomenclature	Chemical Abstracts System	CAS
Surface Characterization	X-ray Photoelectron Spectroscopy	ISO TC 201	ISO 14976
Engineering Materials	Description and Properties	ISO TC 184 SC4	ISO 10303-45

Where Does CODATA Fit In?

CODATA is the Committee of Data for Science and Engineering. The then International Committee of Scientific Unions (ICSU, now the International Council for Science) founded it in 1968 as an independent committee. CODATA is concerned with the collection, quality and accessibility of all types of scientific and technical data. CODATA has considerable experience in the development of S&T data reporting requirements and has issued many reports on this subject. During recent years, CODATA has begun examining how best to serve the scientific community in terms of facilitating the development of data and database standards in a computerized environment. Several of its Task Groups have addressed aspects of this problem. The most relevant to biology is the Commission on Standardized Terminology for Access to Biological Data Banks. This commission has been instrumental in helping to establish Species 2000, which activity is well described in other parts of this publication.

What CODATA can and does provide is a friendly environment for scientists to work together internationally on S&T data and database standards. The formality involved in traditional SDOs is often a different culture from that scientists are comfortable with. In the SDOs, the standards are developed by consensus and by voting. The standards often reflect not the state of the art, but rather a methodology that everyone is comfortable with. In contrast, scientists are usually most comfortable with using the state of the art, especially in terms of 'my way is best'.

CODATA wants to continue creating an environment that is helpful to scientists who want to develop S&T data and database standards. It has experience in setting up effective Task Groups, cross-Union cooperation and computerized data in general. CODATA looks forward to working with various disciplines to ensure that the standards necessary for users to exploit the power of computerized collection, delivery and use of scientific data.

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Activity of DIWPA in Relation to IBOY

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Abstract

DIWPA (DIVERSITAS International in the Western Pacific and Asia), which is a regional organization for DIVERSITAS activities, is planning an International Biodiversity Observation Year in 2001 (IBOY-DIWPA 2001). IBOY is one of the activities of DIVERSITAS (an International Program of Biodiversity Science) to launch a year of observations on the status of Earth's biological diversity in the year of 2001, the first year of the 21st century. IBOY-DIWPA aims (1) to establish an international network for preservation and identification of biodiversity information, and (2) to elucidate the functional aspects of biodiversity in ecosystems. To implement these, we will conduct inventory and monitoring of biodiversity in Western Pacific and Asia by using standardized protocols in forest, lake, and coastal marine ecosystems. We have started the discussions on research sites and are examining standardized methodology. Several pilot studies began in 1999, following the development of a manual.

Key Words : DIWPA, IBOY, Biodiversity, International network, Western Pacific and Asia, Protocol manual.

What are DIVERSITAS and DIWPA?

DIVERSITAS is an international program for the study of biodiversity in all its aspects. It aims to promote and integrate research on biodiversity and provide syntheses for not only scientific committees but also policy makers, in response to the requirements of the Convention on Biological Diversity. DIVERSITAS was established in 1991, supported by six international scientific organizations — IUBS (International Union of Biological Sciences), SCOPE (Scientific Committee on Problems of the Environment), UNESCO (United Nations Educational, Scientific and Cultural Organization), IUMS (International Union of Microbiological Societies), ICSU (International Council for Science), and IGBP (International Geosphere-Biosphere Program) (Younés, 1996). The organization is run by a Scientific Steering Committee which includes three scientists (Drs Peter Bridgewater, Setijati Sastraprajda, and Hiroya Kawanabe) from the Western Pacific–Asia region. Detailed information can be obtained from the DIVERSITAS webpage: http://www.icsu.org/DIVERSITAS/index. html.

DIWPA (DIVERSITAS International in the Western Pacific and Asia) is a regional organization for DIVERSITAS activities, established in 1993. Article 7 of the United Nations Convention on Biodiversity requires signatory parties to "identify components of biodiversity important for conservation and sustainable use … and monitor, through sampling and other techniques, the components of biodiversity identified." It also calls for signatories to "identify processes and categories of activities which have or are likely to have significant impacts on the conservation and sustainable use of biodiversity, and monitor their effects" and to "maintain and organize … data derived from identification and monitoring activities." Many Western Pacific and Asian countries have ratified the convention and have developed national biodiversity action plans and national biodiversity strategies. In all of these documents, the need to inventory and monitor biodiversity and to understand its function in ecosystems is seen as an essential prerequisite to the future sustainable management and use of natural resources, nationally, regionally, and globally.

The mission of DIWPA is to promote sustainable management and utilization of biodiversity in the Western Pacific and Asian region through the development of regional programs of collaborative research focused on the inventorying and monitoring of biodiversity and its role in ecosystem processes. The objectives of DIWPA are (1) to promote regional research in biodiversity, (2) to develop joint research projects on biodiversity at the regional level, (3) to establish regional biodiversity networks, (4) to encourage interchange of information among scientists, (5) to conduct training courses pertinent to biodiversity, (6) to provide a scientific basis for the development of common regional policies in biodiversity, (7) to establish a network of databases, (8) to organize meetings, workshops, and symposia periodically on current regional issues and concerns of biodiversity, (9) to develop capacity-building in biodiversity assessment and analysis, and (10) to contribute to the accomplishing of the 10 Core Programme Elements of the DIVERSITAS Operational Plan (Younés, 1996). The main activities up to now are shown in Table 1.

Table 1. Activities of DIWPA 1993–99

Year	**Activities**
1993	1st DIWPA Planning meeting (Kyoto, International Symposium "Ecological Perspective of Biodiversity")
1994	2nd DIWPA Planning meeting (Paris, UNESCO "Biodiversity Forum")
1995	3rd DIWPA Planning meeting (Beijing, PSC) 1st DIWPA International Field Biology Course (Tropical Rainforest, Sarawak, Malaysia) DIWPA Workshop "Biodiversity and Dynamics of Ecosystems" (Singapore) 4th DIWPA Planning meeting (Singapore)
1996	5th DIWPA Planning meeting (Beijing) 2nd DIWPA International Field Biology Course (Lake Baikal, Russia)
1997	DIWPA Symposium "Biodiversity in Island and Marine Ecosystems" (Suva, PSC) 3rd DIWPA International Field Biology Course (Tropical Forests,Thailand) DIWPA Symposium /Workshop "Monitoring and Inventorying of Biodiversity in Western Pacific and Asia" (Taipei) 1st DIWPA Steering Committee meeting (Taipei)
1998	BICER, BDP and DIWPA Joint International Symposium on Lake Baikal (Yokohama) 4th DIWPA International Field Biology Course (Yakushima Island, Japan) DIWPA Workshop "Developing Standards for Global Monitoring on Biodiversity" (Kyoto) 2nd DIWPA Steering Committee meeting (Kyoto) Symposium on Biodiversity in Western Pacific and Asia (Taipei, PSC)
1999	DIWPA Symposium "Biodiversity and Ecosystem Process: Spatial and Trophic Considerations" (Kyoto) 3rd DIWPA Steering Committee meeting (Sydney) 5th DIWPA International Field Biology Course (Cairns, Australia)

DIWPA is focusing on integrating effort and resources towards studying the ecosystems of the Western Pacific and Asia. Unique ecosystems exist in this region, which includes the terrestrial Green Belt from Siberia to New Zealand and the marine Blue Belt along its eastern border (Inoue, 1996), as well as the Pacific East–West Island Belt connecting the tropical archipelagoes (Mueller-Dombois, 1998). The names Green Belt and Blue Belt signify the continuous forest vegetational zones and productive coastal marine ecosystems, with humid climate and high primary productivity, of the region. The Pacific East–West Island Belt has biota derived from continental lands in the Western Pacific. Although DIWPA activities are confined to the region of the Western Pacific and Asia, we welcome from outside the region researchers who are interested in and studying ecosystems in the region. DIWPA aims to create a loose federation of the networks that already exist in each country and the research projects that focus on specific subjects or topics; it does not intend to establish a rigid organization that manages everything under one umbrella. Already more than 400 scientists in 41 countries and/or economies have joined DIWPA. Detailed information can be obtained on the web page: http://ecology.kyoto-u.ac.jp/~gaku/diwpaindex.html.

IBOY and IBOY-DIWPA

DIWPA is planning IBOY-DIWPA (International Biodiversity Observation Year in 2001) as a monumental event in the first year of the 21st century. It comprises "Global Monitoring of Biodiversity" using standardized protocols at as many field stations as possible in Western Pacific–Asian region. The original idea was proposed by the late Professor Tamiji Inoue, Kyoto University, as a regional observation activity named BOY. DIVERSITAS expanded the idea into an *international* observation activity, hence IBOY. DIVERSITAS has a committee for IBOY and projects are already underway. More than 20 international projects were nominated as flagship projects. IBOY-DIWPA is one, entitled "Network study of biodiversity in ecosystems in the Green and Blue Belts in the western Pacific and Asia."

IBOY-DIWPA aims (1) to establish an international network for the preservation and identification of biodiversity information, and (2) to elucidate the effects of biodiversity on ecosystem functioning, by inventorying and monitoring biodiversity using a standardized manual in three ecosystems, forest, lake, and coastal. For the implementation of IBOY-DIWPA, we have examined (i) research sites (IBOY-DIWPA sites) and (ii) standardized methods or protocols for all research sites.

One of the important scientific objectives is to record the situation concerning biodiversity in the first year of the 21st century. The data to be obtained in 2001 may be foundational in monitoring the effects of global climate change on the biosphere in the decades and centuries ahead. We thus identify the activity of IBOY-DIWPA as the first step for a long-term biodiversity-monitoring program to continue throughout "The Century of the Environment." Another objective is to detect patterns of relationship between biodiversity and ecosystem functioning along the primary N–S and secondary E–W gradients in association with human disturbance. Parameters that describe ecosystem functioning, such as primary production, turnover rate, and so on can be compared among different ecosystems along several gradients, as a function of biodiversity.

The other aspect of IBOY-DIWPA is a kind of public campaign. The importance of biodiversity has been publicly highlighted especially since the Earth Summit in Rio de Janeiro, 1992. However, priorities for research and conservation of biodiversity have remained low, and social investments for research and education on inventorying and monitoring and for training the next generation of taxonomists are inadequate. The agricultural and forestry sectors in many countries have to deal with national and international issues related to inventorying and monitoring of biodiversity, but the organization of most of them is too out-of-date to cope with such new issues. The social aspect of DIWPA-IBOY is an activity which evoke public attention to biodiversity research, to build or reorganize infrastructures in many field stations, and to recruit the younger generation into biodiversity research.

Several international workshops and symposia have been held by DIWPA to examine the protocol and related topics (Table 1). The Protocol Manual was discussed at a meeting in Kyoto in 1998, and editing of the manual was started soon after. The first version was completed in July 1999, coinciding with discussions on the implementation of IBOY-DIWPA. In 2000, pilot studies began at several sites to test methodology and decide on the final version of the manual. Following observations obtained throughout the region in 2001, we move to the analyses of the results obtained. It may take several years to realize the goals of IBOY, since the region's biodiversity is tremendous. A regional Biodiversity Summit will be formally proposed for 2005, to include the public and policy makers, at which the analyzed results of IBOY-DIWPA will be presented. We believe the results will greatly contribute to the international debate on biodiversity and its conservation. We hope that activities like IBOY-DIWPA will be the start of long-term global monitoring of biodiversity.

Protocol of IBOY-DIWPA

Key questions relating to the IBOY-DIWPA Protocol Manual have been: (i) Which taxa or functional groups of organisms should be monitored in relation to ecosystem functions? (ii) What methods can be applied in monitoring, including biotic and abiotic factors? (iii) How can we identify the collected specimens, or how can we collaborate with systematists? And, (iv) how can we manage the datasets obtained?

We selected as the target groups: for forest ecosystems (i) vascular plants, (ii) arthropods, (ii) non-arthropod soil animals, and (iv) vertebrates; for freshwater ecostsems (i) aquatic grasses (ii) molluscs, (iii) crustaceans, and (v) pelagic vertebrates; for coastal marine ecosystems (i) macroalgae, (ii) sea grasses, (iii) molluscs, (iv) decapods, (v) echinoderms, (vi) fish, and (v) corals. The methods being applied in IBOY-DIWPA are basically those already well established, while trying to avoid biases introduced by variability in sampling skills. Thus, specific trapping methods are recommended, for example. The same types of data-logging systems and sampling procedures are necessary to provide comparable data. As for collaboration with taxonomic experts, we have to discuss more about the funds necessary for identification, capacity-building, collection deposition, and procedures for analysis. Special care should be paid to the possibility for genetic or biochemical studies. Proposed projects like "GaiaList 21" and "Species 2000" can be good candidates for collaboration.

IBOY-DIWPA includes two types of study sites: "Core Sites" and "Satellite Sites." At Core Sites, intensive studies will be carried out on prerequisite subjects, while at Satellite Sites some studies are not required. Each working group selected candidates for core and satellite sites on the basis of the following criteria: (1) infrastructure (including facilities, accommodation, existing research program(s), and human resources); (2) baseline information; (3) reasonably natural environment; (4) long-term commitment of the site; and (5) potential for monitoring. In total, 44 forest, 25 coastal, and 21 lake sites, respectively, were nominated for ecosystem monitoring (Yumoto, 1999).

International Field Biology Course

One of the main activities of DIWPA so far, is a series of training course, namely IFBC (International Field Biology Course), held since 1995 (Table 1). The aim of the series is training in individual study of field biology, through a range of activities including basic lectures, practicals, and research, in the highly diverse natural environments of the Western Pacific–Asian region. Researchers at each field station will teach biology students of different nationalities. The first course was held in the mixed dipterocarp forest of Sarawak, Malaysia, in 1995, the second at Lake Baikal, Russia, in 1996, and the third in the various tropical forests of Thailand. The fourth course was held on Yakushima Island, Japan, a World Natural Heritage site.

The fifth IFBC was held in March 2000 at a tropical rainforest area near Cairns, Queensland, Australia. This was specially designed to be a part of the IBOY-DIWPA Training Program. The Cooperative Research Centre for Tropical Rainforest Ecology and Management (Rainforest CRC) in Australia has organized a Training Course on Insects and Forests as part of the DIWPA and IBOY. Courses are led by Professor Nigel Stork (Chief Executive Officer, Rainforest CRC), Professor Roger Kitching (Griffith University), and Professor Richard Pearson (James Cook University) who provide training in the sampling, sorting, and identification of arthropods in tropical forests. Lectures cover various group of arthropods and various aspects of entomology, ecology, and forest science using experts from Australia, Japan, and elsewhere. Courses are designed to cater for the needs of postgraduates and field and laboratory technicians and, once completed, allow trainees to carry out independent sampling and research on arthropod diversity in forests. The courses also include training in the establishment of permanent forest plots and measurement of trees.

Pilot studies can be started at several sites in forest, lake, and coastal marine ecosystems. The 5th IFBC, in fact, was an intended Pilot Study. Others were held in 2000 at Lake Biwa and the Tomakomai Experimental Forest, Japan.

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The "GaiaList 21" Project: Toward the Enrichment of Baseline Knowledge of Biodiversity and its Conservation

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Abstract

A brief introduction was made of GaiaList 21, the project that aims to provide a firm basis for our understanding and conservation of the biodiversity of the earth. The GaiaList 21 committee members are going to undertake a pilot study at a cool temperate deciduous forest in Tomakomai, Hokkaido, northern Japan, in order to establish a sample management system for site surveys, which includes a data feedback system between ecologists and taxonomists.

Key Words: GaiaList 21, Comprehensive description, Management system, Biological specimens

GaiaList 21

Recognizing the importance of the existence of a diverse range of life forms on the earth and striving to preserve them should be given the highest priority among the numerous tasks confronting us today. The "GaiaList 21" project was proposed in 1995 by the Zoological Society of Japan as a fundamental and concrete project for preserving the diversity of life on the earth. The framework of the project is reproduced in Table 1. GaiaList 21 aims to describe comprehensive biological information of every species now present on the earth, and preserve their specimens, cells and genome DNA for future generations of human beings. The project will be carried out on an international basis, although Japan is expected to be the chief sponsor. Place of storage and ownership of taxonomic specimens and other biological materials will be determined based on a full understanding of all the nations and organizations concerned.

Table 1. The framework of the GaiaList 21 project.

1) Classification of all species of living beings present on the earth and comprehensive description of their biological information.
2) Storage and management of cells and extracted genome DNA in addition to individual specimens of all species described.
3) Training and education of taxonomists, molecular biologists and technicians required for these tasks.
4) Establishment of the GaiaList Center (tentative name) to be responsible for implementing these tasks.
5) Implementing this project on a global scale consisting of ten 5-years periods.
6) Japan will serve as the executor of the project and will be responsible for the majority of its financing. However, nationality will not be a factor in the hiring of researchers and technicians.

The aim of GaiaList 21 thus greatly overlaps with those of other international projects of biodiversity, such as *DIVERSITAS* that lists inventorying and classification of biodiversity as one of the five major programme elements (DIVERSITAS, 1996), and *Systematis Agenda 2000*, in which description and inventorying are major components of the first mission (Systematics Agenda 2000, 1994).

The Zoological Society of Japan organized the GaiaList 21 committee in 1996, and has made effort to realize this project in cooperation with other academic societies and organizations.

Although GaiaList 21 envisions a rather wide range of topics, here I would like to focus on taxonomic inventorying. It is because only a fraction of the world's species, perhaps accounting to no more than 10%, are known scientifically (Erwin, 1982; May, 1988, 1990; Stork, 1997). At the face of the rapid decrease of biodiversity now occurring on the earth, enhancement of taxonomic activities is evidently most urgently needed (Janzen, 1993; Janzen and Hallwachus, 1994; Systematics Agenda 2000, 1994; Wheeler, 1995; Wheeler and Cracraft, 1997). The most straightforward measure to this issue may be to expand and support taxonomists and taxonomic infrastructure (Wheeler, 1995; Wheeler and Cracraft, 1997). But we need other devices that enhance activity of individual taxonomists. Below is an attempt toward this direction.

Ecological Samples and Taxonomic Specimens

Biodiversity surveys tend to concentrate to particular regions that are ecologically important, or are expected to harbor diverse arrays of unique organisms. In surveys in such regions, which are usually done by the initiative of ecologists, a vast amount of specimens are obtained from various environments, such as forest canopy, that might not be easily accessible by taxonomists. These specimens are potential sources of unknown, or poorly known species. Furthermore, accurate identification of these specimens is a prerequisite of any further ecological analysis. Hence, cooperation between taxonomists and ecologists, the two major groups of scientists investigating biodiversity, is indispensable to make the site survey successful.

However, it is not always easy. The reason might be multifold. Here I only point out that there is salient difference between ecologists and taxonomists in the attitude toward biological specimens (Table 2).

Table 2. Some different views of ecologists and taxonomists regarding scientific specimens.

	Ecologists	Taxonomists
Main interest	Site-specific; understanding of local biota	Taxon-specific; revision on global scale
Specimens		
1) Purpose	Identification, counting, etc.	Taxonomic studies
2) Condition	Often un-sorted; many common species + some rare species; not appropriate for taxonomic purpose	Selected; prepared according to taxon-specific preparation methods
3) Weight on	Common species	Rarer species
4) Storage	Large space but temporal	Permanent

First of all, ecologists and taxonomists are interested in different aspects of biodiversity. Ecological researches are usually site-specific, and ecologists want to know the number of species and the number of individuals (or the biomass) of each species in the target area as the very basic information. They gather specimens using various devices, such as trapping, primarily for counting, weighting, etc. Ecological specimens were consequently often unsorted and composed of many common species and a few rare species. Ecologists lay weight on common species, and their samples are voluminous, requiring a large temporal space for storage. The specimens are often not appropriate for taxonomic purposes owing to their bad preserved conditions. Ecological samples might been discarded after they were sorted, counted and weighted.

On the other hand, taxonomists are taxon-specific but not site specific. They are interested in a particular group of organisms all over the world, but have little interest in the composition of whole local fauna or flora. For taxonomists, specimens are indispensable for their researches, and so the specimens must be carefully treated, selected and well prepared according to taxon-specific methods. Taxonomists usually lay weight on rarer species. Since taxonomic specimens must be kept permanently, they eventually need a very large space for permanent storage, although they need smaller space for a short run.

In short, ecological samples are often neither suitable for taxonomic practice nor are interesting (except for a small proportion of samples) to taxonomists. Hence, we need an appropriate sample management system for samples collected by ordinary ecological methods. In this system, samples are appropriately sorted before they are handed to taxonomists, and taxonomists rewards ecologists with promptly idetifying the specimens except for those poorly or unknown species. This system should include a data feed back system between taxonomists and ecologists, and should be beneficial to both fields of scientists.

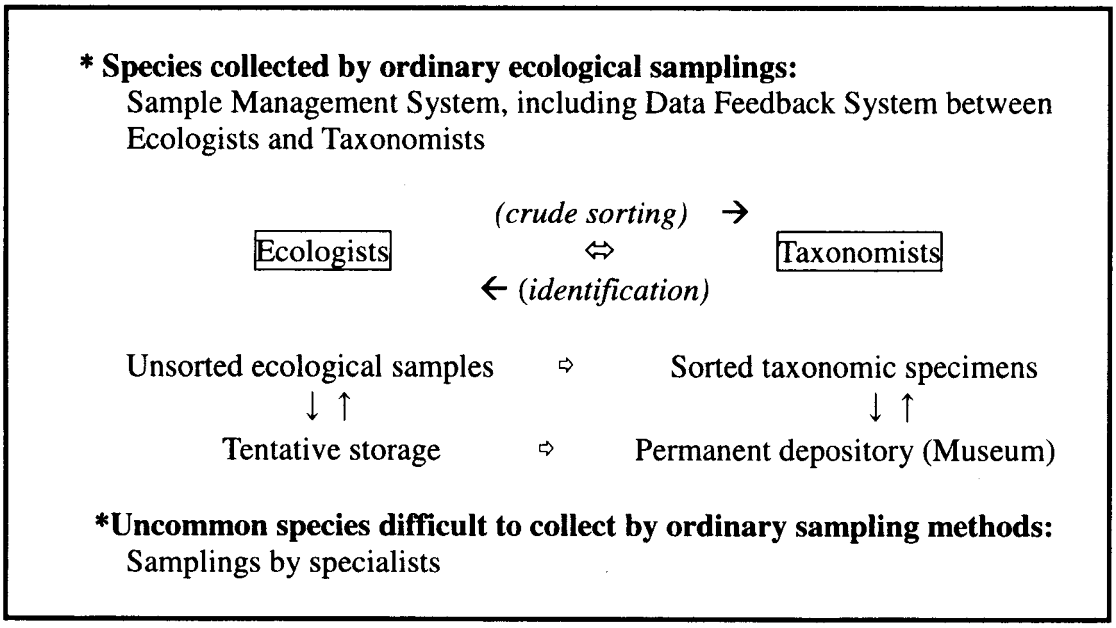

Fig. 1. Scheme of inventorying and a sample management system for site surveys.

DIWPA (International Network of Diversitas Western Pacific and Asia) is going to hold IBOY (International Biodiversity Observation Year) in 2001, and the forest ecosystem group is going to make a preliminary study at a cool temperate forest in Tomakomai, northern Japan in 1999 and 2000. They are planning to test various kinds of sampling methods there. In parallel with this pilot study, the GaiaList 21 committee members will undertake a pilot study of taxonomic inventorying, in which a sample management system as mentioned above will be tested and the cost, space and time required for these tasks will be estimated. Since ecological samplings are not sufficient to uncover total biodiversity of a given area, samplings by specialists will be also iocorporated in order to obtain many rarer species that must be overlooked by ecological samplings (Fig. 1).

Mutual understanding and cooperation between ecologists and taxonomists are indispensable for the enhancement of the studies of biodiversity.

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Zoological Record: A Bibliographic Service and Names Resource

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Abstract

Zoological Record (_ZR_) is an index to the world's zoological literature covering all aspects of animal biology. Since 1864, it has provided the international scientific community with both a current awareness service and an archival tool. Animal systematics is at the core of coverage and, to enable users to trace the history and application of names, every new or changed animal name is indexed separately. _ZR_ is regarded by some as an unofficial 'register' of animal names, a role which the ICZN proposed to formalize through provisions of its new Code. As part of _ZR_'s response to this proposal, all names used in the last 20 volumes of _ZR_ were made freely accessible to the scientific community on the Internet as the _Index to Organism Names (ION)_. While the role for _ZR_ was not formalized on this occasion, the idea of a centralized file of names received considerable interest. _ION_ reflects the zoological literature - animal names are recorded as published. It additionally includes non-animal names provided by other collaborating organizations, who see the usefulness of an 'all organism' index giving basic classification and links to further resources, for use by all biologists. As such, _ION_ represents a stage before _Species 2000_ and an alternative source of information about names. Animal name data provided by _ION_ is a small subset of that held in _TRITON_ (_Taxonomy Resource and Index To Organism Names_), which includes full _ZR_ index and citation data for all new and changed names, building a nomenclatural history for each name.

Key Words:* *Animal names, Bibliographic service, ION, TRITON, Zoological Record

Introduction

The following paper describes *Zoological Record*, a long established bibliographic service covering all aspects of animal biology, and its involvement in various new activities related to organism names. The importance of organism names to all aspects of life science research cannot be overestimated. Accurate names are essential for reliable communication of all organism related data and they should be readily available to all who need to use them. Bringing hundreds of thousands of names together through a user-friendly access mechanism is no easy task but, with the international collaboration of all interested parties, we believe that it is one which is achievable.

History

Zoological Record (http://www.york.biosis.org) is an index to the literature of zoology and the oldest bibliographic service covering the life sciences. The first volume, covering the literature of 1864, was published in 1865 and an annual volume has been published each year since. Until 1980, *Zoological Record* was published by the Zoological Society of London, but at that point the Society was unable to continue to fund compilation and entered into a joint publication agreement with BIOSIS – a not for profit organization based in Philadelphia, and publisher of *Biological Abstracts.* Under this agreement the Society retained a broad editorial interest, but production and management were transferred to BIOSIS, U.K., a wholly owned subsidiary of BIOSIS created for this purpose. Also transferred was the financial burden of producing *Zoological Record.* From its inception, *Zoological Record* has never made a profit and is now heavily subsidized by BIOSIS; the 'not for profit' status referred to above is, unfortunately, a particularly appropriate description for *Zoological Record,* which seems to be an essential tool which everyone needs but for which few are willing to pay.

The main offices of BIOSIS, U.K. are located in York, though there is also a small unit of staff at the Natural History Museum in London.

Coverage

Zoological Record reflects what has been published in the literature. We do not make judgements on the work indexed, but provide a faithful representation of the literature. This is particularly relevant in the context of animal names, and the aims of the Species 2000 project - a point to which we will return later in this paper.

All aspects of the biology of all recent and fossil animal groups – protozoan behaviour, mollusc ecology, insect evolution, mammal distribution, trilobite morphology to name but a few – are indexed in *Zoological Record,* offering users a current awareness service in animal biodiversity. Such biodiversity coverage accounts for over eighty percent of the items indexed. The remaining material is animal systematics which, while also an aspect of biodiversity, receives special attention in *Zoological Record.* Each newly published or changed name is indexed individually making *Zoological Record* not only a current awareness service, but also an archival tool providing users with a complete history of the creation and application of names. Each year some 20,000 entries for new names, and a further 8,000 entries to cover changes in the synonymy or combination of existing names are recorded.

In our attempt to achieve comprehensive coverage, about 4,500 serials and 1,200–1,500 books are scanned for relevant material for each annual volume, and these generate some 72,000 items of literature. Most of this material is obtained from the holdings of various UK libraries (principally those of the British Library Document Supply Centre and the libraries of the Natural History Museum in London), though some is also received as review copies directly from publishers. The support of all these resources is gratefully acknowledged.

Coverage is international, not restricted by language or country of publication, and the type of material indexed varies widely, including primary scientific literature, local natural history publications, monographs, electronic publications, etc.; as long as a publication is relevant, publicly available and can be located in one of our source libraries, it will be indexed. Any omissions are the result of lack of accessibility or human error, not of any kind of exclusion policy, and users are encouraged to alert us to any material that has not been indexed.

Names Resources

During the past 135 years of indexing *Zoological Record,* extensive files of animal names have been compiled. Until relatively recently these have been used for internal production purposes only, but with the advent of the Internet it has been possible to make the files more widely available.

We are also building on what some regard as our role as an unofficial register of names by working with the International Commission on Zoological Nomenclature (ICZN). The Commission sought to formalise this unofficial role by proposing a change to the International Code of Zoological Nomenclature, which required that names must be indexed in *Zoological*

Record before they could be regarded as properly published. This proposal, for 'international notification of new names' received a mixed reception and in the end was not adopted, though the Commission has shown continued interest in the idea of a centralized list of names. However, our response to the initial proposal – provision of an access tool called the *Index to Organism Names* – continues to be available, and is one of several name tools on the *Zoological Record* web site.

Index to Organism Names (ION)

ION (http://www.york.biosis.org/triton/nameind.htm) was created partly in response to ICZN's suggestion for 'international notification' of names, but also to try and make names data in general more widely accessible. The ION database provides access to all of the names indexed in *Zoological Record* since 1978, over one million names, and over 400,000 non-animal names from various collaborators. That part of CABI previously known as IMI, and the USDA Systematic Botany and Mycology Laboratory have provided fungal names; the Missouri Botanic Garden has provided moss names; Professor Michael Guiry of the Martin Ryan Marine Research Institute Galway has provided marine algae, and BIOSIS has provided its own Register of Bacterial Nomenclature.

ION is freely available to anyone who wants to find out more about any, recent or fossil, organism name. It can be used, for example, to identify the taxonomic group to which an organism belongs, or to check whether or not a proposed new name has already been used. It also allows users to view all occurrences of a name in *Zoological Record* over the last 20 years and look at how that name has been applied in the literature. When a homonymous name is entered, the system returns all occurrences of the name and allows the user to view the different placements and further data. Since its introduction the site has proved very popular – there are currently 400 searches from some 70 unique hosts each day. For animal names, ION returns only a subset of the data held in the TRITON database: the Taxonomic Resource and Index to Taxonomic Organism Names.

Taxonomic Resource and Index to Taxonomic Organism Names (TRITON)

TRITON (http://www.york.biosis.org/triton/triton.htm) is a mechanism, still under development, for making organism name-related data available on the Internet. Currently there is only restricted access for demonstration purposes, though ultimately it could become a full subscription-based service. TRITON returns all the data provided by ION, with the addition of complete index and bibliographic data for all new and changed (new synonyms, new combinations etc.) animal names, indexed in *Zoological Record* since 1978.

Nomenclator Zoologicus

Published by the Zoological Society of London (ZSL), *Nomenclator Zoologicus* is a record of every new generic and subgeneric name, with its full bibliographic citation, described since Linnaeus' *Systemae Naturae* in 1758. Nine separate printed volumes cover the period 1758—1994, providing an unrivalled source of nomenclatural data for generic names. However, nine volumes, each with its own supplement and addenda, do not provide a convenient means of searching the data and there have been many requests for an electronic version. Some progress has been made towards this; all nine volumes have been electronically scanned by *Zoological Record* staff, and the approximately 358,000 names, and associated bibliographic data contained in them, have been extracted. While extraction is complete, the files require further attention before they can be made publicly available. Nevertheless, the possibility of offering them through a web search facility is under discussion with the ZSL.

Zoological Record and Species 2000

In relation to the Species 2000 project, it is important to note that neither TRITON nor ION provide access to 'valid' organism names. As mentioned earlier, *Zoological Record* does not make judgements on what is published but records names as used in the literature, e.g. if it is clear that a new name does not fulfil all the requirements of the ICZN, this will be indicated, but the name will still be indexed as new. As a result of this policy there are no preferred or approved names in *Zoological Record;* taxonomists are left to draw their own conclusions about the validity or otherwise of the work indexed. The only control applied by *Zoological Record* is to place names in a standard classification hierarchy to allow consistent retrieval. Therefore *Zoological Record* data complements the work of Species 2000 and provides an additional source of data to which the approved names in Species 2000 could be linked.

Conclusion

Names are crucial to all life science research and communication. Whether in bibliographic databases such as *Zoological Record*, in international biodiversity discussions, in genetic engineering programmes or in legal documents for the protection of endangered species, accurate names are essential for correctly identifying organisms. Much has been done by individuals and organizations, but it is only by collaboration in such projects as Species 2000 that it is possible to link all these disparate sources and provide seamless, global, access to names and related data wherever it resides.

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Flora of Japan Database for Integrated Information of Japanese Native Vascular Plants

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Abstract

Flora of Japan Database is a database of vascular plants native to Japan, consisting of about 5,500 species. This database is now constructing by the Japan Society of Plant Taxonomist based on new series of books entitled 'Flora of Japan' published by the Kodansha. This database contains not only fundamental information on each species, including synonymic lists, description, distribution and literature lists, but also some biological information such as chromosome numbers and chemical substances. Also we are now adding photographs of the species included to show their natural habitat. This database is opened to everyone and can be accessed using WWW browsers via Internet. We now intend to adopt the data structure of this database to Global checklist of IOPI, and also to integrate information of the other database by adding pointers to such as type specimens (some Japanese herbaria databases) or DNA sequence data (DDBJ/EMBLE/Genbank DNA database).

Key Words: Flora Database, Flora of Japan, vascular plants, Species Plantarum Project

Introduction

The Japanese Islands have climates that vary from tropical to cold temperate, lying between 25 and 46 degree north latitude. Steep mountains present a complicate topography, which promotes speciation through geographical isolation. Over 5500 species of ferns and seed plants have been identified within the narrow confined of the Islands. In recent survey, we have 5629 native species of vascular plants in Japan, including 10 % of Pteridophyte and 1% of Gymnosperms. About 30% of them are endemic to Japan.

Taxonomic research of Japanese plants is started from Thunberg. Thunberg made extensive plant collections and observations, which formed the basis for this seminal work, *Flora Japonica*. Its publication in 1784 was the beginning of true scientific botanical research in our country. A century later, Franchet and Savatier, published *Enumeratio plantarum in Japonia sponte crescentium*, 1873-1879. It covered 2,743 species of vascular plants, and established the foundation for Japanese plant taxonomic research. From the end of 19th, several prominent Japanese made detailed observations on plant habitats and more clearly delimited both the genera and species in the flora. These efforts made it possible to better understanding which taxa were present in Japan and to apply the correct names. Studies of the floras of neighboring countries were also made. Since the 60's, a great deal of information about Southeast Asian and Himalayan plants has been gathered through oversea field research and it has helped clarify the relationships of plant between Japan and adjacent regions.

From 60's, a number of new editions of descriptive and illustrative floras have been published in Japan. However, all of these new floras, have been written in Japanese. So, internationally, English version of Jisaburo Ohwi's *Flora of Japan*, published in 1965, has been regarded as the standard flora of Japan. But with a few exceptions, Ohwi treated only native species found in Japan proper and omitted most naturalized species and taxa from the Ryukyu and Bonin Islands from his flora. In the 30 years since the publication of Ohwi's flora, studies of Japanese plants have progressed noticeably through comparisons with related taxa from outside Japan and through detailed analysis using a variety of new techniques. It has now become necessary to revise the treatments in numerous families in Ohwi's Flora as well as to extend the coverage of the flora to include plants from Ryukyu and Ogasawara Islands.

Even though biodiversity is now recognized internationally as the basis for the richness of potential gene resources, the diversity of life is now faced with an unprecedented crisis that is regarded as one of the most serious global problems. In Japan, a number of plant species is now threatened their survival. Japan Society of Plant Taxonomists has made a committee for survey of these threatened plants under Prof. Yahara. And last year they compiled all surveyed data and 1428 taxa were listed as threatened vascular plants.

Recently the *Species Plantarum Project* has been organized to produce a database for a worldwide flora. And we must have a contribution of information about Asian plants. In spite of well-studied vascular plant flora in Japan, we had no organization to compile results of new researches. On these background, we started to compile a new floral of Japan in 1990. These efforts are largely in response to the circumstance mentioned above and seek to provide inventories of plants as soon as possible. Under the editorial of Prof. Iwatsuki and other persons, this new 'Flora of Japan' is made as a collaborative effort of many plant systematists. Besides of book version of Flora of Japan, we feel a necessity of digitized version of Flora of Japan for preparing toward the IOPI's *Species Plantarum Project.*

Flora of Japan Database

Upon the above mentioned background, we decided to develop a database of Vascular Plants of Japan. In 1996, special committee for plant database had been established in Japan Society of Plant Taxonomist. The purpose of this committee is making database of Japanese vascular plants and out their information to the world. As mentioned, we were compiling a new flora of Japan, and at first we started to make a plant database based on this new flora, and then modifying its data structure to adopt to international standard such as Global Plant Check List of IOPI. Fortunately, we could get grants from Expo 90 Foundation and Monbusho, we could start to this project.

Fundamentally, each record has same items to the book version. It includes scientific names, synonyms and their original literatures, description, distribution and habitat information, chromosome number, reference to illustrations and note (Table 1).

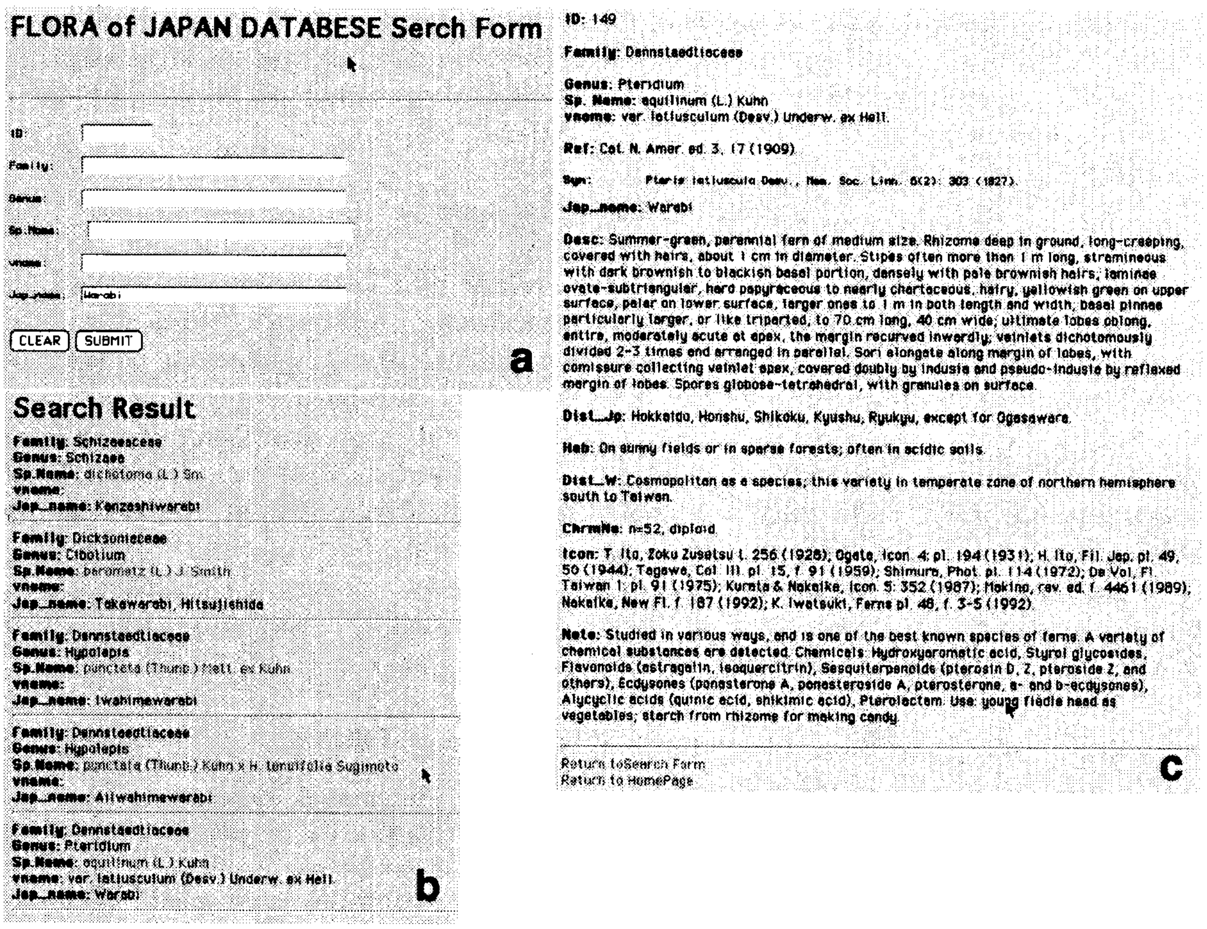
Table 1. Data structure of Flora of Japan Database

ID:	Record ID Number	ChromNo:	Chromosome Number
Status:	Current status of name	Dist_Jp:	Distribution in Japan
Family:	Family name	Hab:	Habitat Description
Genus:	Genus name	Dist_W:	Distribution in the world
Sp_Name:	Species name	Icon:	Figure References
Vname:	Variety or subspecies name	Note:	Note
Ref:	Original literature		
Syn:	Synonyms	PICT:	Tag for Photographs
Jap_name:	Japanese name	DNA:	Tag for DNA sequence data
Desc:	Description		

We add record whose name is not used currently, which corresponding to synonyms of former records. Although the references, both for literature or illustration are now including in the fields all together, they will be move to separate files and connect by relation to each species record.

Also we added some fields for the purpose of control or linking to other databases. Now, each species record has two fields to connect to other databases named PICT and DNA. The former is referring to a photograph Database and the latter contains accession no. to DNA sequence database. We are planning to add further field for connecting other database, which I will mention later.

At this time we have inputted all species data of Pteridophytes, Gymnosperms and Sympetalae of Dicotyledons corresponding to Volume I and Volume IIIa and b. For convenience to use we made an interface for accessing from Internet (http://lycoris.s.chiba-u.ac.jp/jspt/FJ/FJ.html). And we already opened a part of Pteridophytes of this database to a public and anyone can access this database via Internet using standard Web browsers. Figure 1 shows a homepage of Flora of Japan Database from which we can search Japanese plant record.



ID:
Family:
Genus:
Sp.Name:
vname:
Jap_name: Warabi

Search Result

Family: Schizaeacese
Genus: Schizaea
Sp.Name: dichotoma (L.) Sm.
vname:
Jap_name: Kanzashiwarabi

Family: Dicksoniaceae
Genus: Cibotium
Sp.Name: barometz (L.) J. Smith
vname:
Jap_name: Takewarabi, Hitsujishida

Family: Dennstaedtiaceae
Genus: Hypolepis
Sp.Name: punctata (Thunb.) Mett. ex Kuhn
vname:
Jap_name: Iwahimewarabi

Family: Dennstaedtiaceae
Genus: Hypolepis
Sp.Name: punctata (Thunb.) Kuhn x H. tenuifolia Sugimoto
vname:
Jap_name: Aiiwahimewarabi

Family: Dennstaedtiaceae
Genus: Pteridium
Sp.Name: aquilinum (L.) Kuhn
vname: var. latiusculum (Desv.) Underw. ex Hell.
Jap_name: Warabi

ID: 149

Family: Dennstaedtiaceae

Genus: Pteridium
Sp. Name: aquilinum (L.) Kuhn
vname: var. latiusculum (Desv.) Underw. ex Hell.

Ref: Cat. N. Amer. ed. 3. 17 (1909)

Syn: Pteris latiuscula Desv., Mem. Soc. Linn. 6(2): 303 (1827).

Jap_name: Warabi

Desc: Summer-green, perennial fern of medium size. Rhizome deep in ground, long-creeping, covered with hairs, about 1 cm in diameter. Stipes often more than 1 m long, stramineous with dark brownish to blackish basal portion, densely with pale brownish hairs; laminae ovate-subtriangular, hard papyraceous to nearly chartaceous, hairy, yellowish green on upper surface, paler on lower surface, larger ones to 1 m in both length and width, basal pinnae particularly larger, or like triparted, to 70 cm long, 40 cm wide; ultimate lobes oblong, entire, moderately acute at apex, the margin recurved inwardly; veinlets dichotomously divided 2-3 times and arranged in parallel. Sori elongate along margin of lobes, with comissure collecting veinlet apex, covered doubly by indusia and pseudo-indusia by reflexed margin of lobes. Spores globose-tetrahedral, with granules on surface.

Dist_Jp: Hokkaido, Honshu, Shikoku, Kyushu, Ryukyu, except for Ogasawara.

Hab: On sunny fields or in sparse forests; often in acidic soils.

Dist_W: Cosmopolitan as a species; this variety in temperate zone of northern hemisphere south to Taiwan.

ChrmNo: n=52, diploid

Icon: T. Ito, Zoku Zusetsu I. 256 (1928); Ogata, Icon. 4: pl. 194 (1931); H. Ito, Fil. Jap. pl. 49, 50 (1944); Tagawa, Col. Ill. pl. 15, f. 91 (1959); Shimura, Phot. pl. 114 (1972); De Vol, Fl. Taiwan 1: pl. 91 (1975); Kurata & Nakaike, Icon. 5: 352 (1987); Makino, rev. ed. f. 4461 (1989); Nakaike, New Fl. f. 187 (1992); K. Iwatsuki, Ferns pl. 48, f. 3-5 (1992).

Note: Studied in various ways, and is one of the best known species of ferns. A variety of chemical substances are detected. Chemicals: Hydroxyaromatic acid, Styrol glycosides, Flavonoids (astragalin, isoquercitrin), Sesquiterpenoids (pterosin D, Z, pteroside Z, and others), Ecdysones (ponasterone A, ponasteroside A, pterosterone, a- and b-ecdysones), Alycyclic acids (quinic acid, shikimic acid), Pterolactam. Use: young fiddle head as vegetables; starch from rhizome for making candy.

Return toSearch Form
Return to HomePage

Fig. 1. Search sample (*Pteridium aqualinum*). a, Search Form; b, Search Result; c, Record of *Pteridium aqualinum*

At present time, we can search by family, genus and species name, as well as by Japanese name. Figure 1 shows an example of search *Pteridium aqualinum,* whose Japanese name is Warabi, a common fern in Japan. Two records were shown as a result of this search, the above one is *Pteridium aqualinum* and the lower one is var. *latiusculum.* By cricking the lower record, we can access and see all field of this record. Also we can access information of other database with in this form. Firstly, to crick PICT button causes showing the photograph of this species. This will complement the absence of figure or photograph in the book version of flora. Also it will be helpful to understand a habit or habitat of plants. To crick DNA button, the list of accession no for DNA sequence database will appear. At the present time these accession numbers have no direct connection to each record of DDBJ/EMBL/Genebank, however, technically we can refer directly to them. I think this DNA link is important in two points. Firstly, by the recent development of molecular technique, we can easily access DNA sequence data and now, molecular systematic methodology become very common in our field. And often we must change plant scientific name by the result of molecular systematic studies. Secondly, we believe that DNA sequences could become important for identification of plant species. At present time, *rbcL* genes were sequenced more than three thousand species, and this kinds of data are accumulated rapidly. And also we can know the DNA sequence in a day. And thus, we think they become to identification key in near feature. We are planning to develop this kind of identification system, but unfortunately not yet granted.

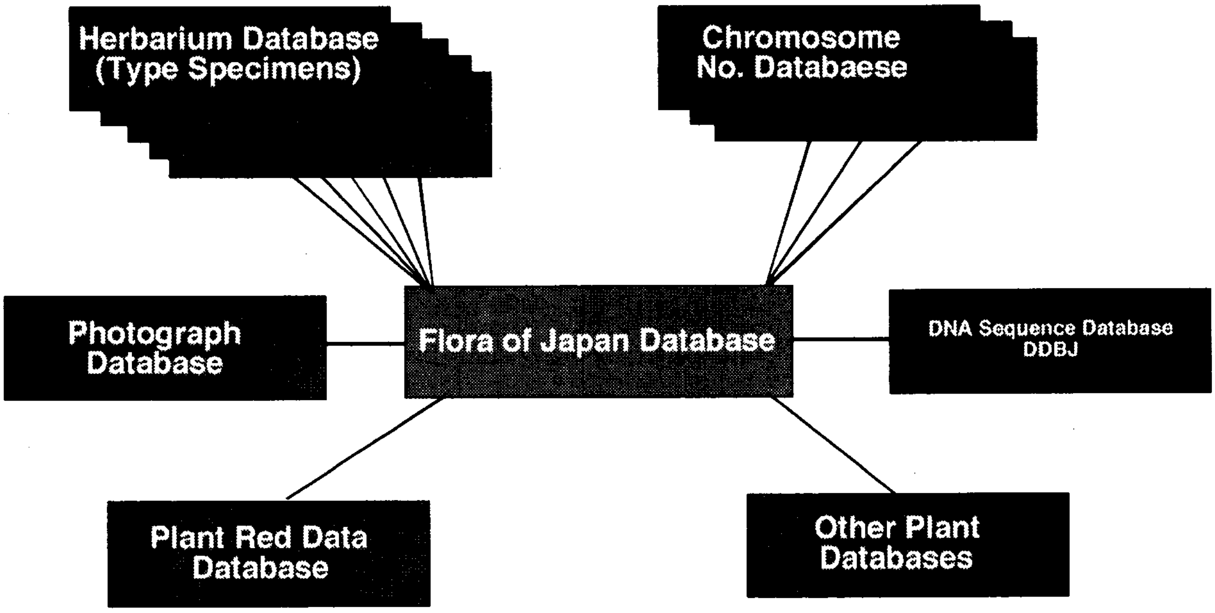


Fig. 2. Links of Flora of Japan Database to other Plant Information Database.

Feature Developments

At present, this database has link to two additional database. But we would like to make links to all possible information of Japanese plants, and hope to develop it as a core and gateway database for accessing plant information of Japan. At this viewpoint, we now planning to extent record structure to link following database (Fig. 2). For a taxonomic study, it is very useful to access type specimens of each name. Now, some herbaria made their type specimens databases. In Japan, type specimen databases are established or planning in University of Tokyo, Kyoto University and Tokyo Metropolitan University. I asked the managers of this database to link and directly use their picture data from our database, and in near feature this photograph will become available from our database. Also we want to link type specimen of Japanese plant in other countries. Secondly, we are planning to link chromosome databases. Now, chromosome database of Asian fern becomes available via Internet by Japan Fern Society. Dr. Takamiya of Kumamoto University and I agreed to refer each other and these data also will be available in near feature. Moreover, we have compiled and continue to collect chromosome data of Japanese Asteraceae, and we also take these data in the database.

Committee of Threatened Plant of our society is planning to make a database of Threatened Plant in Japan. Off course detailed information of present precise distribution data that should not be opened to public, but it still contain useful information.

Now, we have many resources of plant information and many databases are made based on them. And development of computer network made it possible to link these databases efficiently, and to use as a virtual huge database. We would like to link our database to other plant information databases and to be able to refer each other.

Acknowledgements

We would like to express our thanks to Expo 90 Foundation and Monbusho for their financial supports for our project.

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From Linking to Integration of Biological Databases

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Abstract

Since late Dr. Skerman compiled and published in 1966 the first edition of the World Directory of Collections of Cultures of Microorganisms, the developement of databases in culture collections and the linkage and integration of the distributed databases have been a key issue for the establishment a comprehensive network of Microbial Resource Centers (MRCs) . WFCC-MIRCEN World Data Centre for Microorganisms (WDCM) has developed databases on MRCs and their holdings. WDCM has also created tools for data retrieval and data analysis for the study of microbiology. We introduce here the recent activities of WDCM, especially the software that WDCM developed based on the Common Object Request Broker Architecture (CORBA).

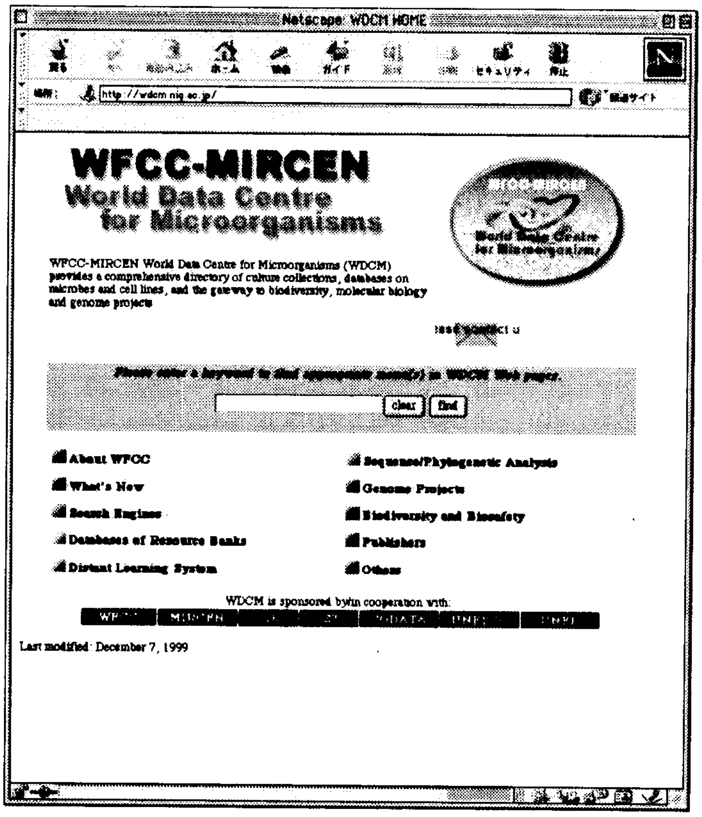
Key Words: culture collections, microorganisms, database, interoperability, distributed system, INTERNET, CORBA, JAVA

Introduction

WFCC-MIRCEN World Data Center for Microorganisms (WDCM) published the fifth edition of the World Directory in 1999. The World Directory includes 495 culture collections from 60 countries. These collections are the fundamental resources for the research and development in the era of biodiversity and post-genomics. Culture collections have provided scientific communities and bioindustries with data, information and knowledge on microbes for many years. In the age of the Internet, culture collections are required to provide their intellectual resources in the digital form by improving their informatics literacy. We also need the network of culture collections that are distributed in groups of microbes, research subjects and locations. WDCM has contributed to improve the network of culture collections and their users by publication of the World Directory and databases.

The need of networking culture collections was recognized by an UNESCO meeting in 1966, followed by the first International Congress for Culture Collections (ICCC-1) in Tokyo in 1968. The late Professor V. B. D. Skerman of the University of Queensland (Australia) published the first edition of the World Directory recognizing that there had been no information on the status of culture collections. After his retirement, the center was transferred to the Institute of Physical and Chemical Research (RIKEN) in Japan based on the evaluation of proposals from several institutions in the world.

WDCM at RIKEN introduced the International Packet Switching System (IPSS) to provide the information on culture collections on-line and improved the system in 1994 by implementing a World Wide Web (Web) server. In 1996, WDCM created Agent for Hunting Microbial Information on the Internet (AHMII) for searching multiple databases distributed in the Internet. WDCM was moved to the National Institute of Genetics (NIG) where DNA Data Bank of Japan (DDBJ) is also located. The HomePage of WDCM at NIG is shown in Fig.1.



Netscape: WDCM HOME

http://wdcm.nig.ac.jp/

WFCC-MIRCEN
World Data Centre
for Microorganisms

WFCC-MIRCEN World Data Centre for Microorganisms (WDCM) provides a comprehensive directory of culture collections, databases on microbes and cell lines, and the gateway to biodiversity, molecular biology and genome projects

Please enter a keyword to find appropriate menu(s) in WDCM Web pages.

- About WFCC
- What's New
- Search Engines
- Databases of Resource Banks
- Distant Learning System
- Sequence/Phylogenetic Analysis
- Genome Projects
- Biodiversity and Biosafety
- Publishers
- Others

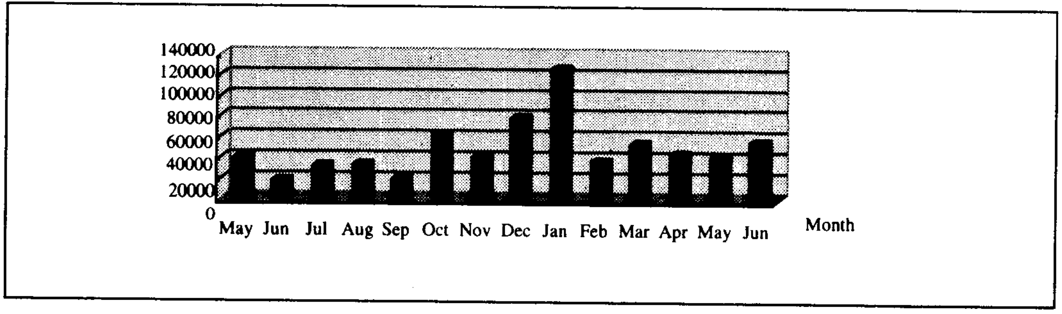
WDCM is sponsored by/in cooperation with:

Last modified: December 7, 1999

Fig.1. WDCM Home Page

The URL address is http://wdcm.nig.ac.jp/ and the statistics of the access is given in Fig. 2.

1) Monthly number of requests



2) Requests by domains on INTERNET

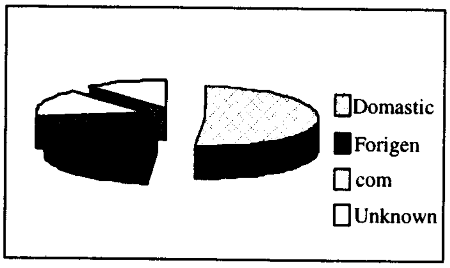


Fig. 2. Statistics of the Access to the WDCM Web Server

The current WDCM WWW pages provide original databases such as CCINFO (the World Directory) and STRAINS (a databases of microbial strains and cell lines) and links to distributed databases. Based on the experience from the development of AHMII, we aim at the development of an information system that makes it possible for novice users to integrate contents from multiple distributed databases and further to analyze the data.

Methods

Hardware

The WDCM Web server is implemented on DELL personal computer with 4 CPUs of 450Mhz. The operating system is Linux. The microbial database and application programs for search, data analysis user interface are developed on DELL Dimension PC with 450 Mhz × 1CPU model and DEC DIGITAL PC with 300Mhz × 1CPU, respectively.

Software

We apply the Common Object Request Broker Architecture (CORBA) to our system. The object request broker is a set of libraries and programs, which make distributed databases and application programs interoperable. If the Interface Definition Language (IDL on the Fig. 3) as the meta-data is defined for each database, we are able to develop a CORBA interface program with which any kind of servers and clients can communicate with each other. In CORBA environment, users can carry out detailed search to squeeze arbitrary subset of the database with no knowledge on the schema of member databases. They can also implement results of searching the distributed and heterogeneous databases into their own local database. We selected JDBC and ORBacus to introduce CORBA environment and ObjectSotre for the database management system.

All application programs reported in this paper were written by JAVA language that is a language of "Write Once, Run Anywhere". Therefore, each application as it is will run on almost all operation system such as WINDOWS, Mac-OS, UNIX and Linux.

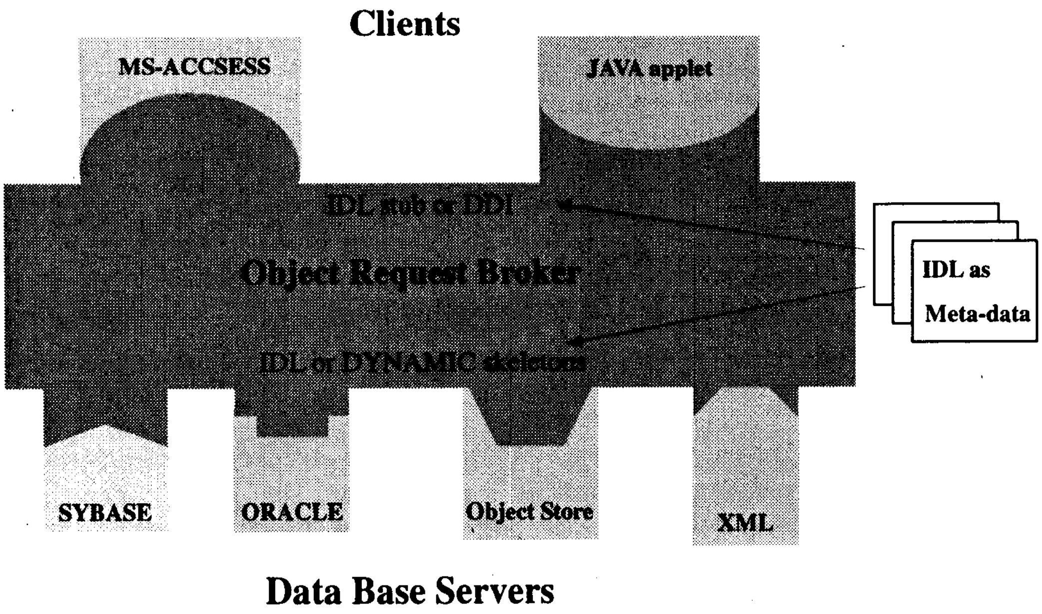


Fig.3. Basic Idea of CORBA

Results and Discussion

Agent for Hunting Microbial Information on INTERNET (AHMII)

WDCM developed a "one-stop" query system on the Internet to link databases of culture collections, research institutes and a DNA sequence data bank that are distributed in Japan, EC and US. A user could simultaneously search some or all of the sites that are set beforehand by WDCM. Through graphical user interfaces, he/she can type in a scientific name as a keyword, for example "*Lactobacillus plantarum*", to triger the search. Then AHMII visits the selected sites with the scientific name to fetch the results from them. AHMII will display the results on the first come first served base in a HTML file format (Fig.4). It is feasible for AHMII to allow free terms for the search.

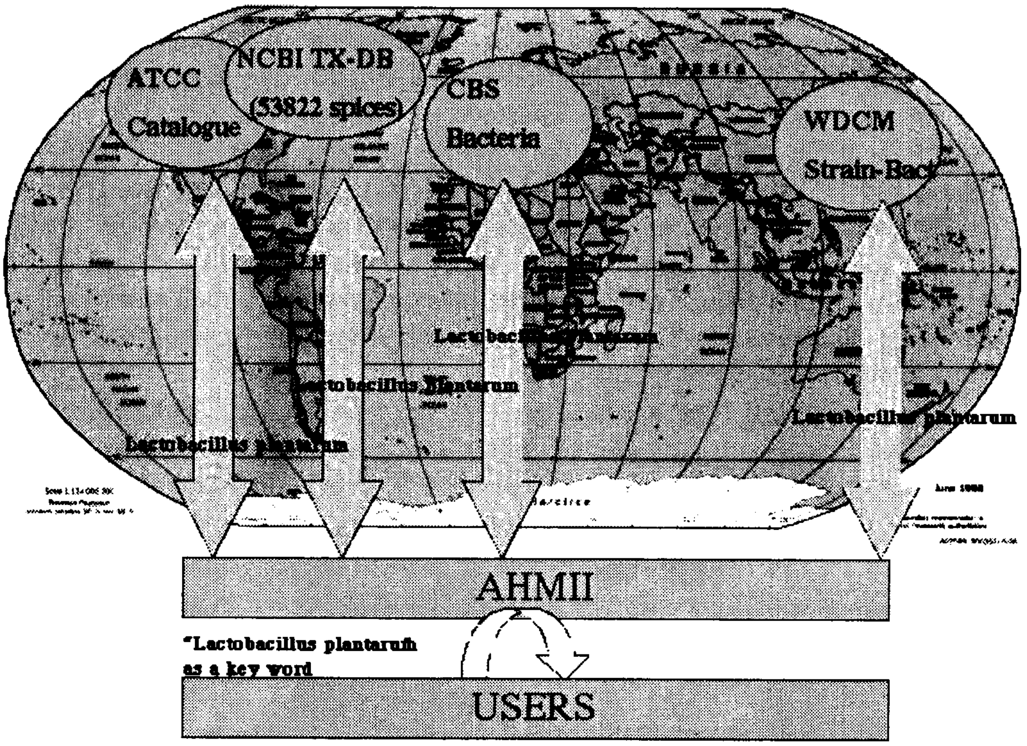
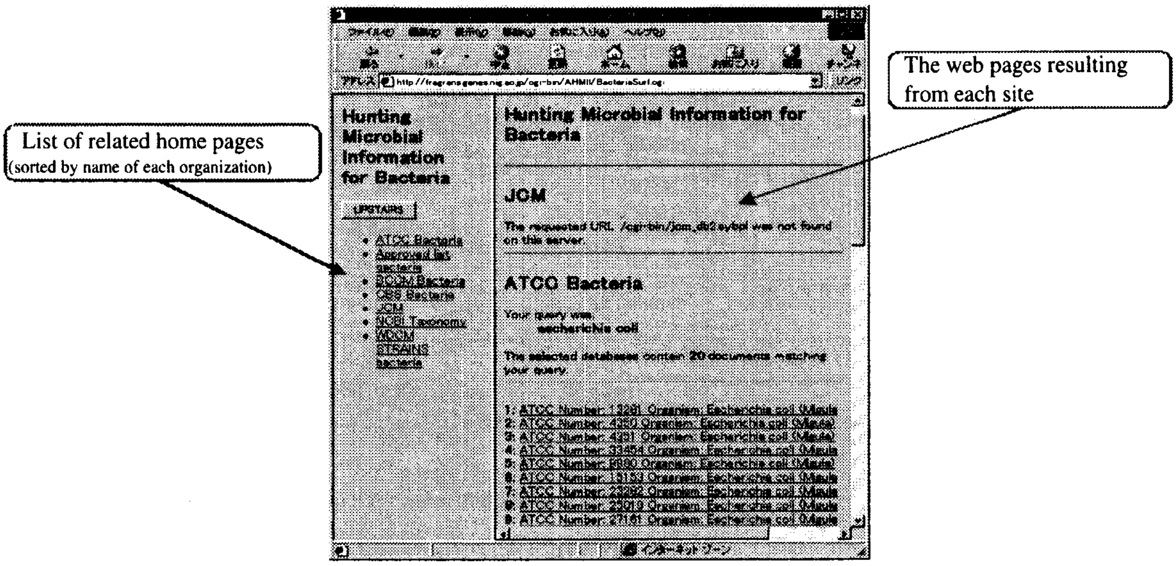


Fig. 4. Overview of AHMII

The first version of AHMII was written by Perl language and the socket function library was used to establish the connection to the sites in a sequence. That is the connection is not made in parallel. Recently, we released the second version of AHMII. Thanks to the thread function of JAVA language, the new version visits the sites in parallel. This parallel execution reduced the retrieval time remarkably. The sample of AHMII is shown in Fig. 5.



Hunting Microbial Information for Bacteria

- ATCC Bacteria
- Approved list bacteria
- BCCM Bacteria
- CBS Bacteria
- JCM
- NCBI Taxonomy
- WDCM STRAINS bacteria

Hunting Microbial Information for Bacteria

JCM

The requested URL /cgi-bin/jcm_db2sybpl was not found on this server.

ATCC Bacteria

Your query was
escherichia coli

The selected databases contain **20** documents matching your query.

1: ATCC Number: 13281 Organism: Escherichia coli (Migula
2: ATCC Number: 4350 Organism: Escherichia coli (Migula)
3: ATCC Number: 4351 Organism: Escherichia coli (Migula)
4: ATCC Number: 33454 Organism: Escherichia coli (Migula
5: ATCC Number: 8890 Organism: Escherichia coli (Migula)
6: ATCC Number: 15153 Organism: Escherichia coli (Migula
7: ATCC Number: 23282 Organism: Escherichia coli (Migula
8: ATCC Number: 25919 Organism: Escherichia coli (Migula
9: ATCC Number: 27161 Organism: Escherichia coli (Migula

List of related home pages
(sorted by name of each organization)

The web pages resulting from each site

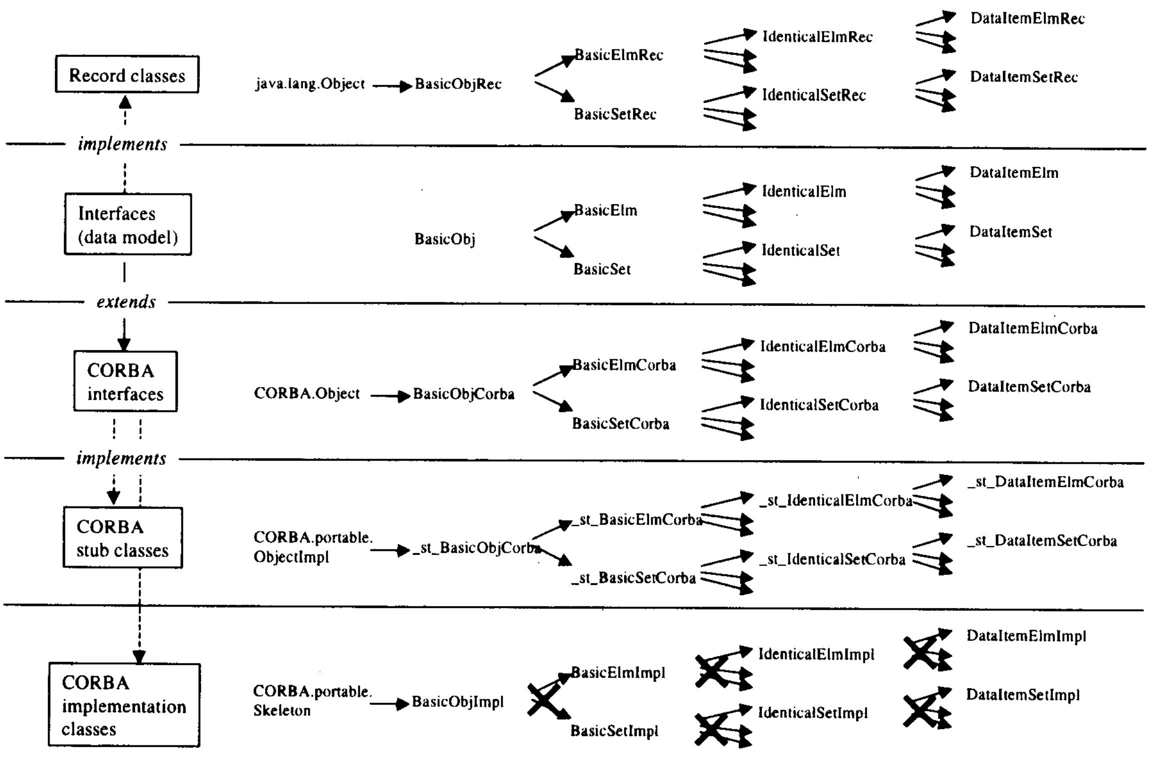
Fig. 5. User Interface Window of AHMII

Information Workbench for the analysis of microbes

AHMII provide links to relevant web pages and database entries by a single query. The user need not repeat the query one site by one site. However, AHMII is not capable of the integrating data from distributed databases. We need a system more sophisticated than AHMII for retrieving arbitrary subsets of the distributed databases to integrate the contents into a private local database for the analysis. Therefore, we designed the Information Workbench that has the following three features:

1. To be easy to modify the database schema
    - To cope with addition of new fields for tests and the update of scientific names
    - To develop a modular system
2. To support the classification and the identification of strains in the database
    - To be easy to compare results derived by various analysis methods
    - To suggest the user of the supplemental information to improve the classification and identification
3. To set link to other biological databases on the Internet
    - To construct distributed environment
    - To be platform (machine) independence

We rely on the object oriented technology to realize above functions. We defined objects and classes and designed a system of three layers. First we designed classes for the establishment of the data model. The classes have a hierarchical structure as shown in Fig, 6. The classes are then extended to two directions: one is a set of record classes, which are in charge of data accessing and retrieving from the database; another is a set of CORBA interfaces.



(every each class extends CORBA.portable.Skeleton directly)

Fig. 6. Inheritance Hierarchy of Classes

The system has the three layers of database layer, middle layer and client layer. At the database layer, we implemented database server by use of object oriented database management system. The middle layer is introduced for the adaptability to the distributed environment of resources such as databases, modules for analysis, clients and so on.

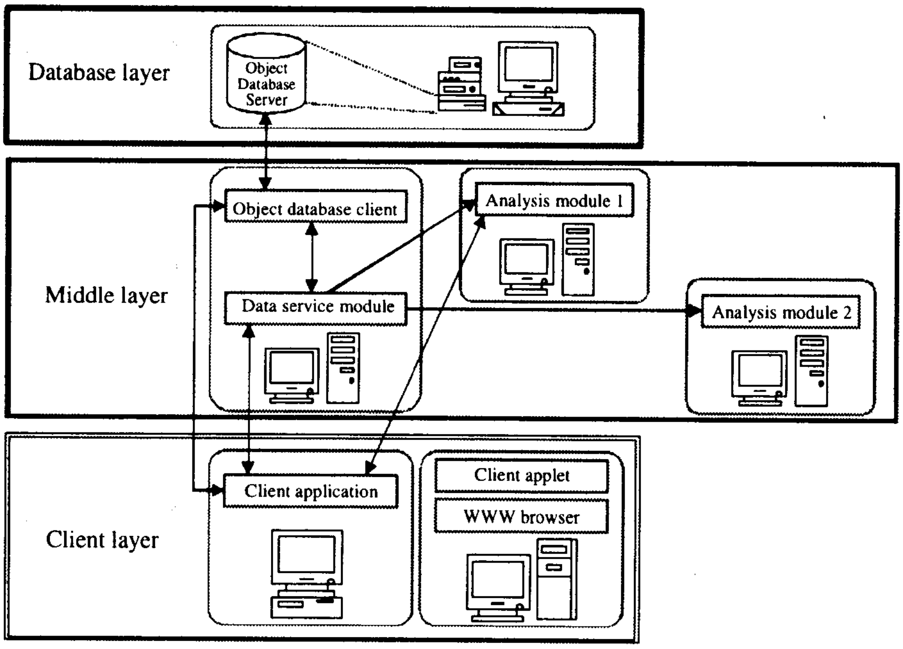


Fig. 7. Overview of System Configuration

In the case the server-client system (2-layer system), programs in the middle layer in the 3-layer model should be implemented in either the server site or the client site. In the 3-layer model, we can use not only resources fixed in the server or client but also those installed in other machines on the network. Thus, the 3-layer model is more flexible than the 2-layer model. At client layer, we develop two types of client programs by JAVA. One is a Java application and another is Java applet. As a prototype, we loaded s1,200 strains of yeast with biochemical tests and 18srRNA sequence data.

The user interface programs for the maintenance and update of the database are shown in figure 8. We also developed the application programs to support the identification or the classification of a selected set of strain data including drawing dendrogram by cluster analysis methods, three-dimensional plot of the strain based on numerical analysis-III and phylogenetic analysis based on DNA sequence data (Fig.9). These application programs are composed of modules to be integrated when necessary. Therefore, we can use each program as not only the part of system but also an independent application program. The application programs have CORBA interface, so that the information workbench can be customized to re-use the set of data retrieved from other servers on INTERNET.

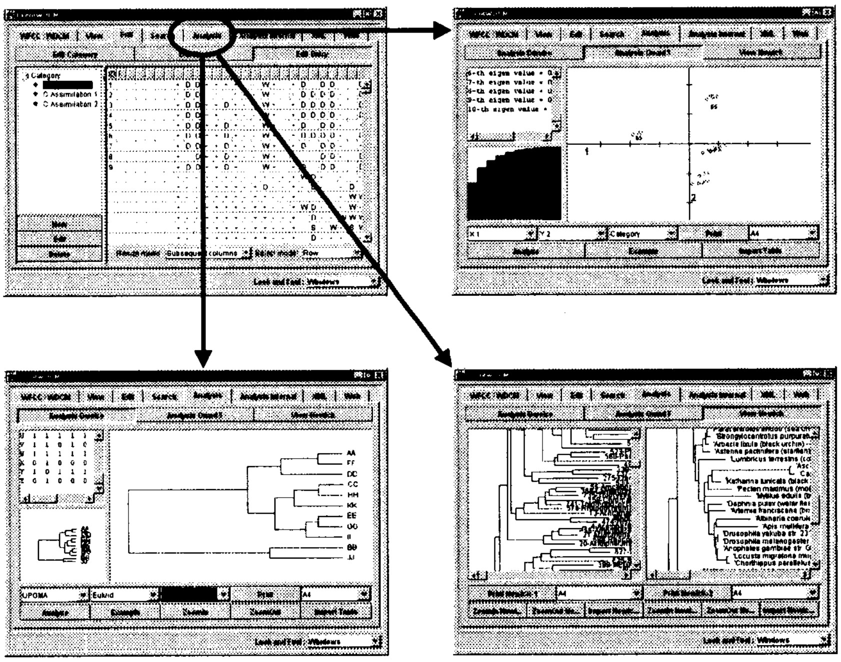


Fig. 8. User Interfaces to the Strain Database

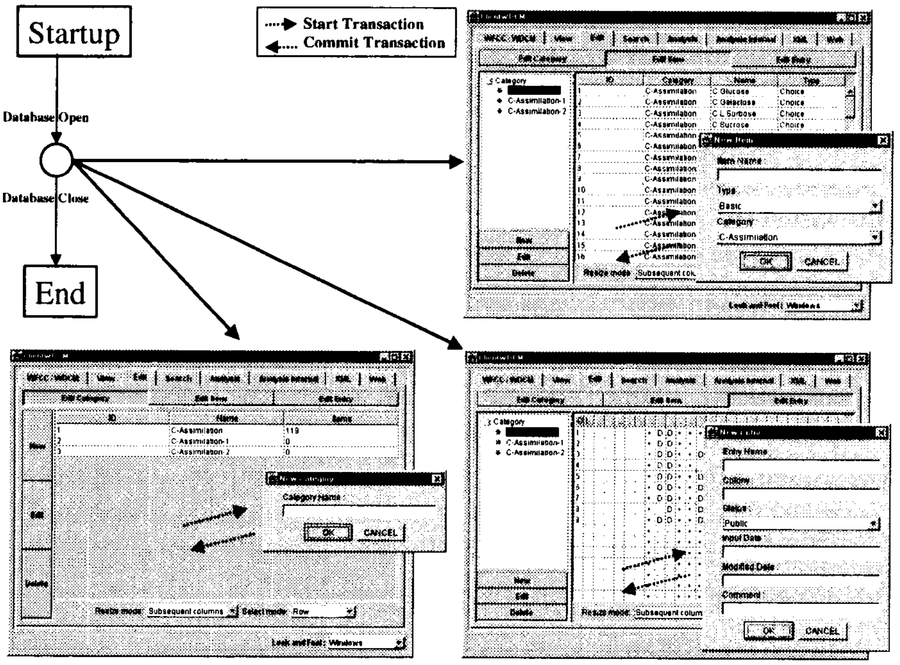


Fig. 9. Application Programs for the Support of the Identification and the Classification

Conclusion

In this report, we introduced the activities of WDCM and the application programs that will support the creation of networking and enhancement of culture collections that will be a new age Microbial Resource Centers in the 21st century.

For reaching an integrated view on microbes we need to:

- strengthen Microbial Resource Centers (MRCs) that create and maintain microbial resources and data
- promote the digitization of data in MRCs
- encourage MRCs to disclose meta-data
- identify promising technologies such as CORBA, XML and etc.

The items mentioned above will be discussed elsewhere in feature.

Acknowledgement

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http://wdcm.nig.ac.jp

http://www.javasoft.com

http://www.orbacus.com

TreeBASE: A Database of Phylogenetic Information

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Abstracts

Phylogenetic systematics brings added value to the species lists and taxonomic inventories that form the groundwork of our understanding of biodiversity. But this added value is lost without a central database to store what we know about historical patterns and evolutionary relationships. TreeBASE was developed to harness this information and to provide a tool to study the evolution of biodiversity. Access to phylogenetic trees, and to the data underlying them, is needed for a wide variety of purposes, including comparative studies of morphological and molecular evolution, biogeography, coevolution, and studies of congruence of results based on different sources of evidence. Such data are also needed to monitor progress in phylogenetic research, to test new methods of analysis, and to address immediate practical problems in conservation of biodiversity. TreeBASE stores published phylogenetic trees, character and molecular data matrices, bibliographic information, and some details on taxa, characters, algorithms used, and analyses performed. The database is designed to be explored interactively and to allow retrieval and recombination of trees and data from different studies. TreeBASE therefore provides a means of assessing and synthesizing knowledge of phylogenetic information and biodiversity. The URL is: *http://phylogeny.harvard.edu/treebase*.

Key Words: TreeBASE, database, phylogeny

Introduction

In the early 1980's, the advent of personal computers and PCR techniques together precipitated an explosion of phylogenetic knowledge. Personal computers made it easier, faster, and more affordable for biologists to analyze phylogenetic data, and DNA sequencing made large amounts of raw phylogenetic data available to the non-specialist. By 1989, publications of phylogenetic trees were growing by 15 to 20% per year without any sign of abatement (Pagel, 1997, Sanderson, et al., 1993). In addition, trees were increasingly used to answer questions outside of systematics, such as in coevolution and adaptation (Coddington, 1988, Mitter and Brooks, 1983, Mitter, et al., 1988, Mitter, et al., 1991).

For reasons similar to those that drove the molecular biology community to develop DNA databases, Sanderson et al. proposed that the systematic community develop a phylogenetic database to harness this rapidly-growing field (Sanderson, et al., 1993). In addition to providing a central repository of tree and character data, a phylogenetic database promised to become an important tool for biologists studying coevolution, biogeography, conservation, phylogenetic methods, or character congruence. In 1994, M. Donoghue, T. Eriksson, W. Piel, K. Rice, and M. Sanderson began work on a prototype phylogenetic database called TreeBASE, with support from Harvard University Herbaria, University of California at Davis, and a SGER NSF grant (DEB9318325). Since then, TreeBASE grew from a prototype to a more mature database. At present it is endorsed by a growing number of journals as a site for prospective authors to deposit their data.

TreeBASE Database Model

TreeBASE assumes that published phylogenetic works can boil down to a basic plan: each publication should contain one or more distinct phylogenetic analyses, each of which applies a particular algorithm using a particular weighting scheme on a set of data matrices to produce a set of trees. A tree, therefore, is always the product of one analysis, but matrices can be used by several different analyses. Authors invariably publish papers that are more complex than this simple plan envisions, but usually what is presented can be reduced to approximate it. Since TreeBASE only paraphrases the original work, we strongly recommend that the scientific community not use TreeBASE without consulting the author's published paper.

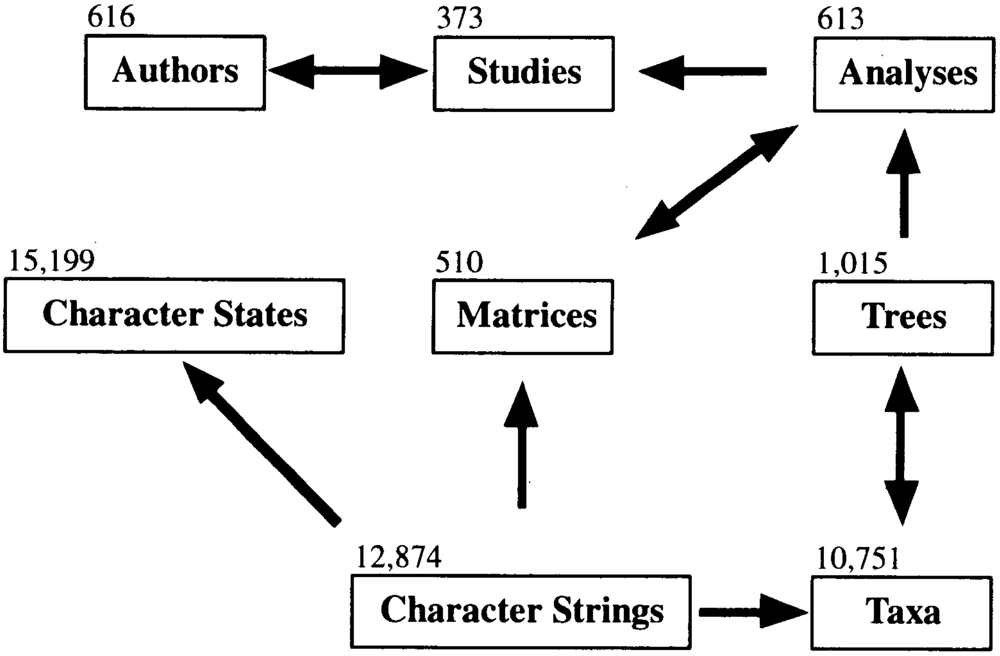


Fig. 1. Schematic of TreeBASE relational tables. Relations between tables are indicated by arrows from the "many" table to the "one" table. In other words, there can be many records of analyses for each study record, many trees for each analysis, etc. Two headed arrows indicate many-to-many relations, thus each tree can have many taxa and each taxon can exist in many trees. The number above each table indicates the number of records in TreeBASE as of November 1999.

In order to build this basic epistemological plan into the database model, we chose to use a relational database, which means that different types of data are stored in separate tables, each linked to another in a hierarchical chain. If a set of records in one table links to a single record in another table, the relations between the tables are said to be in a "many-to-one" relationship. Alternatively, a non-hierarchical "many-to-many" relationship is when a record from either table can relate to many records in the other (Fig. 1). TreeBASE's model is fairly complex and forms a circular loop: two separate paths link the table of studies with the table of taxa, one by way of the trees and one by way of the matrices (Fig. 1). Separating the data into numerous relational tables gives us more power over the stored data. For example, it allows us to combine matrices or recreate matrices with different sets of taxa—a procedure that would be much more difficult with a flat-file database. In addition, the separate tables approximately mirror the nexus phylogenetic data format, in which different types of data are stored in their respective data blocks (Maddison et al., 1997). Figure 2 illustrates how the modular segmentation of data in the nexus format parallels the database model in TreeBASE.

Central to TreeBASE's model is the *Studies* table, which contains the citation of the published data and the paper's abstract. The names of authors are stored in a separate table with a many-to-many relation with the *Studies* table. Each study is linked to one or more records in the *Analyses* table, which stores information on the cladistic algorithm and the software used to perform it. The *Analyses* table also acts to associate matrices with resulting trees. Thus, each *Analyses* record simultaneously points to one or more *Trees* records and one or more *Matrices* records. The *Trees* table stores the phylogenetic tree in parenthetical notation (i.e. newick notation), the name of the figure in the publication, a generalized title for the tree, and the type of tree (consensus or single).

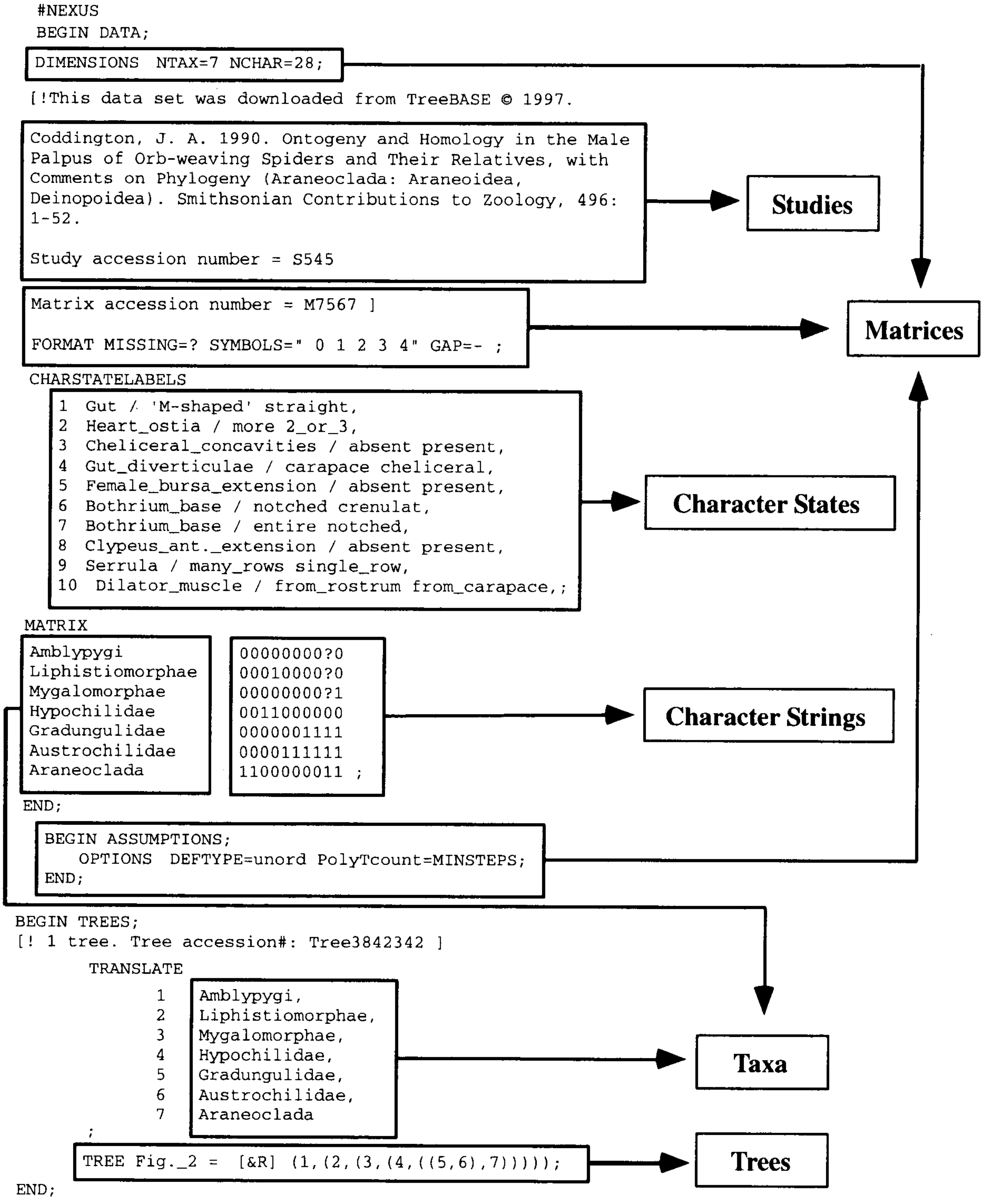
An alternative strategy would have been to store the tree as a set of parent-offspring records, where each parent-offspring record represents an internode segment within the tree (as implemented in HICLAS, http://aims.cps.msu.edu/hiclas/). Trees are then recreated by following the branching chain of parent-offspring records, starting from the most ancestral node and ending with the terminal taxa. This method would have allowed for more sophisticated manipulation of trees, such as combining them into supertrees, or skeletonizing them by pruning branches. However, we determined that this method would slow down the speed of tree retrieval and excessively burden the database with additional records—storing the tree in a single coded text field proved more effective, albeit less elegant.

The *Trees* table has a many-to-many relationship with the *Taxa* table (i.e. each *Trees* record can have several *Taxa* records, and each *Taxa* record can link to more than one *Trees* record). Each *Matrices* record stores the name of the matrix, the data type, and the format of the data. In addition, it has a one-to-many relationship with the *Character Strings* table, which stores each row of character data in the matrix. As of November 1999, TreeBASE has 510 matrices, which amount to 12,874 rows of character data (Fig. 1). Rather than store the columns of the matrix as separate records, we chose to put each row in a single text field in the *Character Strings* table. For the database program 4th Dimension, this limits each matrix to no more than 32,000 characters per taxon—the maximum number of characters in a text field. We felt safe with this strategy, seeing as the entire mitochondrion is about half this number.

Browsing and Searching Records

The scientific community can access TreeBASE using an HTML web browser pointing to the following URL: *http://phylogeny.harvard.edu/treebase*. The browser interacts with the web server through the Internet, which in turn passes instructions to and from the 4D database engine that is running on the same computer as the server. Users can initiate a search using five criteria:

1. *Author Search*—searches on the last name of an author of a publication.
2. *Citation Search*—searches on the full citation of the paper.
3. *Study Accession Number*—searches on a unique code that is assigned to each study.
4. *Matrix Accession Number*—searches on a unique code that is assigned to each matrix.
5. *Taxon Search*—searches on a taxonomic name that appeared in either the data matrix or the phylogenetic tree.



```
#NEXUS
BEGIN DATA;
DIMENSIONS  NTAX=7 NCHAR=28;
[!This data set was downloaded from TreeBASE © 1997.
Coddington, J. A. 1990. Ontogeny and Homology in the Male
Palpus of Orb-weaving Spiders and Their Relatives, with
Comments on Phylogeny (Araneoclada: Araneoidea,
Deinopoidea). Smithsonian Contributions to Zoology, 496:
1-52.

Study accession number = S545
Matrix accession number = M7567 ]

FORMAT MISSING=? SYMBOLS=" 0 1 2 3 4" GAP=- ;
CHARSTATELABELS
 1  Gut / 'M-shaped' straight,
 2  Heart_ostia / more 2_or_3,
 3  Cheliceral_concavities / absent present,
 4  Gut_diverticulae / carapace cheliceral,
 5  Female_bursa_extension / absent present,
 6  Bothrium_base / notched crenulat,
 7  Bothrium_base / entire notched,
 8  Clypeus_ant._extension / absent present,
 9  Serrula / many_rows single_row,
 10  Dilator_muscle / from_rostrum from_carapace,;
MATRIX
Amblypygi           00000000?0
Liphistiomorphae    00010000?0
Mygalomorphae       00000000?1
Hypochilidae        0011000000
Gradungulidae       0000001111
Austrochilidae      0000111111
Araneoclada         1100000011 ;
END;
 BEGIN ASSUMPTIONS;
    OPTIONS  DEFTYPE=unord PolyTcount=MINSTEPS;
 END;
BEGIN TREES;
[! 1 tree. Tree accession#: Tree3842342 ]
        TRANSLATE
                1   Amblypygi,
                2   Liphistiomorphae,
                3   Mygalomorphae,
                4   Hypochilidae,
                5   Gradungulidae,
                6   Austrochilidae,
                7   Araneoclada
        ;
   TREE Fig._2 =  [&R] (1,(2,(3,(4,((5,6),7)))));
END;
```

Fig. 2. Schematic illustrating where nexus elements are stored in TreeBASE tables. The boxes on the right represent TreeBASE tables; the boxes on the left represent blocks of nexus-formatted phylogenetic data. Arrows point to where the blocks of nexus data are stored in TreeBASE.

An initial search leads to a preliminary short-list of results. The user can then select from this list to display the resulting studies. A study is presented following the basic plan outlined above, i.e. the reference is followed by a list of analyses, and under each analysis is listed the matrices used and the trees that result. Selecting a listed matrix downloads the data to the user's local computer; selecting a listed tree displays it in a separate frame.

Interacting with Trees

Displayed trees are interactive—clicking below a branch zooms in on a clade, clicking above a branch returns all descendant taxa to the shortlist to be searched on again. The first feature is designed to make it easier to explore larger trees; the second allows users to jump from one tree to another by searching on what is known about taxa on a particular branch. For large trees, users can also choose to see them in hyperbolic style, thanks to a Java program called Hyperbolic Tree™, provided by Inxight (*http://www.inxight.com/*). Hyperbolic trees compress and prune branches that are more distant from a given point, removing the clutter and confusion that would otherwise occur when displaying large trees in the more usual way.

Tree surfing in a "small-world" network—The tree surfing feature allows users to locate "neighboring trees" by searching for other trees that contain one or more taxa found in the starting tree. The resulting set of trees is said to be related to the starting tree by one degree of separation; if newly encountered taxa in these related trees are searched on again, another set of trees will result—these are now related to the starting tree by two degrees of separation. As this task is repeated, more distantly related trees are discovered, and soon the entire island of trees has been explored. The associations among trees by way of shared taxa are neither completely random nor completely regular, but somewhere in-between. Consequently, collections of trees, even if spanning a large area of phylogenetic space, are all within relatively short "reach" of one another. This phenomenon is known as a small-world network (Barbási and Albert, 1999, Watts and Strogatz, 1998).

Various tendencies and characteristics of modern systematic methodology and productivity affect the small-world dynamics of a tree database. For example, a linked series of generic-level analyses might together form a "loose" island that requires many degrees of separation to traverse; but if just one family-level tree were added, this addition might suddenly "tighten" the island, markedly reducing the average degrees separating trees. The tendency of systematists to produce deep trees as compared to shallow trees, or the use of many outgroups as compared to just one or two, will shape the dynamics of taxon connectivity.

TreeBASE allows submitting authors to provide higher taxon names for internal nodes. While this feature has the advantage of increasing the connectivity among trees, authors do not always use it. The extent to which authors provide higher taxon names strongly affects the small-world dynamics of the database, since higher taxa are usually well connected with many distant trees. Consequently, future tree connectivity can easily change depending on the attitude and habits of submitting authors.

Presently, TreeBASE has a single super-island comprising over 70% of trees in the database—the remainder being distributed among 114 small islands (see figure 3 in Sanderson et al. 1998). Moreover, trees in the super-island are fairly well dispersed, with a mean distance of 11.5±3 iterations. While we can expect the super-island to tighten as more trees are added, we hope that the mean distance will not decrease too much, as the tree surfing feature will loose its effectiveness if it traverses the database too quickly. If this happens we may need to raise the stringency of the definition of a neighbor.

Eventually all trees in TreeBASE will be linked together to form a single super-island. But at present there are too few trees in TreeBASE, relative to the whole tree of life, for them all to overlap. The number of additional trees needed in order that the entire database join the super-island depends, again, on the characteristics of systematic productivity. A simple simulation where subsets of randomly selected trees are tested for their degree of connectivity, demonstrates a distinct pattern of island growth and conglomeration. The lowest amount of connectivity occurs when the database has only 70 to 180 trees. At around 250 trees, the rate of new island formation begins to drop and the average island size surges. The number of islands no longer grows after 500 trees, where presumably the rate of conglomeration of separate islands, due to the addition of well-connected trees, matches the rate of new island creation. Since the database is not much larger than 1000 trees, we cannot say when the number of islands will begin to drop until there is just one super-island. However, judging by the fact that island growth already flattened at just 500 trees, we may achieve complete coverage surprisingly soon.

Building Supertrees using TreeBASE—One of the applications of tree surfing is to build collections of related trees that can then be fused together to form a supertree. Building supertrees is a powerful way of summarizing and synthesizing current systematic knowledge for a group of taxa. There are several different methods of supertree construction (Sanderson, et al., 1998)—matrix representation with parsimony (MRP) being the most popular for trees with incomplete overlap of taxa (Baum, 1992, Purvis, 1995, Ragan, 1992, Ronquist, 1996). Currently we are developing an MRP supertree construction tool to work together with our tree surfing tool. This combination will make it fairly easy to summarize and synthesize phylogenetic knowledge using TreeBASE.

Submitting Data

Authors of published phylogenies are strongly encouraged to submit their data to TreeBASE. The submission process is automated and fairly flexible, allowing authors to interrupt their submission and return to it at a later time. Author, reference, and abstract information are entered in HTML forms and processed by a common gateway interface program. Data are uploaded to TreeBASE as nexus-formatted data, and entered into a HTML form using the client browser's copy-paste feature. We strongly recommend that submitters use MacClade (Maddison and Maddison, 1992) to prepare their data because this program insures correspondence in spelling and accuracy in nexus syntax. Authors who do not have access to nexus-editors can contact our staff for assistance.

Submission Policy—TreeBASE will only accept data used in scientific work that has been or will be published in a peer-reviewed publication, such as a journal or book. Authors can initiate a submission prior to the manuscript being accepted for publication, but the data will only be made available to the public once the paper is treated as "accepted," "in press," or "published" by the journal's editorial board. Normally, trees in TreeBASE directly correspond to figures in the publication, however up to twenty additional unpublished trees may be included if their existence is mentioned in the paper's text. For example, they might be the set of most parsimonious trees, even if only a single consensus tree appeared as a figure in the publication.

Initially, authors are given a temporary submission tracking number (e.g. "SN123"). Later, when the paper has been accepted, the data are made public and TreeBASE issues a permanent study accession number (e.g. "S123") and a permanent matrix accession number for each data matrix (e.g. "M456"). The author can insert these numbers into the last version of the manuscript or in the galley proofs so that readers can easily locate the data in TreeBASE. In some instances, authors can have the data withheld from public release until the journal has reached the library shelves.

Growth of TreeBASE—Submissions are vital for helping TreeBASE keep up with the tremendous growth of phylogenetic knowledge. An excellent source of data comes from those journals that require or recommend that authors submit data to TreeBASE, and we urge more journals to do the same. Recently we have seen an increase in the rate of new fungal data in TreeBASE, largely because several journals in this field are now directing prospective authors to submit their data to us.

For sequence data, the principle advantage of TreeBASE over GenBank (*http://www.ncbi.nlm.nih.gov/*) is that TreeBASE stores aligned datasets, as well as weighting schemes and step matrices that are peculiar to phylogenetics. It is critical that the readership of journals be able to recover the exact alignment used in a published analysis, particularly for non-coding sequences that are difficult to align (Cohen, et al., 1998). Without the alignment, the researcher's original hypotheses of homology are forever lost to the scientific community. Other on-line services, such as EMBL (*http://www.ebi.ac.uk/*), accept aligned data but only as non-searchable, passive files. Unlike TreeBASE, none of these sites accept other types of phylogenetic data, such as morphological characters, RFLPs, allozymes, and the trees themselves. Consequently, we hope that TreeBASE offers a unique and valuable service for both scientists and scientific journals.

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A Master List of the World's Plant Species

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Abstract

There are ever-increasing numbers of collaborative international and regional biological taxonomic database projects, many now with interactive websites. The Global Plant Checklist is a project of the International Organization for Plant Information, aiming to bring together a unified and taxonomically edited master list of plant species of the world. This will provide a framework for users to access all kinds of information on these species. The pilot Checklist is at http://iopi.csu.edu.au/iopi/. The current emphasis is on bringing together existing datasets while user-friendly software is developed for editing the database. Editing will be done by botanists specialising in each group. Several general lessons can be drawn from our experiences to date.

Key Words: Global Plant Checklist, potential taxon, IOPI Data Model, vascular plants, global species databases, biodiversity, taxonomic impediment

Introduction

It is generally agreed that electronic master lists of species are needed as the first step in organising and making accessible information on the world's organisms, but there is no straightforward, commonly agreed way to achieve these lists. This is becoming a major problem with the recent increased interest in biodiversity issues worldwide and the consequent demand for authoritative information on what species exist where. What are we as biologists doing to meet that need, and what more can we do?

There are ever-increasing numbers of collaborative biological taxonomic database projects, both international and regional, many now with interactive websites. Although some of these projects have been built up through the efforts of dedicated individuals, a general feature of these projects is the participation of taxon specialists from around the world. An additional feature of such projects is that they do not exist just as a list of the names of taxa but rather they provide the most authoritative way to access information about those taxa. They can be divided into four categories:

- **Name-based projects**. These aim to list all names ever published for a particular group of taxa. These nomenclator projects do not usually express a taxonomic opinion on the status of the published names. An example is the International Plant Name Index (IPNI) project, which aims to provide a comprehensive authority file for the names of all seed plants (flowering plants and 'gymnosperms'). This is a co-operative venture, uniting the efforts of the *Index Kewensis* project of the Royal Botanic Gardens Kew (UK), the *Gray Herbarium Card Index* at Harvard University Herbaria (USA) and the *Australian Plant Name Index* at the Australian National Herbarium in Canberra.

- **Species- or classification-based projects.** These aim to list all known species of a given group of organisms. Many are compiled by individual specialists as they study the systematics of a particular group but others rely on international collaboration, particularly for larger taxon groups. Two successful pioneering examples are the International Legume Database and Information Service (ILDIS; http://www.ildis.org/) covering the legumes (plant family Fabaceae) and FishBase (http://www.fishbase.org/) for the fish species of the world. The Global Plant Checklist of the International Organization for Plant Information also falls into this category. These three projects are all members of the Species 2000 project. Species 2000 (http://www.sp2000.org/) is working to provide a uniform and validated index of names of all known species, providing links to member databases for further information on each taxon.

- **Hierarchy- or phylogeny-based projects.** These aim to show the phylogenetic relationships of groups of organisms, and give access to other information about these taxa. Two such projects are TreeBase (http://herbaria.harvard.edu/treebase/index.html) and Tree of Life (http://phylogeny.arizona.edu/tree/phylogeny.html).

- **Geographically based projects.** These present a census of all species of a group that occur in a particular region. Many of these only cover one country or one region within a country, but some projects do cross national boundaries and therefore qualify as international projects. Examples of this include the Integrated Taxonomic Information System (ITIS; http://www.itis.usda.gov/plantproj/itis/index.html), which is a collaborative project covering North American organisms of all kinds, and the ESFEDS database of European plants (http://www.rbge.org.uk/Welcome.html) that was based on the hardcopy *Flora Europaea* and is now being extended by collaboration with the Med-Checklist Project in the Euro+Med Project to include plant species of the whole Mediterranean region.

What is IOPI?

The International Organization for Plant Information (IOPI; http://iopi.csu.edu.au/iopi/) is a collaboration amongst the world's botanical and IT specialists that aims to make available a modern, unified, computerized inventory of the plant species of the world, linked to data on their distribution and attributes. It had its genesis in a wide-ranging information-system conference in Delphi (Bisby, Russell and Pankhurst 1993). The first phase of this worldwide plant information system is a Global Plant Checklist of the world's species of vascular plants. It also has an on-line Database of Plant Databases, which is a metadatabase listing plant database projects around the world. Its third activity is the Species Plantarum Project (http://www.anbg.gov.au/abrs/flora/spplant/spplant.htm), which is writing a *Flora of the World* (the first few fascicles of which are now published, in English and Chinese).

The Global Plant Checklist

The Global Plant Checklist (GPC) aims to cover the species of vascular plants initially. These include about 270,000 described species (represented in the literature by about 1,000,000 names, that is, on average each species name has three synonyms) with an estimated 30,000 species still to be formally described. The broad strategy is to merge data held by IOPI members (mainly in databases, Floras and monographic treatments) into a computer-accessible format. Input of data from both regionally based and taxonomically based sources will be tackled in stages, aiming to use the most readily available datasets first, namely large regional and monographic databases already existing in electronic form.The merged data will be edited for consistency by a worldwide network of specialists. The Checklist will become increasingly useful through refinements from taxonomic editing and the incorporation of additional datasets.

Representing in a database the possible combinations and variations found in taxonomic classification and nomenclature is complex (Bisby 1993). The IOPI Data Model (Berendsohn 1997) is based on the concept of potential taxa (Berendsohn 1995). One name may represent more than one concept of a taxon, as seen by the frequent use of expressions such as *sensu lato, sensu stricto* and *pro parte* after a name to indicate different concepts of the variation included under that name. This model aims to distinguish between these different concepts of a taxon so that the database user is confident that the information given under a name does indeed represent information about a single concept of a taxon. Further discussion of 'potential taxa' by Berendsohn can be found on the web at http://research.calacademy.org/taf/proceedings/Proceedings.html. The IOPI data model also makes allowance for alternative classifications. This is necessary, given the lack of agreement in taxonomic circles about the delimitation of certain taxa.

As a collaborative project, a key feature of the GPC is the intention to involve all specialists, using the plant family as the basic organising unit. These specialists will compile and edit data for each family, and have responsibility as a group for maintaining the data for that family in the Checklist. This will be facilitated by implementing a distributed database structure, which is becoming more feasible as Internet connections become more widely available and reliable.

Basic data included in the GPC for a taxon are:

- Its name (genus, species, plus infraspecific names as relevant)
- Author and protologue details
- Type information (to be added as it becomes available)
- Known synonyms
- Its placement in a classification, at least at family level
- Its geographic distribution, both in plain language and in the standard geographical units (Hollis and Brummitt 1992) of the International Working Group on Taxonomic Databases (TDWG)
- Bibliographic reference to a recent treatment, either hardcopy or electronic, that includes this taxon
- Acknowledgement of source of data (either a hardcopy publication, electronic dataset, or individual botanist).

There are three levels of data present in the GPC: (i) source datasets (the data shown as originally contributed by the dataset owners or custodians), (ii) partly coordinated /edited entries, and (iii) fully coordinated entries that conform to all the GPC specifications. It is important that the source datasets are stored and maintained in their original form because each of their entries represents a certain view of a taxon at the time of the publication of the reference cited. This taxonomic concept, represented by a scientific name and its source reference, is a potential taxon (see above).

Given the slow pace of taxonomic revision and publication – the 'taxonomic impediment', as the Global Taxonomy Initiative (ABRS 1998) calls it – there are considerable numbers of known species that are as yet unnamed. These can be included in the GPC as long as a reference specimen is clearly indicated.

The GPC is still in start-up phase, with a provisional version on-line (http://bgbm3.bgbm.fu-berlin.de/iopi/gpc/) that demonstrates how the Checklist works, and serves as an aid for developing data entry and botanical editing procedures. The preliminary Checklist started with three regional datasets, namely those for:

- Australia (part of the Australian Plant Name Index; used by permission of the Australian Centre for Plant Biodiversity Research, Canberra)
- Peru (used by permission of the Missouri Botanical Garden), and
- Europe (Flora Europaea - ESFEDS database; used by permission of V. Heywood).

Such regional datasets can present the problem of overlapping data records when amalgamated in the GPC. Incorporating family-based datasets is obviously simpler in that there will be no overlap in names (Bisby 1993). However, the regional datasets are important in that they bring in more information about the distribution of the taxa than may be available in family-based datasets.

A list for the family Casuarinaceae, from the research of the late Dr L.A.S. Johnson and K.L. Wilson, Royal Botanic Gardens Sydney (used with their permission), was then added as an example of a whole family. Other datasets that have been added more recently include the Magnoliaceae and Fagales datasets from the Royal Botanic Gardens Kew (forming part of the publications Frodin and Govaerts (1996) and Govaerts and Frodin (1998)), Irvingiaceae (the first family published in the *Flora of the World* (Harris 1999)), the PLANTS dataset for North America (by permission of the United States Department of Agriculture – PLANTS is now part of the ITIS data network), the S.K. Czerepanov 1996 list covering the former USSR (by permission of the Komarov Botanical Institute, St Petersburg, Russia), and data from published volumes of the *Med-Checklist* for the Mediterranean region (by permission of W. Greuter, Botanischer Garten und Botanisches Museum Berlin-Dahlem).

We are now seeking funds to implement the relational, distributed database planned for the full version fo the Global Plant Checklist. This will fully implement the IOPI Data Model.

Lessons from Our Experiences

Several general lessons can be drawn from our experiences in developing the Global Plant Checklist to date.

- Rate of achievement: Nothing is achieved as simply or quickly as first expected. This is particularly true of such international collaborative efforts, involving extensive consultation. However, this is partly offset now by the rapid pace of change in information technology (development of hardware and software). What was in the realms of IT research some years ago is now becoming commonplace and comparatively more affordable, particularly in terms of the Internet and interoperability of database programs, even on different platforms. Even so, there is still a need to adapt software to fit the particular needs of one's own project and that process does not seem to be getting cheaper.

- Funding: Think globally but act locally. International funds are very limited for such international collaborative projects. Much of that funding is politically influenced and is allocated nationally or to a consortium of several countries, particularly developing countries. The most successful strategy for projects such as ours seems to be to seek funding locally for individual components. However, this can lead to problems because it is easier to get funding for data-entry than for key administrative coordinating functions.

- Expert input: Local involvement is of supreme importance in building and maintaining such an authoritative checklist because it will not succeed without the input of local experts in the various taxa (Stirton 1993).

- Activists: To achieve such international collaborative projects, we need committed scientific organisations but we need committed individuals just as much. There are few people who are willing and able to do the many tasks, even if their organisations are generally supportive of a project. The pressures on working biologists are intense and becoming ever more so with the increased community interest in biodiversity. At the same time, economic pressures are frequently leading to reduced staff numbers in scientific organisations. The resolution of this situation is uncertain.

Final Remarks

I would conclude by saying that there are no simple formulas for a successful collaborative checklist project, whether within a country or internationally. However, I hope that this talk has given you some pointers on ways to go or pitfalls to avoid.

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Current Status of the Fish Database in Taiwan and its Future Perspective

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Abstract

The total number of fishes in Taiwan comprising 250 families and 2450 species has reached about 1/10 of the world's fishes. This number does not include some unidentified species, especially deep-sea fishes. The curatorial and distributional data of these Taiwanese fish have been integrated into a single database which can be accessed interactively on the internet at http://fishdb.sinica.edu.tw. The database includes the following contents:

1. **Basic information and a specimen photo of each species – One can make inquiries by fish names, body contours, or fish pictures, etc. A list of newly added species and the reasons for changing scientific names are also provided.**
2. **Distributional database – Through the GIS, users can check the actual distribution areas of each species on the map (in a grid system, 10' each) or obtain a list of species for each grid.**
3. **Bibliographic database – To the present, 274 taxonomic, ecological, or distributional pieces of literature of fishes in Taiwan have been collected since 1909 including local Chinese articles.**
4. **Curatorial database – One can inquire about the approximately 5000 lots and 2000 species of fish specimens deposited at the Institute of Zoology, Academia Sinica (ASIZP) and 1000 species deposited at the National Museum of Marine Science & Technology (NMSMP).**
5. **Chinese fish names of the world fishes – The Chinese names of 26,600 valid species in Wu et al. (1999) are provided for promoting the unification of Chinese fish names.**
6. **Miscellaneous – New version of errata of "Fishes of Taiwan" (Shen et al. 1993), Chinese character fonts, and the pronunciation of characters with "fish" radical are furnished.**

The above regional database of Taiwanese fishes already can link and access to fish data for each species in the global fish database, *FishBase*, of ICLARM (http://www.fishbase.org). Through the collaboration with FishBase, the users of *Species 2000* can also get the most updated data of Taiwanese fishes via *FishBase* (http://www.sp2000.nies.go.jp/index.html). It is believed that the establishment of global biodiversity information exchange system, like "GBIF" (Global Biodiversity Information Facilities) or "BioNet—International" (the global network for taxonomy) all will need local database workers to provide regional databases to provide their content so that their goal of information sharing throughout the world can be reached.

Key Words: Not assigned by the author.

Introduction

Among many missions in the biodiversity research and conservation, systematics and inventory are the most fundamental and basic tasks. Recently, the DIVERSITAS program (An International Programme of Biodiversity Science) promoted by several international academic societies, including IUBS, SCOPE, UNESCO, ICSU, and IGBP, also declared the importance of taxonomic work. The biodiversity in the soil, marine, and freshwater environment, and microorganisms are the special target areas of research (IUBS, 1997). For surveying, monitoring, and conservation work in marine and freshwater ecosystems, fishes always are the most important component and have received peoples' attention and consideration because fish have long had intimate relations with human lives. According to the infrastructure of "Systematic Agenda 2000", the assembly of systematic knowledge into efficient databases and creating international information networks are the keystone to whether the use of biodiversity resource will be successful or not. This is also one of the major tasks that the Convention on Biological Diversity (CBD) requests all its party countries to follow. Thus, many countries have established or are establishing their national biodiversity database centers to manage their accumulated biodiversity-related information. Several international scientific organizations are also promoting the establishment of global biodiversity databases or networks, such as the GTI (Global Taxonomy Initiative) requested by CBD, BioNET-INTERNATIONAL for establishing global taxonomy network, or GBIF (Global Biodiversity Information Facility) proposed in the CBD/COP4.

For different purposes, there are different kinds of biodiversity databases, among which, the taxonomic databases contain five kinds: nomenclatural, distributional, curatorial, bibliographic, and descriptive data (Allkin and Bisby, 1984). Specimen and temporal–spatial distributional data as well as local literature published in native languages have to be collected and organized by local scientists of each countries as well as to create their own regional database. It is difficult to ask foreign experts to help them accomplish this. Thus, ways to get correct regional taxonomic data and establish databases are becoming very important missions of local taxonomists. Then, through the cooperation with global database via the internet, exchanging and sharing the most updated information with each other are crucial to whether the database establishment can be successful or not.

The most difficult part for building a taxonomic database is the frequent changes of species names and their classification systems. Using fish as one example, it was estimated that 1/10 of species names need to be replaced every 10 years on the average (Froese and Pauly 1998). The main reasons are because of misidentifications, typographical errors, different taxonomic viewpoints, and proposed new classification systems after using new techniques or examining more specimens by fish taxonomists. Consequently, many synonyms or undetermined species status have resulted. Correct species identification and accurate distributional data are essential for users' proper experimental design, field sampling, and publishing. Thus it should be one unavoidable duty of taxonomists to establish their own fish taxonomic and distributional database for public use.

Currently, there are many existing biological taxonomic databases in the world. However, most of them were constructed by taxonomists for their own research convenience. So their purposes, data format, and both hardware and software systems are quite various. Additionally, because only some of these databases are available to the public on the web, they have not contributed to scientific cooperation and development. Nevertheless, there are some global taxonomic databases which were quite successfully. They include *FishBase* developed by ICLRAM, *Prokaryobase, World Virus Database, Legumes*, IOPI, etc. by various institutions. The nomenclature data in these databases now can be inquired via *Species 2000* (Indexing the world's known species).

The purpose of the present article is to summarize our experiences with establishing our fish database over the past 10 years as well as some future prospects. Although our regional database has collaborated with the global *FishBase* and periodically provided updated Taiwanese fish data since 1993, it was not until 1999, that both databases could exchange their fish data for each species with each other directly on the web. There is no need to search the data by going through different home pages as usual. This approach achieves our goal of working locally but sharing our information internationally.

Background and History

Since 1984, the Laboratory of Fish Ecology and Evolution has been working on the faunistic study of fishes in Taiwan. The survey sites cover almost all coastal waters around Taiwan and some islets, the South China Sea, Quemoy and Matsu as well as the watersheds of the Tamshuei, Nanao, and Holong rivers. The temporal and spatial distributional data have increased very rapidly. For example, the total number of species of Taiwan has increased to 2450 within the past 6 years despite those unidentified or doubtful species. The history of our database establishment is summarized as follow:

- 1984-1989 -- The National Science Council (NSC) supports a 5-year research project on a family-by-family faunistic study each year. All study results were summarized in a synopsis book of *Fishes of Taiwan* (Shen et al., 1993).
- 1991-1992 -- The cataloged data of fish specimens deposited at the National Museum of Marine Science and Technology were computerized using the MUSE system.
- 1989-1994 -- The NSC sponsored another 5 year project to collect and establish distributional database in the coastal waters around Taiwan, mostly on coral reef fishes by underwater census.
- 1991-1996 -- The Council of Agriculture (COA) sponsored a 6 year project to collect and build a coastal and offshore economic fishery resources database; most data were obtained from fishermen's questionnaires.
- 1991 to the present -- The promoting the establishment of fish database for CODATA/DSAO (Chiu & Shao 1991).
- 1993 to the present -- We collaborate with *FishBase* of ICLARM.
- 1996 to the present -- We joined the team project of "Networking of Taiwanese Research" funded by Academia Sinica, and cooperated with the Institute of Information Sciences to incoporate the GIS (GRASS) system into distributional database.
- 1997 to the present -- The web station of *Fish Database in Taiwan* is officially established.
- 1999 to the present -- Direct access of the fish data from *FishBase.* Under the support of the first year project of the Digital Museum of NSC, a popular version entitled *Fish World of Taiwan* was released; The GIS system was changed from GRASS to ArcView/MapInfo under the technical support of the Computing Center, Academia Sinica.
- 2001 and beyond -- We expect that the project of "Fish Fauna of Taiwan", one of the "National Archive Digitizing Projects" can be approved and carried out.

The purposes of building a fish database in Taiwan include:

a. Provide the most up-to-date results of fish taxonomic studies in order to strengthen information exchange and research cooperation in research communities.

b. Provide ecological data of the aquatic environment for assessment, conservation, exploitation, and management of marine biological resources.

c. Promote the unification of fish names especially for Chinese fish names, and Chinese and English common names.

While building a regional fish database, we also provide our data to a global fish database – *FishBase* periodically. *FishBase* should be one of the most successful biological databases because it collects information not only from English books or research papers but also from non-English local publications via many collaborators in different countries. Because *FishBase* gived credit to all data suppliers, it is naturally easier to gain the support of scholars. The most significant progress is that *FishBase* has been well recognized by many distinguished fish taxonomists in the world. So, *FishBase* has correctness and authority beyond a doubt, especially when it received the support from W.N. Eschmeyer to include his digitized data of two books entitled: *Catalog of the Genera of Recent Fishes* (Eschmeyer,

1990) and *Catalog of Fishes* (Eschmeyer, 1998). Since 1999, users have already been able to inquire about information of *FishBase* from the internet (http://www.fishbase.org) instead of purchasing CD-ROM as in the past 3 years. Furthermore, through the link of fish species names, we can also look up regional information of that particular species in other countries. Because our database in Taiwan has already made much progress and has a lot of experience, we were initially invited by R. Froese, the leader of the *FishBase* project, to develop this function with them. At the moment, users can get descriptive fish information in *FishBase* instantly while browsing our Taiwanese fish data and vice versa. In other words, if the data format is confirmed, the concept of accessing the data from other database is feasible. Through the channel of *FishBase*, the users of Species 2000 or other global information exchange systems, like BioNET-INTERNATIONAL (the global network for taxonomy) or the GBIF (Global Biodiversity Information Facility) can also access species information in our fish database from Taiwan (Fig. 1).

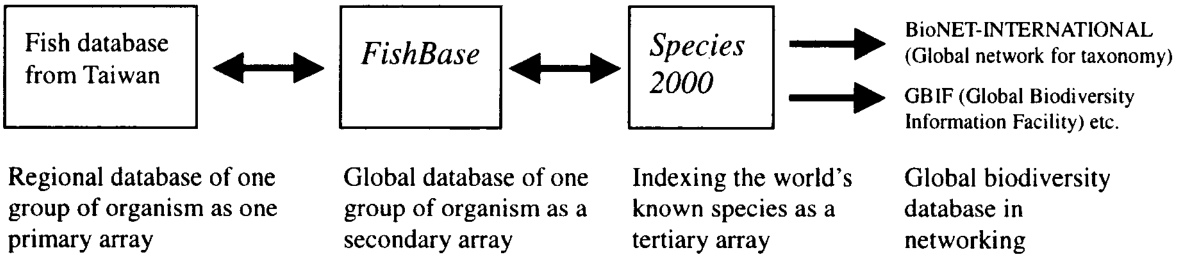

Fig. 1. Interrelationships and cooperation between regional and global databases.

Current Status of Fish Database in Taiwan

Figure 2 shows the infrastructure of the fish database in Taiwan. All data are linked using the scientific name. Through the names, users can inquire about all different kinds of data in the regional database or global database.

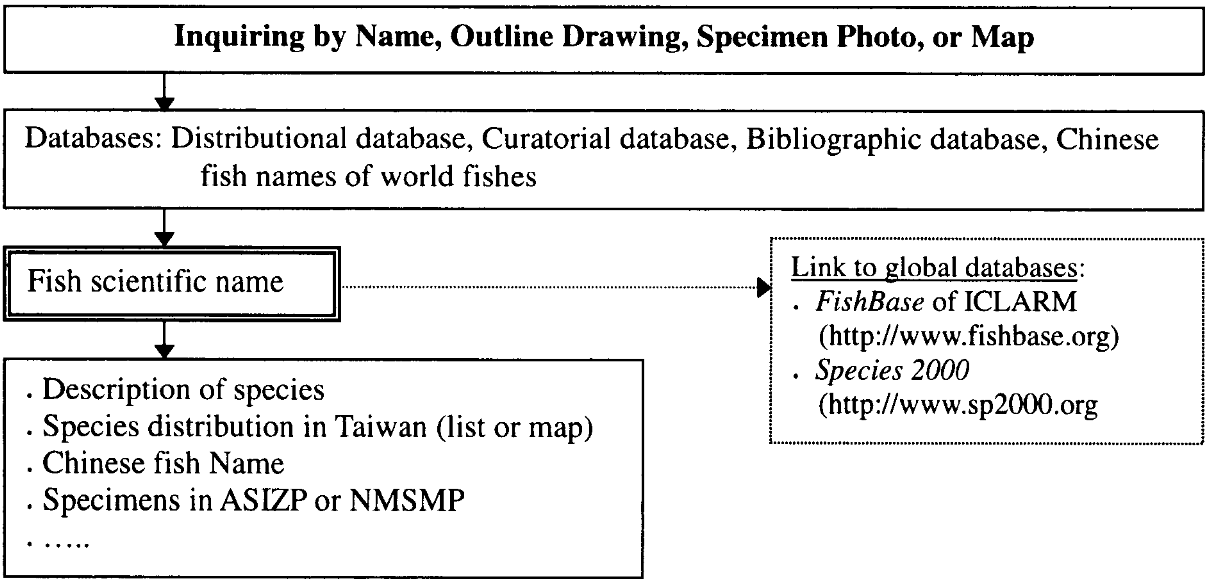

Fig. 2. Flowchart of *The Fish Database of Taiwan* (Inquiry and output)

Currently the *Fish DataBase in Taiwan* includes the following 8 parts:

1. Updated checklist of fishes from Taiwan and the reason for change – To March 2000, there are 250 families and 2450 species of fishes included in that checklist. Unpublished new records of species are included in cases where their occurrence has been established by specimens or by *in situ* photos. The reasons for each addition, deletion, or modification of a name in the list are provided.
2. Distributional database -- Users can check the actual distribution areas of each species on the map (in a grid system, 10' each) or obtain a total list of species for each grid based on the selected conditions of fishing gear, month, and abundance. The monthly abundance variation of selected species can also be obtained. To date, the inshore economic fishes within 12 nautical miles have been included, but we still lack the coastal and freshwater fishes. A checklist of fish at Nan-Sha (Spratly Island) and Tung-Sha (Prata's Island) in the South China Sea are provided. The relation between the distribution of each particular species and the water surface temperature (remote sensing map of NOAA satellite) can be inferred using the GIS system of ArcView/Map Info.
3. Basic information and specimen photo of each species – Inquiries can be made by fish names, body contours, or fish pictures, etc. The basic information contains morphology, ecology, habitat, and world distribution. A list of newly added species along with the reasons for changing scientific names are also provided together with the most updated number of family and species of fishes in Taiwan.
4. Curatorial database - The fish specimens collections including the Institute of Zoology, Academia Sinica (ASIZP) and the National Marine Science Museum (NMSMP). So far, a total number of 242 families, 2029 species and 5022 lots have been included for ASIZP and 175 families, 1000 species, and 1444 specimens for NMSMP.
5. Bibliographic database – 237 taxonomic, ecological or distributional pieces of literature of fishes in Taiwan are provided, including local or non-SCI journal articles since 1909 have been listed. Some of them are written in Chinese.
6. Inquiry system for Chinese fish names of the world fishes (Wu *et al.,* 1999) – includes 26,600 species.
7. Inquiry of Chinese character fonts and the pronunciation of characters with the "fish" radical – currently 64 characters are included using graphic mode.
8. Miscellaneous – A new version of the errata of *Fishes of Taiwan* (Shen *et al.*, 1993). All 1800 specimen photos in this book were scanned and are used as the major image source in the database.

Future Perspectives

Although the overall structure and items of our fish databases look well organized, the actual data entry is still far from complete. For example,

(1) Currently we have only photos for approximately 1900 species altogether, of which only 800 species are underwater photos. Descriptive text is available in Chinese for only 500 species. Additionally, we wish to scan all color photos of deposited specimens when they were fresh, so that the important color pattern can be used.

(2) We need to complete the English version of this database.

(3) We need to actively provide our local fish data or photos to global fish databases, like *FishBase* of ICLARM, BioNET, or GBIF.

(4) We will cooperate with *FishBase* of ICLARM to search for collaborators from different Asian-Pacific countries so that different languages of fish names can be incorporated into *FishBase* like Chinese, Japanese, Korean, Thai, Russian, and so on. Then all Asian people,

regardless they are taxonomists or not, can easily access all the detailed information on each species from the Internet by keying in or browsing their local fish names without knowing the scientific names of the fishes.

(5) We need to solve the problems of missing fonts of Chinese characters, continuously develop the new technique of metadata, intellectual property protection, water mark, query by image content (QBIC), GIS, and multi-media systems etc.

(6) We need to continuously revise and promote the unification of Chinese fish names across the Taiwan Strait.

We hope that our experience in database construction is useful to other countries in developing their own fish databases or even building up the databases of other organisms. Sharing the most complete and updated biodiversity information is the most fundamental and economic approach to conserving the biodiversity of our world.

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Taxapad 1999 and the Interactive Catalogue of World Ichneumonidae *(Hexapoda, Hymenoptera)*

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Abstract

Taxapad, a Microsoft Window based program that presents catalogue database in a graphical form, is described, showing the inherent data structure used to present published information dealing with the family of parasitic wasps, Ichneumonidae. The interactive catalogue is a useful source of information on Ichneumonidae that has over 21,000 valid species distributed worldwide, and the Taxapad is useful as a notepad for entering personal information to any of the over 228,000 scientific names and over 10,000 common names in the system.

Key Words : Database, Catalogue, Ichneumonidae, Scientific names

Introduction

The limitation of the printed media to present a mass of interconnecting taxonomic information becomes evident with the publication of 'The Catalogue of World Ichneumonidae' (Yu & Horstmann, 1997). Although it is divided into two volumes and covered 1,558 pages, much of the information compiled during the study of this group was not included due to the inadequacy of the linear form of a printed catalogue to present such information. For example, it is possible to show the distribution by country of an ichneumonid wasp in a catalogue, but it is unlikely that a catalogue will show lists of ichneumonid wasps that are found in individual countries. And yet, the information base is the same. This example can be expanded to all information that a database covers: hosts, biological attributes, morphological attributes, etc. With the advent of the compact disk, such mass of information can now be made available, with no loss of accessibility, by the use of appropriate software to present the information.

Software created to handle taxonomic database must take into account that these databases are governed by the rules in the Nomenclatural Codes and by the taxonomic hierarchical structure of the scientific names. In the Nomenclatural Codes, the rule that species-epithet ending must agree with the gender of the generic name makes the child object (species) dependent on the parent object (genus). And by their taxonomic relationship, some child attributes (for example, distribution information) become the parent attributes, but some (for example, type information) are confined to the child only. This type of 'reverse inheritance' can in theory go all the way up to the kingdom level.

Taxapad is created specifically to handle such taxonomic information, and is used as a platform to present information gleaned from over 8,000 references dealing with the family Ichneumonidae.

Taxapad 1999

Taxapad is a Microsoft Window based program for presenting taxonomic, biological, and bibliographic information. It was written in Delphi 3, a Pascal based language produced by Borland International Inc. (Scotts Valley, California, U.S.A.). The predecessor of Taxapad was Taxa, which was used in the 'Catalogue of the Chalcidoidea of the world' (Noyes, 1998). The 'pad' in Taxapad denotes that the general user is able to enter his own observations to any scientific names in the system, making this a notepad for biologists.

Taxapad uses the hierarchical structure of scientific names made available by the Zoological Code or made valid by the Botanical Code to store and retrieve information. The 1999 version of Taxapad has over 228,800 scientific names and over 10,000 common names, divided into 25 major taxonomic groups as follows:

1. Animalia – Chordata
2. Animalia – Mollusca
3. Animalia – excluding Arthropoda
4. Arthropoda – excluding Heaxapoda
5. Hexapoda – Coleoptera (Adephaga, Archostemata, Myxophaga)
6. Hexapoda – Coleoptera (Bostrichoidea, Buprestoidea, Elateroidea)
7. Hexapoda – Coleoptera (Chrysomeloidea)
8. Hexapoda – Coleoptera (Cleroidea, Cucujoidea, Tenebrionoidea)
9. Hexapoda – Coleoptera (Curculionoidea)
10. Hexapoda – Coleoptera (Hydrophiloidea, Scarabaeioidea, Staphylinoidea)
11. Hexapoda – Diptera (Brachycera)
12. Hexapoda – Diptera (Cyclorrhapha)
13. Hexapoda – Diptera (Nematocera)
14. Hexapoda – Hemiptera
15. Hexapoda – Hymenoptera (Aculeata)
16. Hexapoda – Hymenoptera (Apocrita – Chalcidoidea)
17. Hexapoda – Hymenoptera (Apocrita – Cynipoidea, Evanoidea, Proctrupoidea)
18. Hexapoda – Hymenoptera (Apocrita – Ichneumonoidea)
19. Hexapoda – Hymenoptera (Symphyta)
20. Hexapoda – Lepidoptera (Macrolepidoptera – Noctuoidea)
21. Hexapoda – Lepidoptera (Macrolepidoptera – others)
22. Hexapoda – Lepidoptera (Microlepidoptera)
23. Hexapoda – Orthoptera
24. Hexapoda – others
25. Plantae, Monera, Protista & Fungi

Although Taxapad started as a platform for Ichneumonidae, it becomes necessary to expand the scientific name structure to include all the above groups because Ichneumonidae interacts with many other insects (especially Hymenoptera, Lepidoptera and Diptera) and plants. Also the rule of homonymy covers all scientific names governed by the Zoological Codes, so some Ichneumonidae names are in conflict with names of many other organisms, from Amphibia to Tribolites.

On this taxonomic structure, any amount of information can be appended, and using the concept of 'reverse inheritance', information of the child (species) can also become the information of its parents (genus and supra-generic names). With this form of data structure where the scientific name structure is independent of the information structure, instability of the scientific names caused by changes in combinations or synonymy will not affect the information database. For example, if the information section initially points to 'taxon X' as a host, and later on, 'taxon X' becomes a junior synonym of 'taxon Y', the information section need not be changed, because the program will automatically retrieve the current valid name, which is now 'taxon Y'.

Interactive Catalogue of World Ichneumonidae

The family Ichneumonidae is a group of parasitic wasps in the order Hymenoptera. There are currently over 21,000 valid species distributed worldwide. It is an important factor in the biological control of many agricultural and forestry pests. The object of the catalogue is to gather published information on this family, and extract pertinent taxonomic, biological, and distribution information to be entered in the Taxapad information section.

The information section is made up of information units, each of which is made up of a field, a content, a reference, and an appendix.

There can be a maximum of 255 fields, but in Ichneumonidae, only 61 are defined as follows: associate, associate (plant), biocontrol of, biology, combination, common name, compared with, competitor, country, country (error), disease, emendation, emendation for, ex synonym, food source, gender, higher group, host, host (error), host food, host habitat, host location, host selection, host suitability, image, infra-subspecific name, introduced into, isotypic with, lapsus, level status, misidentified as, misidentified for, morphology, new name for misidentification, new name for primary homonym, new name for secondary homonym, original level, original subgenus, original subgenus of, original subspecies of, parasite, parasitism, parasitoid, past homonym, predator, primary homonym, region, secondary homonym, subgenus, subgenus of, synonym, taxonomy, taxonomy (alternate), type, type (invalid), type of, type of (invalid), unnecessary new name, and validate.

The content qualifies the field and can be a literal or a scientific name. A scientific name is merely a pointer to another name. The reference identifies the source of the information. The appendix contains further information to the content, and can be a literal name, a scientific name, a number, an image, a geographic co-ordinate, a file name, or a dissenting reference.

The information of each scientific name is divided into four 'pages' — taxonomy, biology, morphology, and distribution, and the field and content is arranged alphabetically on each page. Although the reference for each information is hidden, the complete reference citation can be brought up by clicking on the content.

Three functions are available to better understand the taxonomic relationship of a group. The taxonomic tree function creates a tree-like structure, using the highest taxon as the root, and branches down to subspecies level. The catalogue-style listing creates a list of all the scientific names in the group, with their junior synonyms, in a format used by most printed catalogues. And lastly, an overview of the whole group shows the subgroups and how many genera and species each has.

Searching for Information

Information in a database is only useful if it is easily searchable. To search for information in a database, a common approach is by questioning the database using a search string. This assumes that the user knows all the searchable keywords contained in the database, which is very unlikely. An alternative is to present the user with a list or an index of all available key words and let the user select one or more items. Since a taxonomic database contains a large number of scientific names, complicated by many homonyms and synonyms, the latter approach is more appropriate. This is the approach used by Taxapad.

Taxapad has seven pre-created indexes for searching the whole database, and a number of ad hoc lists to search for information within a group of names. The seven indexes are as follows:

1. The taxonomic index: Each taxonomic group has its own taxonomic index, with a total of 583,530 names. All binominal names appear twice on the index, once with generic name first (for example, '*Venturia canescens*') and the second time with specific name first (for example, '*canescens, Venturia*'). By selecting a name, all available information related to that name will be shown. By selecting more than one name, a list of the selected names will be created for further processing (see below).
2. The subject index: There are 73,064 subject headings in Ichneumonidae. Each subject heading is made up of a field (for example, biology) and a content (for example, developmental rate). By selecting one or more of the subject headings, a list of taxa that have information related to the subject heading(s) will be created for further processing (see below).
3. The author index: Each taxonomic group has its own author index, with a total of 9,087 author names. By selecting one or more authors, a list of taxa described by the author(s) will be created for further processing (see below).
4. The image index: There are 2,759 images in Ichneumonidae. The name of each image is the scientific name of the organism depicted by the image and the content (for example, fore and hind wings) of the image. By selecting the name of an image, the image will be shown.
5. The generic and supra-generic index: The 64,326 names are from all 25 taxonomic groups, with emphasis and completeness for the orders Hymenoptera (Pagliano & Scaramozzino, 1990) and Lepidoptera (Hemming, 1967; Nye, 1975; Fletcher, 1979; Watson et al., 1980; Fletcher & Nye, 1982, 1984; Nye & Fletcher, 1991). By selecting a generic name from this index, the local taxonomic index of the generic name will appear, so the user will be able to search further for the specific epithet. This is particularly useful if the taxonomic affiliation of a binomen is not known.
6. The common name index: There are 10,139 common names of organisms from groups connected with Ichneumonidae, taken from various official and unofficial common name lists (Thomas & Hanson, 1957; Werner, 1982; Greiff, 1989; Naumann, 1993; Brako et al., 1995; Braby et al., 1997). By clicking on a name, the valid scientific name and the taxonomic affiliation of the organism will be shown.
7. The reference index: The 15,565 references pertaining to the superfamily Ichneumonoidea are listed either in alphabetical order by authors, or in chronological order by date of publication. Each reference has four fields: author, title, source, and notes.

The window containing a single taxon or a group of taxa created by the indexes 1 to 3 above, has statistics and reference functions that create ad hoc lists of field and content to search for information. The list will contain only information related to the group, so the search can be narrowed down as the search progresses.

Concluding Remarks

With the exponential increase in publications and scientific names, a system that uses taxonomic relationship to organise information will be very useful to researchers in the biological sciences. Taxapad is an attempt to provide a framework to present such information to researchers in a user-friendly way. As the electronic media is inherently graphical, a literary exposé of the system as I tried to do in this article will be inadequate. For those who are interested, a graphical presentation can be seen on the website at http://www.taxapad.com.

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Preparation of the World Cyanobacterial Database

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Abstract

The taxonomy of cyanobacteria was radically changed recently, and the species concept, criteria of species delimitation and characterization, and knowledge of their ecological and phytogeographic distributions were corrected fundamentally. As the ecological significance of cyanoprokaryotes increases, the preparation of the world cyanobacterial database is more and more urgent. The principles, framework and structure of the prepared world database of cyanobacterial taxa are presented, respecting changes in their modern system.

Key Words: Cyanobacteria, cyanophytes, cyanoprokaryotes, taxonomy, genera, species, distribution, ecology, database

Introduction

The elaboration of species database of cyanobacteria (cyanophytes, cyanoprokaryotes) is connected with several problems. Cyanobacteria were traditionally treated taxonomically as microalgae according to morphological criteria, based on characteristical phenotype diversity in nature, but the palaeobotanical and ecological investigations, and introduction of molecular and ultrastructural approach, yielded a lot of new knowledge on cyanobacterial organisms. Their prokaryotic bacterial structure and type of diversification and speciation are substantially different from eucaryotic algae, and the consequent definition of new classification criteria was necessary. However, the application of taxonomic criteria, used for eubacteria, cannot be applied for cyanoprokaryotes without problems as well. A complicated morphological diversity, life cycles, oxyphototroph mode of life and function in nature classify them rather to plant microorganisms.

Thus, the system of cyanoprokaryotes was changed radically in last three decades of 20th century, and taxa, revised after introduction of the modern ecological, electron-microscopical and molecular methods are often incompatible with traditionally described species. The modern taxonomy of cyanobacteria is, therefore, not easy, and numerous authors prefer the more simple, traditional old identification (comp. Whitton and al. 1998). Main complications are as follows:

1. Numerous misinterpretations and ill-defined taxa occur in literature. It is a result of the old, still surviving idea about the ubiquitous character and cosmopolitan distribution of almost all cyanoprokaryotes. Old identification books, based mainly on the knowledge of European species, are used often for study of cyanobacterial populations all over the world including tropical regions, what results in many mistakes.
2. The modern taxonomy uses phenotype ultrastructural, molecular and ecological characters as much as possible to reach integral characteristics of various taxa. However, numerous taxa, described by old scholars, are incompatible with these evaluations, and almost unidentifiable for lack of information.

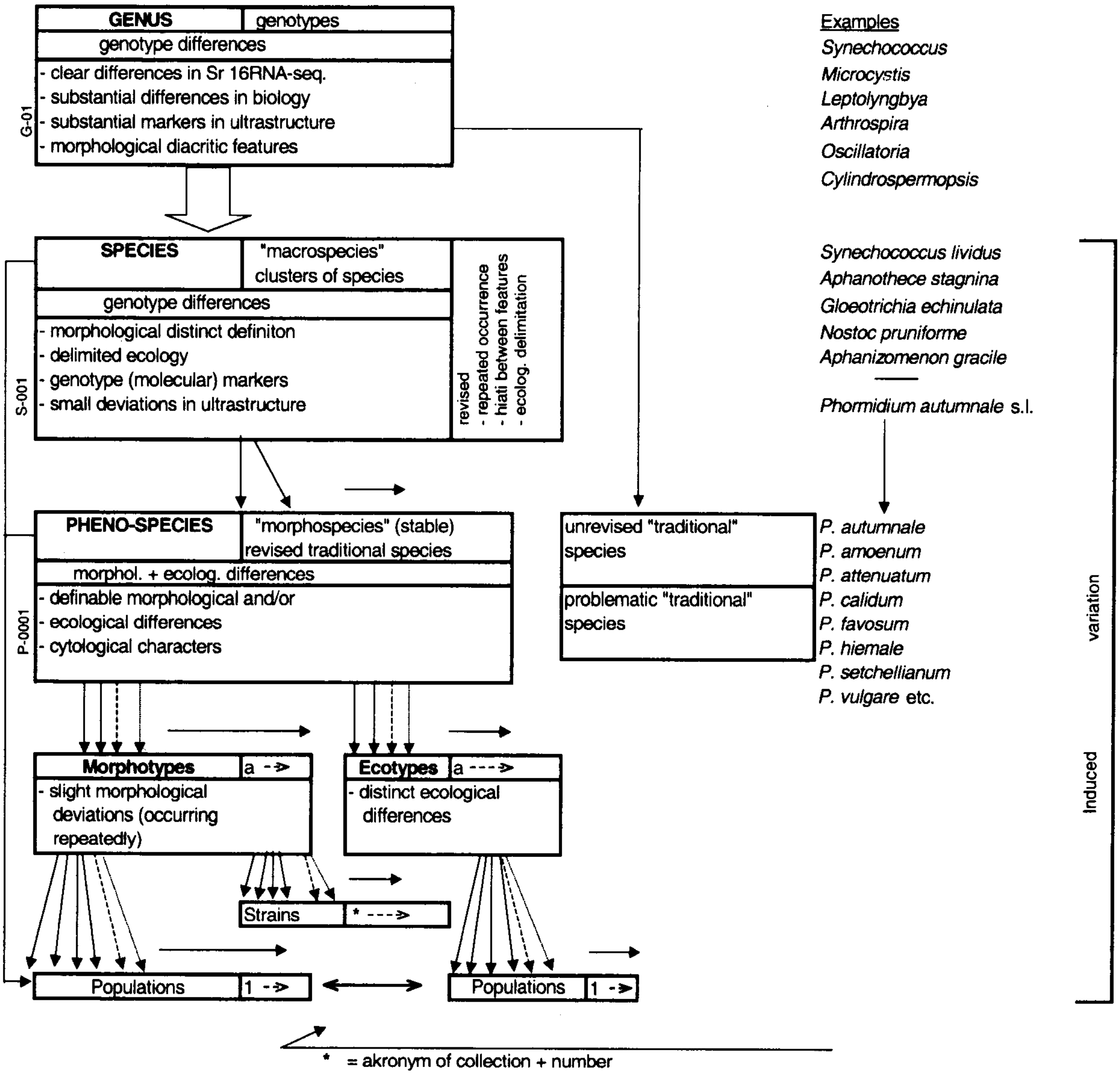
3. The ecological specificity and distinct ecological limits were proved in numerous species. The geographic distribution is dependent therefore on the ecological demands of species. The underestimation of species ecology results in numerous incorrect identifications. Up to now, regions and biotopes exist (particularly in tropical regions), where only less than 5% of cyanoprokaryotic species are known.
4. The taxonomic revisions are still at the beginning. Particularly, the integrated phenotype and genotype evaluation of taxa will bring surely numerous further changes in the cyanobacterial system in few next years.

In spite of all mentioned problems, the preparation of cyanobacterial database is possible and necessary. Up to now, several databases including cyanoprokaryotes were already initiated (Soeder and al. 1981, Dor in Grilli-Caiola and Albertano 1996, Whitton and al. 1998). The information database of the world's known genera and species of cyanoprokaryotes is prepared also at the Institute of Botany (Academy of Sciences of Czech Republic) at Třeboň, which should be compatible with "Species 2000" project (Bisby 1999).

Species Concept

The cyanobacterial diversification and genus- and species- concepts are not now clear, but intensely studied and discussed (Anagnostidis and Komárek 1985, Castenholz 1992, Komárek 1994, Miller and Castenholz 1999, Rippka and al. 1999). The definitions of taxonomic categories are, however, conventional to a certain degree, particularly in prokaryotic organisms. We are sure, that molecular and phenotype taxonomy must be in agreement, and that the modern system must be in consequence with the up to date knowledge of cyanoprokaryotic diversity. The scheme of registered taxa in the database is presented in Table 1.

Table 1. Generic and species concept



Database Structure

The database should summarize all the known data on the species (genus) as a basis for the utilization in both the scientific research and ecological practice. Therefore, several requests must be accomplished:

1. Each species sheet (item) should include as much as possible information published about the species before the year 2000.
2. The database should respect the traditional binomial botanical system (genus/species concept), which is recently the only system available and used in practice.
3. As the database should serve the source for further taxonomic study, the items should contain all the available synonyms.
4. The database should enable changes, corrections, transfers, additions etc. to reflect new knowledge on the taxon.
5. Each item should be integrated by a drawing and photograph, if available. As the photographs are rather memory consuming, they can be arranged into the special gallery linked to the main database.
6. As the database will be rather large (about 3200 accepted species of Cyanobacteria were described and revised up to now) the necessary "browse" and "look up" systems should be applied to make the orientation easy. The request as: Find species that produce heterocytes; Find species that are used for laboratory experiments; Find species that can form the water-blooms in tropics etc. can be involved.
7. The question of keys arrangements should be discussed in large.

Methods

The literature and compendia will be used as a basis for the electronic modification of the database:

- The genera will be divided into the higher taxonomic units (orders): Chroococcales (93 genera), Oscillatoriales (45 genera), Nostocales (34 genera) and Stigonematales (48 genera).
- Genera and their species inside of the order will be arranged alphabetically.
- The main item will be the sheet of the species.
- The sheet of each species with full description will contain main characteristics as listed in Table 2.

A frame will be formed for the drawings showing the appurtenant picture(s) automatically. The request for microphotograph will be linked with the database of microphotographs and will be demonstrated after pressing a button.

The most important data (see Table 2) should be organized to the widely utilized software database system (Microsoft Access under the Windows, for example which can be linked to M. Word and M. Excel), that would enable easy approach through the computers of given capacity.

Table 2. Required data items in Cyanobacterial Database

Genus:
- number, valid name, author, year
- full citation
- synonyms with full citations
- type species
- taxonomic position (higher taxonomic hierarchy)
- original diagnosis
- full description, phenotype characters
- notes to the taxonomy
- reproduction strategies, life cycles, reproduction, cell division
- ecology, ecophysiology, ecological significance
- physiology
- distribution (proved), resp. maps, endemism, problematic citations
- ultrastructure
- biochemistry
- molecular data
- misinterpretations
- generic schemes
- literature, monographs, citations
- application, technology

Species:
- number, valid name, author, year
- full citation
- synonyms with full citations
- diagnosis
- full description, phenotype characters, morphological variation
- intraspecific variation
- misinterpretations
- ecology, ecophysiolog. variation, citations of false ecologies
- distribution
- citations (occurrence) under invalid names
- drawings
- microphotos
- taxonomic notes
- spec. literature, monographs
- literature: experimental papers
- links to other taxa
- spec. ultrastructure
- biochemistry
- strains, collections (revised, unrevised); collections:akronym, source ([ecol.], media, isolator, date of isolation)
- herbaria, specimens

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Species 2000: New Zealand — The Challenge of Biodiversity Assessment, with Special Reference to the Marine Environment

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Abstract

Species 2000: New Zealand is a regional activity that is linked to _Species 2000_ International. Its goal is an all-biota species inventory (including fossils) that will serve as a baseline for future biodiversity studies. The activity is progressive. It will begin with a millennial symposium (February 2000), to be followed by published volumes of all-taxon reviews and species checklists that can be made available on the internet. The checklists will serve as a platform for production of taxonomic databases, emended to conform to the requirements of _Species 2000_ International. The symposium activity will expedite the formulation of a biosystematics strategy for New Zealand. Given that New Zealand has a very large Exclusive Economic Zone, a particular challenge for the future will be that of marine taxonomic inventory leading to a census of marine life. Five major challenges are outlined and solutions suggested.

Key Words: Not assigned by the author.

Introduction

Species 2000: New Zealand is a regional activity that aims to review and inventory the entire New Zealand biota, living and fossil, native and adventive. The boundaries of the region, for the purposes of the symposium, constitute the land and fresh waters of New Zealand and the sea area within the 200 nautical mile Exclusive Economic Zone (EEZ). The symposium venue is the new Museum of New Zealand building, Te Papa, in Wellington on 1–5 February 2000. A formal proposal to hold the symposium was made to New Zealand's Foundation for Research, Science & Technology in November 1997 in order to allow more than two years of planning prior to the meeting date of 1–5 February 2000.

Species 2000: New Zealand took its name from the well-known global biodiversity agenda *Species 2000*, with which it became formally linked in July 1999. Coordinated by Dr Frank Bisby of Reading University, England, *Species 2000* is to be a cumulative register of the world's known species, partly achieved by the linking of databases worldwide. So far, only about 1.75 million of an estimated 12.5 million to 13.6 million species of organisms on Earth have been described (Hawksworth & Kalin-Arroyo, 1995; Stork 1999) and it will be some years before they are fully catalogued. Remarkably, all-species catalogues do not yet exist for any country on Earth (including New Zealand, until the symposium volumes are published). Yet biological inventory has never been more needful. Why?

It has been estimated that the world's species are becoming extinct at a rate 100 times the natural background rate. Destruction of rain forests is particularly contributory to this accelerated rate because of elevated biodiversity in the tropics, but much of the globe, including the sea floor to 1500 m depth, is under threat of massive biodiversity loss because of human activities (Eldredge, 1998; Roberts & Hawkins, 1999; Tegner & Dayton 1999). New Zealand is not unaffected. It is becoming increasingly appreciated, however, that healthy ecosystems provide irreplaceable goods and services. In the new "Century of the Environment" human health, national security, and economic and social well-being will become increasingly contingent on environmental well-being (Lubchenco 1998). Science will have a critical role in informing policy and management relating to the environment, but there is still a considerable lack of fundamental knowledge about biodiversity, biological interactions, and ecological processes.

Achieving a Baseline Inventory

To begin the twenty-first century with a baseline inventory of the entire New Zealand biota will provide a valuable contribution to the nation that will also be of interest to a global audience. The inventory will capitalise on the historic and ongoing work of New Zealand and overseas taxonomists and contribute to new government strategies, like *Environment 2010* and *Fisheries 2010*, that aim to achieve more ecosystem-friendly resource extraction (Ministry for the Environment, 1995; Ministry of Fisheries 1996).

For New Zealand, such an inventory represents quite a challenge, which nevertheless appears to be achievable. At the outset, the biggest challenges seemed to be, and remain, the availability of taxonomists and time and resources for them to do the task of inventory. At this point in time, now three months before the symposium, more than 160 prospective contributors (including 24 overseas) are involved to a greater or lesser degree in compiling species checklists and/or writing reviews for the symposium and volumes. This number is unexpectedly high given the relatively small number of systematists in paid part-time or full-time employment in New Zealand, but is augmented by ecologists and geneticists, whose work requires them to clarify the taxonomic status of the organisms they are studying, and retired systematists who are willing to work unpaid because of their commitment to and love of New Zealand's natural history.

Timing and rationale for a baseline inventory

Why was it decided to undertake a complete biotic inventory now? Two considerations dictated the timing of the activity. First, the New Zealand government has shifted its emphasis from outputs to outcomes in evaluating the effectiveness of science funding, i.e., politicians require that scientists not only produce papers and other outputs but demonstrate how the new knowledge will benefit actual and potential users of that knowledge. It is also required that scientists identify at least some local and immediate end-users and solicit their input and written support when formulating research objectives. Apart from other scientists, easily identifiable corporate end-users of biodiversity information include government departments with responsibility for the environment (Department of Conservation, Ministry for the Environment, Ministry of Fisheries & Forestry) and regional and public-health authorities.

The second reason was calendrical — New Zealand's planning for end-of-millennium celebrations highlighted an opportunity to celebrate the nation's biodiversity as a special heritage to be respected and treasured by all New Zealanders. The timing is also eminently practical — the end of a century is a useful time marker for a baseline review. The New Zealand symposium will result in an authoritative checklist of species names (initially without synonyms) for all, or almost all, taxonomic groups, current to 31 December 1999. After this date, only publications with a year-date beginning with 2 need be searched for additions to the biota.

Benefits of a baseline species inventory

Included in the rationale for a review and inventory of the New Zealand biota were the following reasons and anticipated benefits.

1. The task of inventory needs to be carried out before it becomes too large to accomplish with present resources. The known biota is fast reaching a size where it is becoming somewhat incomprehensible. Inventories have not yet been made for many groups and the literature is frequently scattered and disparate.
2. The inventory needs to be carried out while there are still taxonomists available who can accomplish the task. In New Zealand, as elsewhere, the present cohort of competent systematists is getting ever closer to retirement, or already in retirement (and dying), with inadequate numbers of new recruits.
3. Benefits of cross-disciplinary information. Systematists have little cognisance of the size, taxonomic composition, etc., of groups beyond their own speciality. There is much we can learn from one another.
4. To promote a national appreciation, at the public and political level, of New Zealand's indigenous biota — its nature, variety, degree of endemism, and special features. Special features may include taxic novelty, archaism ("living fossils"), association with special habitats (e.g., geothermal areas, ultramafic/mineral-rich soils, whale bone, hot vents, hydrocarbon seeps, hyporheic, subterranean, or cavernicolous situations, etc.), ecological associations (symbiosis, predator-prey, parasite-host, pollinator-host, keystone role), ecological dominance, habitat-structuring, toxicity, excessive rarity, hyperdiversity, indigenous-resource contribution, bloom-forming ability, etc.
5. To inform conservation needs. What is typical or representative, what is unique, threatened, endangered, and needs protecting?
6. To inform resource needs. What is potentially sustainably usable or exploitable — for food, as sources of pharmaceuticals, cosmetic, agricultural, or industrial (e.g., biocidal) biochemicals, or of other products (materials), as biological or agricultural control agents, or for genetic engineering, etc.? A complete inventory will give some predictive, as well as actual, capacity to answer these questions.
7. To inform biosecurity needs — the inventory will include invasive and other adventive species.
8. To help understand the origins of New Zealand's present-day biota, both ecologically and phylogenetically, and historic effects of climate change. The inclusion of fossil species in the symposium is regarded as crucial, and there is much that New Zealand neontologists and paleontologists can learn from one another.
9. To provide a means of gauging and prioritising the task of inventory of the remaining biota, for the training of biosystematists and allocation of resources. Known undescribed species in formal repositories will be included in the inventory, and estimates given of remaining undescribed species.
10. A public relations opportunity for biodiversity. As a millennial project it will give focus to New Zealand's national biodiversity, allowing it to be highlighted in the media, and to schools, etc.
11. To accomplish the aims of the Convention on Biological Diversity and to contribute to the New Zealand Biodiversity Strategy.
12. To provide a contribution to the global community. Scientists, conservationists, and others interested in biodiversity from a global perspective will appreciate having a complete documentation of the biodiversity of the New Zealand region, a hotspot of endemism (Mittermeier et al., 1997, 1998).

Arising out of the symposium will be one or two published volumes. Chapters will review major taxa and end-chapter appendices will list all known species, including undescribed labelled species in museum collections, in order to provide as accurately as possible an estimate of known species diversity. The checklists will serve as a platform for production of taxonomic databases, with subsequent emendations including the addition of synonyms and other data, to conform to the requirements of *Species 2000* International. New Zealand Crown Research Institutes (National Institute of Water & Atmospheric Research (NIWA), Landcare Research, Institute of Geological & Nuclear Sciences), and Museum of New Zealand will be the main holders of the improved taxonomic databases after the symposium, commensurate with the collections in their care. It is intended that the taxon checklists should be made available in electronic form, the details of which are still being worked out. For the present, the *Species 2000*: New Zealand URL is http://www.niwa.cri.nz/Species2000NZ/.

Beyond *Species 2000: New Zealand* — the Particular Challenge of Marine Biodiversity Inventory

As the most oceanic nation of significant size, New Zealand faces particular challenges in marine biodiversity assessment, living marine resources inventory, and a census of marine life. These are the challenges of sampling, taxonomy, databasing and analysis, policy, and education.

The sampling challenge

A major challenge is imposed by the large size of the New Zealand EEZ (4,053,049 million km^2), 15 times the land area, and possibly the fourth- or fifth-largest EEZ in the world. This challenge is exacerbated by the small population of New Zealand (ca. 3.8 million) and consequent limited resources for high-cost ocean survey and seafloor sampling. Historically, the New Zealand Oceanographic Institute (NZOI) (1954–92) and NIWA, into which NZOI was incorporated, achieved over 9000 benthic stations in the New Zealand region, of which 80 % were made in 0–1000 m depth and 16 % in 1000–2000 m. Despite the excellent density of stations achieved, the total area sampled scientifically by all NZOI/NIWA gear (trawls, dredges, epibenthic sleds, grabs, and corers, but excluding scuba) is only about 1.43 km^2. The addition of all equivalent museum and university sampling to this figure would increase the total to just less than 2 km^2 — about one two-millionth of the area of the EEZ (Nelson & Gordon, 1997). Research trawling by the former Ministry of Agriculture and Fisheries and its successor the Ministry of Fisheries, from 1961 to the present day, achieved more than 19,000 bottom-trawl tows, covering an area of >7400 km^2. Although these surveys added significantly to a knowledge of fish diversity, regrettably little bycatch was added to museum collections until recently. Further, the mesh size used in most trawl surveys (4 cm diameter) will have excluded most components of benthic diversity in terms of numbers of species (K. McKay, NIWA, pers. comm.).

There is some urgency in achieving increased sampling — the impact of commercial trawling appears to be having a significant negative impact on benthic habitats and diversity in New Zealand coastal waters (Battershill et al., 1998; Thrush 1998; Cranfield et al., 1999).

Solutions to the sampling challenge will include a combination of approaches, including increased use of remote technologies, increased quantitative sampling of selected areas of the seafloor (including the deep sea) and of the meiobenthos, application of statistical procedures to identify benthic assemblages and their characterising species, and assessment of the spatial extent of benthic assemblages in relation to sediment and hydrographic factors. Mapping of known benthic distributions (species and assemblages) will help prioritise where to conduct future sampling.

The taxonomic challenge

In New Zealand, as elsewhere, there is a shortage (or lack) of specialists for most taxonomic groups. For example, there is only one macroalgal systematist, and none for marine fungi, Cnidaria, or marine free-living Nematoda. This acute shortage must be urgently solved because most active systematists are older than 45, there is little training of new recruits, and no new systematic positions are available. Validation of shipboard identifications have yet to be carried out for many species records.

To ameliorate the problem, NIWA is working to increase the publication of more and varied identification products, and using overseas specialists to describe the New Zealand biota. It is intended that the *Species 2000*: New Zealand symposium should provide the impetus to formulate a strategy for prioritisation and capacity-building in systematics. From what is known and estimated about New Zealand's marine biodiversity, it will take ca. 87–100 years to describe the remaining species if the present rate of <100 new species/records per year continues.

Databasing and analytical challenges

Most of New Zealand's marine biodiversity data are non-quantitative, of the presence-absence type. For estuarine and shallow coastal areas, most biodiversity distributional data have not yet been captured electronically, residing in student theses and a range of published and unpublished reports. The reliability of many species identifications in these sources is variable. Most biodiversity data have not yet, or have only partly, been analysed (e.g., identifications may have been only to family or genus and few cluster analyses have been performed to ascertain relationships in assemblages). Much ancillary information (e.g., sediment type) has not yet been digitized, and existing databases need upgrading to accommodate new information fields and to permit linkages.

A recent development has been the formulation of a strategy by NIWA to improve biodiversity databasing. The strategy calls for implementation of a National Aquatic Biodiversity Information System (NABIS) (Glasby et al., 1999), with upgraded database systems, increased rate of capture of biodiversity data from published and unpublished sources, digitisation of untransformed ancillary data, and conformity to data-retrieval standards (e.g., ANSI Z39.50).

The policy challenge

In New Zealand there are too many disparate agencies and pieces of legislation relating to the marine environment (Nelson & Gordon, 1997; Weeber, 1998). As a consequence, there is no clear hierarchy of responsibility and no cohesive strategy or time-table for marine-protected areas. Both major political parties in New Zealand have suggested the development of a national oceans policy and simplification of the present complex legislation and management structures. These remedies should improve strategic planning for marine-protected areas and highlight the need for better marine-biodiversity information. Current mapping of the extent of New Zealand's legal continental shelf may lead to increasing the area of the EEZ by up to 20%, likewise highlighting the need to know more about indigenous living marine resources.

The educational challenge

There is a pressing need for more education concerning marine conservation values, but it is hard to make a case for better protection of marine ecosystems and habitats in the absence of hard scientific data about fishing impacts in most areas. Notwithstanding, information about impacts has been slowly increasing in recent years, both in New Zealand and overseas, which has led to a new Fisheries Act (1996) that, for the first time, explicitly acknowledges the need for knowledge about the ecosystems that support fisheries. In the meantime, there is a need for more reviews and syntheses of marine-biodiversity data and communication of findings to all potential users of the information. *Species 2000: New Zealand* will be a helpful contribution in this regard.

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Federal Information System Genetic Resources (BIG) – A National Approach in an International Context

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Abstract

Information requirements on genetic resources are included in the Convention on Biological Diversity as well as in the FAO Global Plan of Action for PGRFA. In Germany, these agreements will be implemented, *inter alia*, by establishing a set of related internet databases. The Federal Information System Genetic Resources (BIG) integrates databases on the wild flora of Germany, collections of botanical gardens, accessions of the largest German genebank, and relevant databases. The German initiatives are seen to be linked into the relevant international information systems. The FAO WIEWS, as amended in line with the International Undertaking for PGRFA, provides a conceptual framework in which German as well as other national and regional databases would be linked. Technologies developed for retrieval systems of distributed databases of the BIG project should offer new opportunities for the integration of national and regional databases in such a World Information Networking for PGRFA (WIN).

Key Words: Genetic resources, Database, Information management, Information systems, XML, Taxonomy

Introduction

International context

Information requirements on genetic resources are included in the Convention on Biological Diversity (CBD) as well as in FAO's Global Plan of Action (GPA). The CBD covers the conservation and sustainable use of biodiversity as two of its three objectives, along with the fair and equitable sharing of benefits arising from the use of genetic resources. Articles in the convention expect parties to facilitate exchange of information relating to conservation and sustainable use. In the case of plant genetic resources for food and agriculture (PGRFA), the same objectives are specified in the GPA. Its *Activity 17* (FAO, 1996) anticipates the construction of comprehensive information systems for plant genetic resources (PGR) to facilitate access to and management and utilization of PGR through the assembly, exchange, and provision of useful information. Thus, the challenge to establish information systems on genetic resources has been recognized internationally, necessitating national and international mandates and activities for implementation.

Information requirements on genetic resources

Biodiversity in the sense of the CBD and the GPA includes diversity at the level of habitats and ecosystems (including human-managed ecosystems for domesticated and cultivated species), as well as genetic diversity at the infraspecific level (e.g., varieties and cultivars) and species level. Conservation of biodiversity has to target genetic resources *in situ* as well as *ex situ*, i.e., in their natural or human-managed habitats, and in collections.

Information systems on genetic resources have to cover this range of diversity levels and reference sites. For the purpose of food production or other uses, such information systems should ideally contain factual data on the properties and performance of the genetic material. For the purpose of conservation and sustainable exploitation, georeferenced data on spatial patterns of biodiversity (species distribution, infraspecific or ecosystem variability in space) are desirable.

National Approach to Establish an Information System on PGR in Germany – the Federal Information System Genetic Resources

Aims and objectives

In Germany, the agreements mentioned above will be implemented, *inter alia,* by establishing a set of related internet databases; the Federal Information System Genetic Resources (BIG) integrates databases on the wild flora of Germany, collections of botanical gardens, accessions of the largest German genebank, and other relevant databases.

The objective of BIG is to integrate the available data on genetic resources provided by agencies of the federal ministries, universities, and other research institutions. BIG aims to provide easy access to these data for decision makers in public institutions (e.g., nature conservation services), for scientists in and outside universities, and for the interested public such as nongovernmental organizations. At the same time, BIG will be important for private industry, in particular breeding enterprises or companies dealing with natural plant substances.

Taking advantage of potential synergies, the BIG project (http://www.dainet.de/big/) aims to develop an integrated information system on plant genetic resources that covers a wide range of taxonomic, genetic, biological, ecological, economic, and geographical information. It will permit complex searches in heterogeneous, decentralized databases, and thus facilitate access to the actual germplasm *in situ* and *ex situ.*

Institutional collaboration

Four German institutions agreed to pool their extensive databases on wild and cultivated plants and their expertise in database management to establish BIG as an online information system on the Internet.

The German Federal Agency for Nature Conservation (BfN) at Bonn holds databases on the wild flora *(in situ),* species distribution and ecology, and the protection status of plant species according to national and EU legislation. It acts as the German Scientific Authority to CITES, the Washington species protection treaty.

The Department for Special Botany and Botanical Garden of the Ruhr University Bochum (RUB) documents the collections (*ex situ*) of botanical gardens in Germany on behalf of the Association of Botanical Gardens.

The Institute of Plant Genetics and Crop Plant Research (IPK) at Gatersleben performs basic research on cultivated plant taxonomy. It maintains a database of nearly 100,000 accessions of cultivated plants (*ex situ*), and is developing a database on "Mansfeld's World Manual of Agricultural and Horticultural Crops".

The Information Centre for Genetic Resources (IGR) within the German Centre for Agricultural Documentation and Information (ZADI) at Bonn has many years of experience providing information systems on the Internet. Besides a number of crop-specific databases, it manages the central German database on plant genetic resources on the Internet.

Technical Realization of BIG as a multi-database retrieval system

Information systems on genetic resources have to cover a wide range of taxonomic, genetic, biological, ecological, economic, and geographical data. Technology is needed, therefore, that can support an open, multipurpose, multiparticipant system. Technically this will be realized by a central view for accessing the online information system of various interlinked, but independent and heterogeneous, databases running under different hard- and software environments.

A user-friendly online interface allows one to query these different databases by a simple and common syntax. This user interface is part of the BIG WWW-server (Fig. 1, BIG's distributed Database Architecture) and can be used by any ordinary browser software. A BIG repository containing a reflection of different taxonomies (including synonyms) and a thesaurus will provide keywords like plant names or attributes (e.g., breeding traits) or other factual data like geographical references for searching the system. The WWW-server will send the query as an http-request to the so called BIG-Kernel (search agent). In the BIG-Kernel only one query will be composed using Extensible Markup Language (XML) as a general exchange format and sent to all relevant databases of BIG. Interfaces at each database will translate the XML-queries in local database syntax and local responses in XML-answers. The BIG-Kernel finally compiles one answer out of all XML-answers and sends this back to the user.

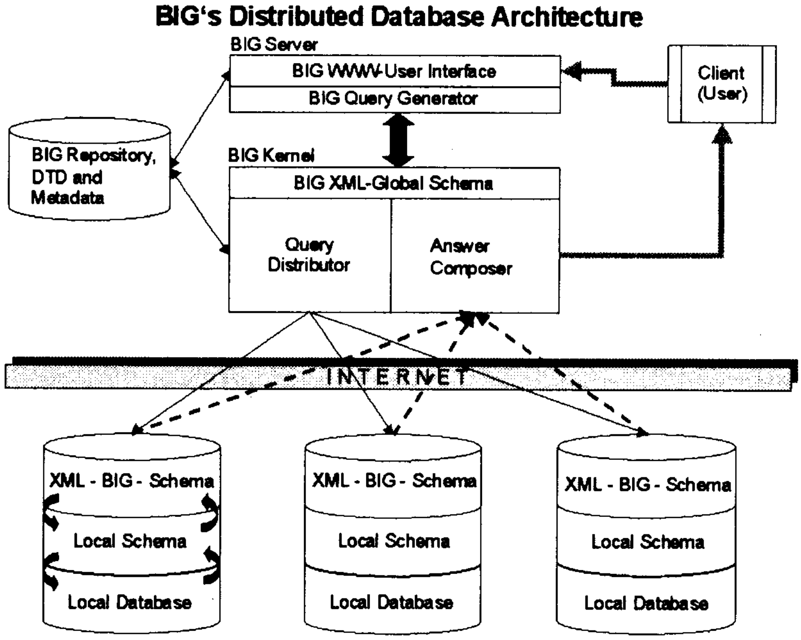

Fig. 1. BIG's distributed database architecture.

Integration of Geographic Information Systems (GIS)

As spatial analysis gets more and more important in the field of managing genetic resources, the need for geographic information systems (GIS) is tremendously growing. Visualisation and exploration of spatial data has to be easy and intuitive. A user-friendly GIS interface is therefore integrated in BIG.

Interactive maps allow the user to define a particular area of interest. GIS will transform the geometry of this area into geographic names or vice versa. This is needed, because the decentralized databases store different kinds of geo-objects. The user interface has, therefore, to compile different queries for each database. GIS is also used for visualisation and exploration of spatial data included in the result set, e.g., the result set includes distribution maps of a taxon on a global scale as well as on a national scale.

Figure 2 shows how GIS can be used to compare and to plan future collecting strategies of genebanks. For historical reasons, there are in Germany two main gene banks (Braunschweig and Gatersleben). The map in figure 2 shows the number of collected *Hordeum* samples of both gene banks distinguished by country of collection. Thus the regional focus of the two genebanks can be compared. Additionally, this helps to coordinate and plan future collecting missions and to identify gaps in the collections.

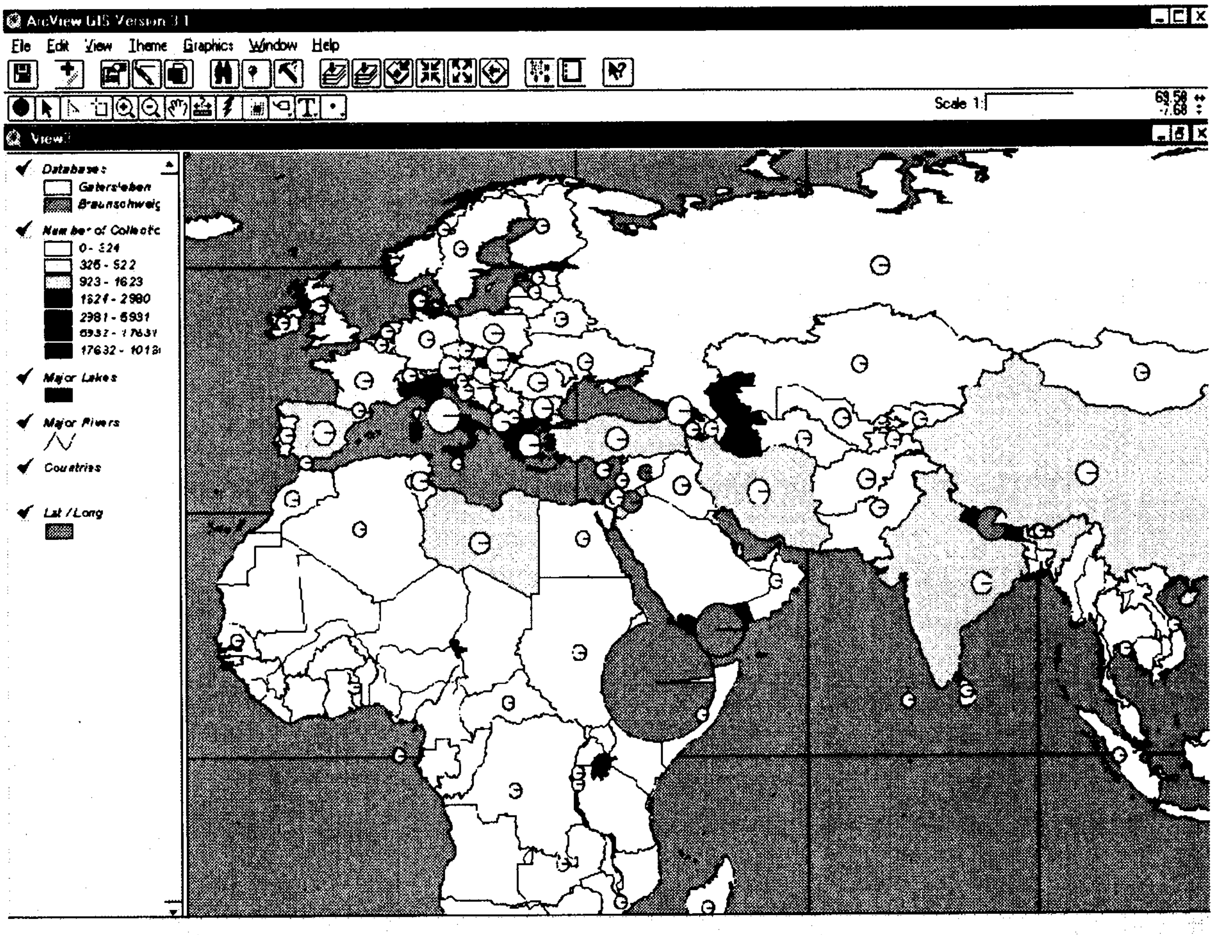

Fig. 2. Comparison of the number of collected *Hordeum* samples in both German genebanks distinguished by country of origin.

Added value through integration of associated databases

The Online-Information System for Evaluation Data EVA (http://www.genres.de/eva) provides specifics on the agronomic and breeding characteristics of germplasm in Germany. Beyond passport data on gene bank accessions, breeders and researchers can find reliable characterisation and evaluation information such as yield, agronomic performance, resistance, and quality from different sources (Harrer, 1999). Currently, the EVA prototype database consists of evaluation data for barley (11,500 accessions), potato (2,000 varieties), and fruit crops (mainly apple, 1,000 varieties). Once fully established, the two online information systems, BIG and EVA, will be integrated, thereby covering the full range of genetic resources *in situ* and *ex situ*, from evaluation data on agricultural crops to data on the distribution of endangered and protected wild species.

International Perspectives

The concept of BIG is generally applicable to taxon-related information. The methodology and tools that are under development for BIG can thus be easily transferred to other databases. The whole system is modular and the communication language XML is international and extensible. In this way, BIG will provide new opportunities for regional or international information networking such as information exchange within the framework of the FAO International Undertaking (under revision) and World Information and Early Warning System (WIEWS). The FAO/IPGRI Multicrop Passport Descriptors could be used as common fields for XML-linked national databases in order to develop a proposed World Information Networking on PGRFA (WIN/PGRFA).

A first step has been initiated between Germany (ZADI) and the USA (Germplasm Resources Information Network, GRIN) to develop a bilateral retrieval system over both national online databases. Another project, named EPGRIS (European Genetic Resources Information System) and coordinated by CGN in the Netherlands, could serve to complement this activity to establish a European Information Network with a central European view (EURISCO). Other participating institutions of EPGRIS will be BRC from France, IPGRI, INIA from Portugal, NGB from Sweden, RICP from the Czech Republic, and ZADI.

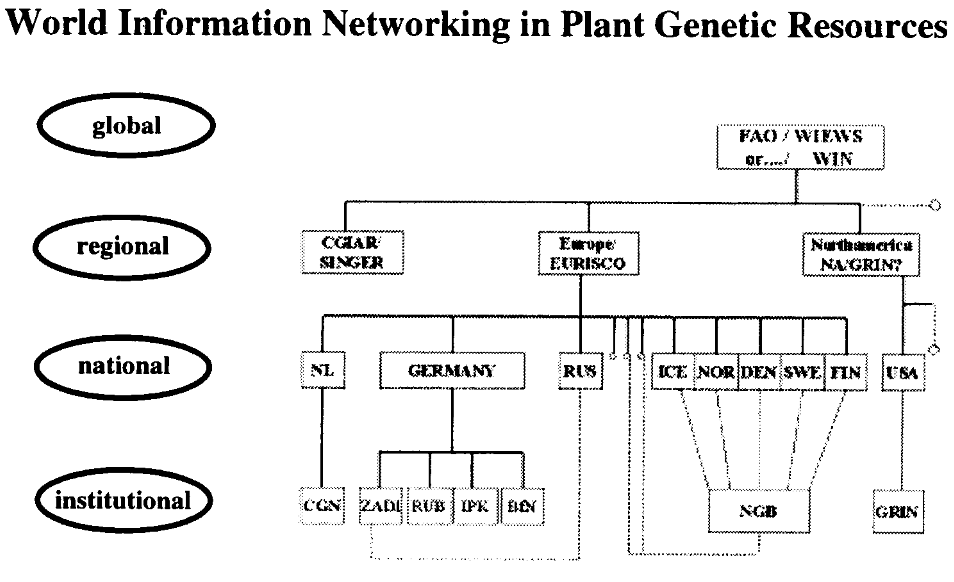
World Information Networking in Plant Genetic Resources

Fig. 3. Model of the proposed World Information Networking on PGRFA (WIN)

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Culture Collection of Microorganisms Networking in Indonesia

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Abstract

Indonesia as a tropical country contains diverse and potential microorganisms. However, awareness of the need for the conservation and sustainable use of these microorganisms is still low. There is no doubt that the role of culture collection in conservation of microorganisms is very important. In the past, several culture collections of microorganisms belong to universities, research institutes, and private companies exist in Indonesia. They have developed independently without any networking or coordination among them. They are actively collect and maintain the indigenous microorganisms related to their research interest in their institution, such as FNCC has mostly food related and industrial microorganisms, UICC with *Rhizopus* collections, BTCC its *Rhizobium* collection, Balivet and CCAM with their animal pathogen and DMUIJ with medical related microorganisms.

Initiated by several curators and researchers, who are involved in culture collection management, *Communication Forum for Indonesian Culture Collection Curators* (FORKOMIKRO) has been established since March 1996. The forum, which conduct regular meeting, represent a medium for members (1) to exchange ideas and experiences, as well as to solve common problems on CC management and (2) to assist the authorities in the implementation of the Convention on Biodiversity with respect to microorganisms.

Recently, sponsored by Yayasan Kehati (Foundation for Biodiversity) the Forum developed software to establish a database system among the members on general information of microbial collection. For the short run, collected database on microbial information, particularly indigenous microorganisms will be used to set up a directory for the indigenous collection. The long term run, the program will be used to browse the microbial information through Internet provider.

Key Words: Not assigned by the author.

Introduction

At present time, there are at least 50 laboratories in Indonesia which claim to have a collection of microbial cultures, most of them situated at Java island. These culture collections usually developed from the research activity at the laboratory, small scale, shortage of expert, facilities and funding. Uncompleted identification of the indigenous cultures and simple method for preservation are common in these culture collections.

About 15 collections are registered at the WFCC-Word Data Center for Microorganisms, but only few culture collections meet the requirement of functional service culture collection. Among these culture collections only few had published lists of their microbial collection (Balitbangtan, 1995; IPB 1996; PAU Pangan dan Gizi-UGM, 1996; PERMI, 1993; Puslitbangbiol-LIPI, 1996).

Initiated by several curators and researchers, who are involved in culture collection management, ***Communication Forum for Indonesian Culture Collection Curator (FORKOMIKRO)*** was established in March 1996 with the sponsorship of Non-Governmental Organization: *Yayasan Kehati* (Foundation for Biological Diversity). FORKOMIKRO is an informal group of curators and researchers who have interest in culture collection of microorganisms. The objectives of FORKOMIKRO are: 1) to serve as a medium for exchange ideas and experiences, as well as to solve common problem on culture collection management; (2) on voluntary basis or upon request from interest client, provide consultation and recommendation to solve problem of culture collection; (3) to assist the authorities in the implementation of the Convention on Biodiversity with respect to microorganisms. At present time for regular meeting, this group is supported by the Foundation for Biological Diversity.

Establishing Microbial Database Among Indonesian Culture Collection

To set up a directory for microbial collection, a microbial database application for general information of microbial collection was established. At least 9 leading culture collections used this database to store and access the general information of their collection, particularly the indigenous ones.

Microbial database application, contain of:

1. Microbial data sheet (to manage the microbial collections data) :
   Page 1:
   - Depositor: Name, Institution, Address, Phone/Fax, E-mail.
   - Isolation and historical: Isolated by, Isolation number, Substrate or Host (Habitat), Geographic sources, Identified by, Institution, Date of identify, History since isolation.
   - Culture deposit and derived from: Culture also deposited at, Accession number(s) in other collection, etc.

   Page 2:
   - Media, method, and pathogenicity: medium, optimum temperature, dark/light, special requirement, recommended method(s) for preservation, and strain pathogenicity.
   - Deposition, use and references: reason for deposition, special use properties (production of, assay of and other) and references.
   - Distribution and remark: fee or restricted, remark/comment.

   Page 3:
   - Microscopic figure: 10 x, 100 x, 1000 x
2. Preparing data for internet transfer. Data communication from each culture collection to data collection center may be sent through Internet or modem.
3. Preparing data for disk transfer. In case of Internet transfer unavailable, disk transfer may be used to send data collection center.
4. Getting data from Internet transfer. Data from internet transfer may be taken and combined with data from certain location.
5. Getting data from disk transfer. Data from disk transfer may be combined with other data from certain location.
6. Blank microbial database. Microbial file may be emptied.
7. Password management. Every user has his/her own password. User may change the password.

Result obtained from this program is a database of the indigenous collection kept at a data collection center (FNCC, IUC Food and Nutrition, Gadjah Mada University) as well as FORKOMIKRO members. For this time being, only 9 culture collections become active member of FORKOMIKRO and store their collections in this database. List of member and their collection is presented in Table 1. Most of these culture collections located at Jakarta the capital city and surrounding (Bogor and Bandung), West Java, and one of them located at

Yogyakarta (Middle of Java). Four of them belong to the University (University of Indonesia - Jakarta, Institute of Agriculture Bogor (IPB - Bogor) and Gadjah Mada University - Yogyakarta), while the others are research centers or company belong to Government Institution.

Due to the limitation of fund, published catalog named: *List of cultures of Indonesian Microorganisms* (1999) only consist of information about: name of species/genus, culture collection accession number and source of collection in the 9 culture collections. Total number of cultures in this List (presented in Table 1) is 1930 strains, with the number of bacteria of 990 strains which belong to 34 genera and 105 species, yeast of 93 strains belong to 9 genera and 34 species, and 847 strains of mold belong to 61 genera and 120 species.

Food and Nutrition Culture Collection

Food and Nutrition Culture Collection (FNCC) is the most recently established culture collection in Indonesia. It was planned and conceptualized in 1985, coinciding with the establishment of the Inter University Center (IUC) of Food and Nutrition at Gadjah Mada University. However, its realization of establishment of FNCC came in 1991. The primary function of FNCC is to collect, characterize, preserve and supply authentic, pure and viable cultures of microorganisms with food and industrial significance. It also serves to contribute the development of education and research related to food microbiology. Occasionally, it offers training courses to microbiologist and technicians regarding fundamental techniques involved in microbial research. To date as shown in Table 1 FNCC maintains a total of 631 indigenous microbial cultures (in the catalog List) and more than 2.000 fungal cultures (not in the list). Cultures were kept in glycerol at – 80 °C and in ampoules (dried specimen). At present, FNCC research deals mainly with lactic acid bacteria. Isolation and identification of lactic acid bacteria as well as their application to food fermentation have been done in cooperation with Japanese and American scientists.

Table 1. FORKOMIKRO member and their indigenous collection (1999)

No	Acronym	Full name, Institution	Cultures held				
			Bacteria	Yeast	Mold	Total	Main collection
1	BCC	Balitvet Culture Collection Veteriner Res.Inst. Bogor	161	6	34	201	Animal pathogenic bacteria (*Salmonella, E.coli, Clostridium*)
2	BFCC	Bio Farma CC, Bandung	0	0	0	0	
3	BTCC	Biotechnology CC, LIPI, Cibinong	197	0	0	197	Lactic acid bacteria, Acetic acid bacteria
4 (U)	FNCC	Food and Nutrition Culture Collection, IUC Food and Nutrition, Gadjah Mada Univ., Yogyakarta	266	0	355	621	Lactic acid bacteria, *Aspergillus, Penicillium, Fusarium, Trichoderma*
5 (U)	IPBCC	Institut Pertanian Bogor CC	0	0	30	30	Fungi
6	LIPIMC	LIPI Microbial Collection, LIPI, Bogor	267	25	267	559	*Rhizobium Aspergillus Penicillium, Mucor*
7 (U)	MUI	Lab. of Microbiology , FKUI Univ. Indonesia, Jakarta	91	0	0	91	Human pathogenic bact. (*Streptococcus, Staphyl. Salmonella*)
8	PAIR-CC	Center for the Appl. Of Isotopes & Rad. P3TIR BATAN, Jakarta	8	0	0	8	
9 (U)	UICC	University of Indonesia Culture Collection , FMIPA-UI Jakarta	0	62	161	223	Rhizopus, Aspergillus
Total				93	847	1930	
Total number of genera			34	9	61		
Total number of species			105	34	120		

(U) = University

Conclusion

In order to promote and conserve biodiversity, the preparation of indigenous microorganism's database collected by Culture Collections in Indonesia is one of the urgent steps. Establishment of culture collection networking will facilitate the improvement of culture collection management and global biodiversity information.

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Microbial Information Network of China (MICRO-NET)

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Abstract

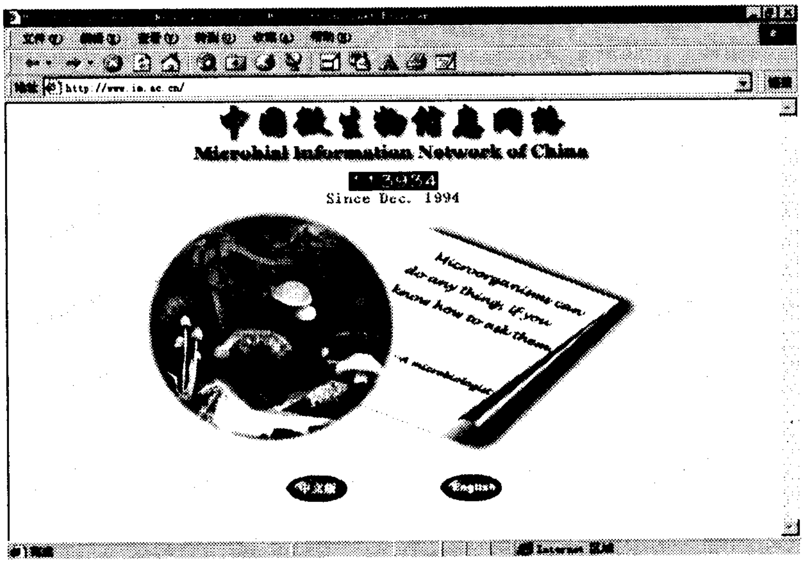
Microbial Information Network of China (MICRO-NET) is from 1994, primitively supported by State Key Laboratory of Microbial Resources, Scientific Database Project and Biodiversity Committee of Chinese Academy of Sciences (CAS). The main aims of MICRO-NET are to collect, arrange and share information resources about microorganisms that located in China. Several tens databases for typical microorganisms in China are constructed. It is also important to introduce newest international biological information to Chinese scientists. Now China Node of International Bio-Mirror Network is located in our center. DDBJ/EMBL/GenBank and several tens international databases are mirrored. *Species-Info* is a special meta search engine to help biologists more easily and more efficiently find biological species information in Internet. Besides the increasing of data and quality users, better computing and network environment is needed. From July 2000, in MICRO-NET some software with large number of users will be set up in super computer, and some important databases will be shared in the national high performance academy network environment. The URL of MICRO-NET is http://www.im.ac.cn, which is the biggest web site in microbiology field in China.

Key Words: Microorganism, Network, Meta Search Engine

China is the country with rich microbial diversity. Chinese have long history to use microbial in industry, agriculture and medicine. Microbial Information Network of China (MICRO-NET) was founded in 1994. Its purposes are to collect and share microbial information resources in China, and to introduce the popular foreign information resources to Chinese scientists.

Our studies are mainly divided into 3 parts: database development, bio-informatic study and special software development. It is the most important works for us to collect the information for the typical microbial resources in China, and create their databases. From 1997, we started to work on bio-informatic databases, such as DDBJ/EMBL/GenBank databases.

Now MICRO-NET and its information resources are financially supported State Key Laboratory of Microbial Resources, Scientific Database Project, Biodiversity Committee, Committee for Type Culture Collection of Chinese Academy of Sciences, China Committee for Culture Collections of Microorganisms, National Natural Science Foundation of China(NFSC), and Ministry of Science and Technology.



MICRO-NET Homepage

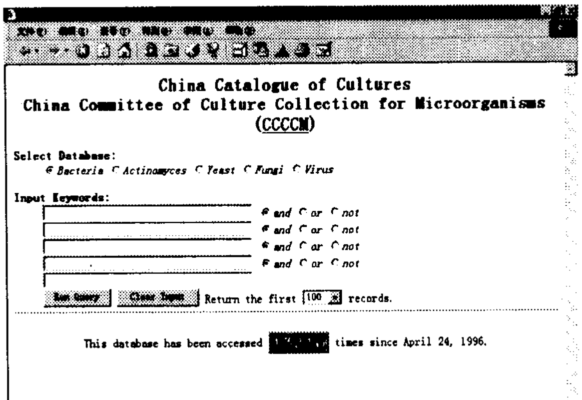
1. Database Development

• Database of China Catalogue of Cultures

CCCCM (China Committee for Culture Collections of Microorganisms) is the only federation for national culture collections in China. In CCCCM, there are twelve national culture collections divided into general microbiological, agricultural, industrial, medical, antibiotic, veterinary and forestry centers, see Table 1 below. The China Catalogue of Cultures (English version) includes 10,716 strains of bacteria, actinomyces, yeast, fungi, and viruses. All the information in this database are online in MICRO-NET, see Fig. 1.

• Database of Type Cultures of the Chinese Academy of Sciences

The Committee on Type Culture Collection of CAS (CTCCCAS) was organized in April, 1996. There are seven Culture banks under CTCCCAS, namely, Microbial Culture Bank, Cell Bank, Gene Bank, Virus Bank, Kunming Cell Bank, Freshwater Algae Bank, and the Rare, Endangered and Endemic Plant Germplasm Bank, see Table 2 below. The Marine Biological Germplasm Storehouse and In Vitro Plant Germplasm Collection are now in the process of being established. Up to the present, 15,418 cultures have been collected and online now, see Fig. 2.


China Catalogue of Cultures
China Committee of Culture Collection for Microorganisms
(CCCCM)

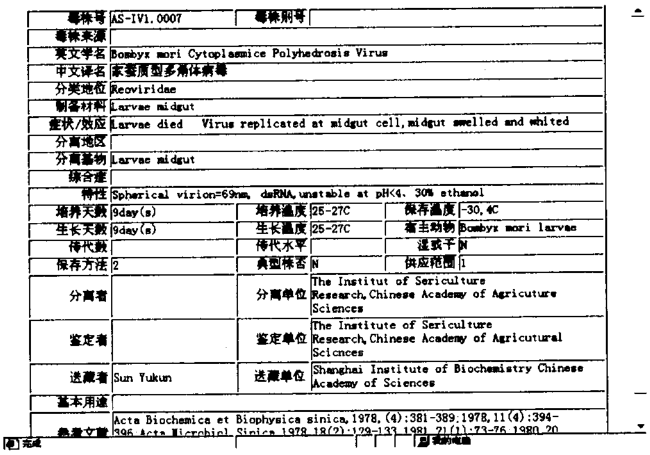
Select Database:
● Bacteria ○ Actinomyces ○ Yeast ○ Fungi ○ Virus

Input Keywords:
● and ○ or ○ not
● and ○ or ○ not
● and ○ or ○ not
● and ○ or ○ not

Return the first 100 records.

This database has been accessed [illegible] times since April 24, 1996.

Fig. 1. CCCCM search menu

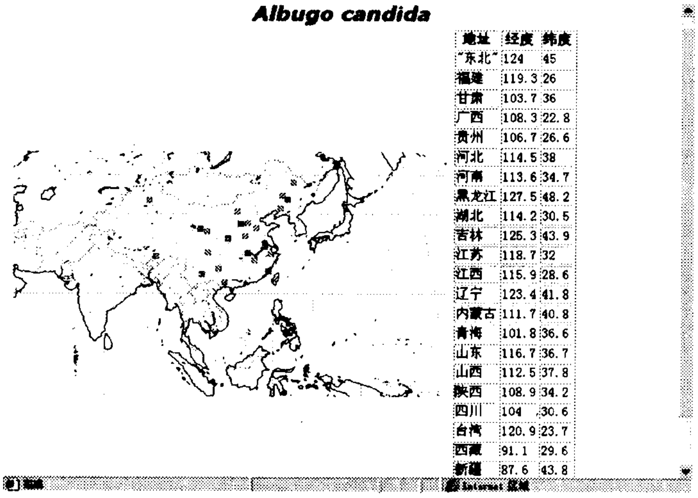


毒株号	AS-IV1.0007	毒株别号			
毒株来源					
英文学名	Bombyx mori Cytoplasmice Polyhedrosis Virus				
中文译名	家蚕质型多角体病毒				
分类地位	Reoviridae				
制备材料	Larvae midgut				
症状/效应	Larvae died Virus replicated at midgut cell, midgut swelled and whited				
分离地区					
分离基物	Larvae midgut				
综合症					
特性	Spherical virion=69nm, dsRNA, unstable at pH<4、30% ethanol				
培养天数	9day(s)	培养温度	25-27C	保存温度	-30, 4C
生长天数	9day(s)	生长温度	25-27C	宿主动物	Bombyx mori larvae
传代数		传代水平		湿或干	N
保存方法	2	典型株否	N	供应范围	1
分离者		分离单位	The Institut of Sericulture Research, Chinese Academy of Agricuture Sciences		
鉴定者		鉴定单位	The Institute of Sericulture Research, Chinese Academy of Agricutural Sciences		
送藏者	Sun Yukun	送藏单位	Shanghai Institute of Biochemistry Chinese Academy of Sciences		
基本用途					
参考文献	Acta Biochemica et Biophysica sinica, 1978, (4):381-389; 1978, 11(4):394-396 Acta Microbiol. Sinica 1978 18(2):129-133 1981 21(1):73-76 1980 20				

Fig. 2. Example of virus database search menu

- **Database of Inventory of Fungi Species**

There is information on 6,500 fungi, including Latin name, Chinese name, host, isolated places, and references. A distribution map of each species can be made automatically.



Albugo candida

地址	经度	纬度
"东北"	124	45
福建	119.3	26
甘肃	103.7	36
广西	108.3	22.8
贵州	106.7	26.6
河北	114.5	38
河南	113.6	34.7
黑龙江	127.5	48.2
湖北	114.2	30.5
吉林	125.3	43.9
江苏	118.7	32
江西	115.9	28.6
辽宁	123.4	41.8
内蒙古	111.7	40.8
青海	101.8	36.6
山东	116.7	36.7
山西	112.5	37.8
陕西	108.9	34.2
四川	104	30.6
台湾	120.9	23.7
西藏	91.1	29.6
新疆	87.6	43.8

- **New Species of Fungi in China**

In this database, we collect information on fungi new species that Chinese scientists have published in Chinese journals. The full text of the original paper on which the new species was published is available in the database.

- **Economic Fungi of China**

We have collected 1,000 fungi with the information on Latin name, Chinese name, taxonomy position, description of behavior and shape, usage and contents of traditional Chinese medicine. All the records have a black/white picture, and some records have color pictures.

- **Electronic version of Flora Fungorum Sinicorum**

The electronic version of **Flora Fungorum Sinicorum** is under structure. From this database, reader can get the full text of each volume including pictures, search every field. Each species name in **Flora Fungorum Sinicorum** is linked to its related species level information in MEDLINE, DDBJ/EMBL/GENBANK, US and Japan patents information, more than one hundred online journals.

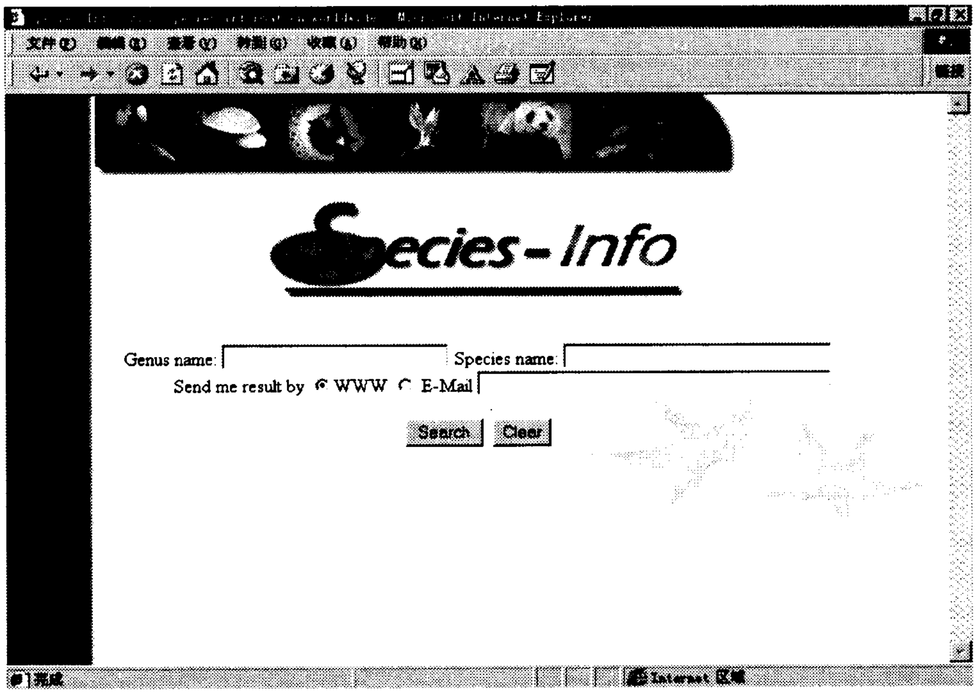
2. Bio-informatic Study

Bio-Mirror is a project under APAN (Asia Pacific Advanced Network). The China Node of ***International Bio-Mirror Network*** is set up in our center. We started to mirror some important international databases in 1997. International Nucleotide Sequence Database (DDBJ/EMBL/GENBANK) is one of them, and this database in our web site is daily updated. A search function is available for it using WAIS. From 2000, we started to use SRS for full text search. In 2000, we started to upgrade our system into a super computer, more and more databases will be mirrored. We also join the national hi-technology project for bio-informatic databases in China.

3. Software Development

Network has become an indispensable tool for daily research study. There are huge number of biological species information in the Internet, such as catalogue information, culture collection information, literature information, genetic information and so on.

We are developing a meta search engine named SPECIES-Info to help biologists find species information in Internet more easily and more efficiently. In *SPECIES-Info*, we focus the information worldwide on culture collection, online journals, genetic data, patents and so on. User just input a species name, then SPECIES-INFO can seek the information on this species automatically, and bring back all the search results together in one html page. All the information that SPECIES-INFO can search at this moment is divided into 7 groups. They are Strain/Cultures Worldwide, Culture Collections Worldwide, Genetic Data, Literature Information, Bacteria Nomenclature, Patent Information and others. In the near future, XML and COLBA will be used for *SPECIES-Info.*



Send me result by ● WWW ○ E-Mail

Acknowledgements

We express the appreciation to State Key Laboratory of Microbial Resources, Scientific Database Project, Biodiversity Committee, Committee for Type Culture Collection of Chinese Academy of Sciences, China Committee for Culture Collections of Microorganisms, National Natural Science Foundation of China(NFSC), and Ministry of Science and Technology for supporting MICRO-NET.

Table 1. China Committee of Culture Collection of Microorganisms

1. **China General Microbiological Culture Collection Center** (CGMCC)
    - Institute of Microbiology, Chinese Academy of Sciences, Beijing
    - Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan
2. **China Agricultural Culture Collection Center** (ACCC)
    - Institute of Soil and Fertilizers, Chinese Academy of Agricultural Sciences, Beijing
3. **China Industrial Culture Collection Center** (CICC)
    - Institute of Food and Fermentation Industry, Ministry of Light Industry, Beijing
4. **China Medical Culture Collection Center** (CMCC)
    - Institute of Dermatology, The Chinese Academy of Medical Sciences, Nanjing
    - National Institute for the Control of Pharmaceutical and Biological Products, Ministry of Public Health, Beijing
    - Institute of Virology, The Chinese Academy of Preventive Medicine, Beijing
5. **China Antibiotic Culture Collection Center** (CACC)
    - Institute of Medicinal Biotechnology, The Chinese Academy of Medical Sciences, Beijing
    - Sichuan Institute of Antibiotic, Chengdu
    - Institute of Antibiotics, North-China Pharmaceuticals Factory, Shijiazhuang
6. **China Veterinary Culture Collection Center** (CVCC)
    - National Control Institute of Veterinary Bio-products and Pharmaceuticals, Ministry of Agriculture, Beijing
7. **China Forestry Culture Collection Center** (CFCC)
    - Institute of Forestry , The Chinese Academy of Forestry Sciences, Beijing

Table 2. Committee on Type Culture Collection of Chinese Academy of Sciences

1. **Strain Bank:** Institute of Microbiology of CAS, Beijing
2. **Cell Bank:** Institute of Cell Biology of CAS, Shanghai
3. **Kunming Cell Bank:** Kunming Institute of Zoology of CAS, Kunming
4. **Gene Bank:** Research Center of Biotechnology of CAS, Shanghai
5. **Virus Bank:** Institute of Virology of CAS, Wuhan
6. **Freshwater Algae Bank:** Institute of Hydrobiology of CAS, Wuhan
7. **In Vitro Plant Germplasm Collection:** Institute of Botany of CAS, Beijing
8. **Marine Biological Germplasm Storehouse:** Institute of Oceanology of CAS, Qingdao
9. **Rare, Endangered and Endemic Plant Germplasm Bank:** Xishuangbanna Tropical Botanical Garden, Xishuangbanna

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Conservation and Sustainable Management of Biological Resources in Malaysia – Current Status of Plant Resource Information

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Abstract

Malaysia is one of the twelve megadiverse countries and is home to a vast diversity of plant species. The cradle of the country's diversity is the bountiful range of habitats and ecosystems found from the lowlands to the mountain summits. The number of flowering plants ranges from 8,500 species in Peninsular Malaysia to 12,500 species in East Malaysia (Sabah and Sarawak) while the number for ferns and fern allies is ca. 1,100 species. Endemism in the tree species is recorded at 26% for Peninsular Malaysia while endemism in a number of predominantly herbaceous families is as high as 80%. Despite the remarkable amount of information that has already been acquired, there are still visible gaps such as the little known diversity of species in families with non-commercial species and plant diversity from East Malaysia. Attempts are on-going to address these gaps and, lately, concerted efforts are being put in by research organisations, universities, government agencies and non-governmental organisations to translate this information into electronic format. Databases for many different groups of biological organisms found in Malaysia are already in place. This paper provides some examples of such databases and the problems of networking between databases.

Key Words: Documentation, Networking, Botanical Research And Herbarium Management System (BRAHMS)

Introduction

Malaysia's superabundant biological diversity is regarded as one of the world's greatest natural heritages. The many types of forests, both climatic and edaphic, support their own unique vegetation. Peninsular Malaysia has an estimated 8,500 species of flowering plants (Turner 1995) while Sabah and Sarawak in Borneo have an estimated 12,500 species (Anon. 1998). The number of species of ferns and fern allies is estimated at 1,100 while Malaysia has about 10% of the total species of orchids in the world (Lamb 1991). For animal species, the country is a proud home to some 300 species of wild mammals, 700–750 species of birds, 350 species of reptiles, 165 species of amphibians and more than 300 species of freshwater fishes (Anon. 1998).

Due to the many varieties of ecotypes, the plant endemicity here is one of the highest in the world. In the project to document the tree flora of Peninsular Malaysia, at least 26% of the indigenous tree species were discovered to be endemic to this peninsula, with many of them being rare (Ng 1990). For families with predominantly herbaceous plant species such as Begoniaceae, Gesneriaceae and Acanthaceae, the percentage of endemism can be as high as 96% (Kiew 1991). Many of these species are very local in distribution and are found in a restricted number of localities. For orchids, over 200 species, i.e. 24% of Malaya's estimated number of species, have some degree of rarity (Lamb 1991; Seidenfaden and Wood 1992). Figures for Sabah and Sarawak are widely expected to be much higher for all groups of plants because of the greater diversity of habitats, ecotypes and geological affinities.

Status of Plant Resource Information

There has been a long history of collection and documentation work in Malaysia. In Peninsular Malaysia, which was at that time known as Malaya, earliest substantive materials on plants collected were made by King and Gamble in their 'Materials for the Flora of the Malay Peninsula' (1889–1915). This represented the earliest efforts to systematically compile botanical monographs, notes and diaries of collectors including the vast information contained in preserved specimens. Collectors who had collected extensively in Malaya before and during this time included Nathaniel Wallich, Alexander Carroll Maingay, William Griffith, Hermann Kunstler, Berthold Scortechini, Leonard Wray, Nathaniel Cantley and Richmond William Hullett. The remarkable effort by King and Gamble set the motion going for further work. Based on King and Gamble's account, H. N. Ridley published the 'Flora of the Malay Peninsula' (1922–1925), a five volume account covering all known Malayan species of Angiosperms and Gymnosperms. An early publication on the uses of indigenous groups of plant species was 'The Dictionary of Economic Products of the Malay Peninsula' (Burkill 1935). Since then, there has been an array of publications for various families and groups of plant species. Some of the more recent noteworthy publications include 'Foresters' Manual of Dipterocarps' (Symington 1943), R.E. Holttum's work on 'The Flora of Malaya, Vol. 1 – Orchids' (1953) and 'Vol. 2 – Ferns (1954)', H.B. Gilliland's 'The Flora of Malaya, Vol. 3 – Grasses' (1971), 'A Manual of the Rattans of the Malay Peninsula' (Dransfield 1979) and 'The Bamboos of Peninsular Malaysia' (Wong 1995). In Sabah and Sarawak, the earliest significant efforts at plant documentation began in the early 19th century (Soepadmo and Wong 1995). The earliest systematic account was by Stapf (1894) on the plant life of Mount Kinabalu in Sabah. Numerous papers on Bornean plant taxa were produced subsequently. In 1921, E.D. Merrill published the first bibliographic enumeration of the Bornean seed plants, listing some 4,924 species excluding the orchid species. His account was later revised by Masamune (1942) and further additions were made by Merrill in 1950. Despite these impressive enumerations, however, Borneo remained deprived of a comprehensive flora of any kind and a concise checklist of species. It is for this reason that the 'Tree Flora of Sabah and Sarawak' project was initiated in the early 1990s, to document and update the taxonomic status of all tree species native to the states.

Improving Data Management and Information Retrieval

The vast amount of information on Malaysia's biological diversity that had been collected throughout the centuries was, until recently, stored in the form of herbarium and museum specimens, reports, diary records, log books and other printed often obscure publications. While these materials are of great importance, the baseline information they contain is often difficult and cumbersome to access and extract because of the rigid structural and physical management of information. The inflexibility to 'juggle and capture' information for different purposes has long been recognised as a non-essential barrier but little could be improved until the advent of computers. Now, computers and database software enable us to build species- and resource-based databases for wide-ranging purposes. These databases are used to monitor growth and yield, derive revenue estimates, improve silvicultural treatments, generate diversity checklists and taxonomic monographs and monitor biological resources. They are, in essence, ultimate tools for managing and conserving biological diversity and natural resources.

Information on vascular plant diversity for Peninsular Malaysia is currently available on the Internet at the following address http://biodiversity.ukm.my/catalog/FloraMalaya. Resource databases for some agricultural crops, ornamental plants and marine flora are available in different formats while others are still under development. These are held in the universities, research institutions, government agencies and non-governmental organisations. These databases will eventually be linked to a website based at the national focal point for the Clearing-House Mechanism (CHM), which is under the auspices of the Convention on Biological Diversity.

Development and Growth of Databases - Some Examples

A database containing information on Malayan plant species is being developed at the Forest Research Institute Malaysia. Networked with other herbaria in the region such as those in Singapore, in Kuching, Sarawak, and in Sandakan, Sabah, this database, when completed, will provide end-users with various sorts of information ranging from general accounts to plant distribution patterns, taxonomic monographs and species checklists. This database, developed with the software known as BRAHMS (Botanical Research and Herbarium Management System) and using the herbarium specimen as the unit, contains information ranging from its occurrence, taxonomic status and nomenclature accounts, collecting notes, abundance and conservation status. BRAHMS includes dictionaries of valid plant names and collectors, and a gazetteer, and is linked to mapping and GIS applications. Primary outputs of BRAHMS include plant checklists, specific or general species distribution patterns. Overlaid with current land-use patterns, topography maps and forest types and forest resources maps, these visually aided outputs present a crucial tool for conservation planning, management and education.

An information management system with GIS and mapping capabilities is currently under construction at the Forest Department Peninsular Malaysia. The areas that are being computerised are planning, operation, resources, revenue, mapping and remote sensing. This project when completed will play a central role in integrating forest resource information, thereby superseding old generation databases and ad hoc data structures.

Future Work and Prospects

Much work is needed in terms of linking all the various databases on biological diversity to the national CHM website. For some institutions, the inadequacy of telecommunication infrastructure, hardware facilities and trained technical support group is a major concern. Other problems include the use of different software applications and data storage methods. Once these can be overcome, prospects for information transfer for a variety of purposes become infinite.

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Indonesia-Japan Collaborative Study on the Biodiversity of Lactic Acid and Acetic Acid Bacteria in Indonesia

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Abstract

Study had been conducted on the taxonomy of lactic acid and acetic acid bacteria isolated from a variety of traditional fermented products and related raw materials, as well as improvement of culture collection system in Indonesia. This study was part of a cooperative project between the New Energy and Industrial Technology Development Organization/Japan Bioindustry Association (NEDO/JBA), Japan and Badan Pengkajian dan Penerapan Teknologi (BPPT), Indonesia on the conservation and sustainable utilization of tropical biological resources which run for four years, from 1995 to 1999. The aims of the study were to elucidate the diversity, the dispersal/ distribution, the taxonomy, and the economic potentials of lactic acid and acetic acid bacteria from Indonesia. In addition, the study also attempted to improve the culture collection system to preserve the cultures obtained. The scope of the study included research and its supportive activities such as exchange of researchers, scientific meetings, provision of essential equipment, and improvement of culture collection and microbial database management. During the course of the study an exchange of respectively five Indonesian and five Japanese researchers had taken place. Moreover, a number of essential laboratory equipment had been provided by the Japanese partner, and a number of scientific meetings had been attended by both the Indonesian and Japanese researchers to present results of their research. A total of 115 acetic acid and 227 lactic acid bacterial cultures belonging to *Acetobacter, Gluconacetobacter*, *Gluconobacter, Enterococcus*, *Lactobacillus, Leuconnostoc, Pediococcus*, and *Streptococcus* had been isolated. As a result of the study a new genus of acetic acid bacteria with the generic name *Asaia* was proposed comprising two new species, respectively *Asaia bogorensis* and *A. siamensis.* Moreover, the classification of the acetic acid bacteria group had been revised in which eight new species, i.e. *Acetobacter indonesiensis* , *A.tropicalis*, *A. orleanensis*, *A. lovaniensis*, *A. estunensis*, *A. roseisyzygii*, *A. cibinongensis*, and *A. orientalis* had been proposed. In addition to the collection of cultures, system for their maintenance in a culture collection had been developed. Results of the study had been published in a number of scientific journals or presented in scientific meetings.

Key Words: Biodiversity in Indonesia, Lactic Acid Bacteria, Acetic Acid Bacteria

Introduction

Rapid Indonesian economic development tends to bring to the declining environmental quality and genetic resources erosion. Being a tropical country and one of the world megabiodiverties, Indonesia needs to take serious action to minimize the undesirable impact of natural resource utilization on its national economic development as well as the survival of its ecosystem.

With respect to microbial resources, two major important groups with high economic potentials, i.e. the lactic acid and acetic acid bacteria deserve our attention. Despite their economic importance, knowledge on their diversity, particularly their wild relatives, is very limited. Only a very small proportion of members of these two groups have been studied and preserved in culture collections in Indonesia.

The aims of the study were to elucidate the diversity, the dispersal/distribution, and the taxonomy of the economically potential lactic acid and acetic acid bacteria from Indonesia. The study is part of a cooperative project between the New Energy and Industrial Technology Development Organization/Japan Bioindustry Association (NEDO/JBA) from Japan and Badan Pengkajian dan Penerapan Teknologi (BPPT) from Indonesia on the conservation and sustainable utilization of tropical biological resources.

Material and Methods

The study was collaboratively carried out by a team consisted of respectively five researchers from the Department of Applied Biology and Chemistry, Faculty of Applied Bioscience, Tokyo University of Agriculture, and five researchers from the Research and Development Centre for Biotechnology, Indonesian Institute of Sciences, Cibinong-Bogor, Indonesia.

There were two components of the study, i.e. (1) Research, which included collection of samples of a variety of traditional fermented products and related materials representing the habitat of lactic and acetic acid bacteria, e.g. soil, fruits, feeds, etc.; isolation, purification, and preliminary identification of the isolates; detailed taxonomic study based on chemosystematic and DNA analysis of scientifically interesting strains, and (2) supporting activities associated with the implementation of the study such as exchange of Indonesian and Japanese experts, organizing scientific meetings, provision of needed equipment, and exchange of information on culture collection maintenance, cultures and microbial data.

The study was started in 1995 and continued for four years. During the first three years the activities included collection of samples from different locations in Indonesia, isolation and preliminary identification of the isolates. These activities were mostly done in Indonesia. For the next three years as of 1996, detailed taxonomic study of the cultures was conducted in Indonesia and in Japan.

Exchange of five Indonesian and five Japanese researchers took place in 1995/96, 1996/97, 1997/98, and 1998/99. During each visit an informal meeting was held to discuss the progress of the study.

Two formal meetings were organized by NEDO/JBA in Tokyo, in 1998, respectively: (1) International Forum on Conservation and Sustainable Use of Tropical Bioresources, 9-10 November, with the objectives to evaluate results of research cooperation between NEDO/JBA (Japan) and its partners in Indonesia, Malaysia and Thailand; (2) International Symposium on Access and Benefit Sharing of Bioresources, 11 November, to discuss on access and benefit sharing of the results of the cooperative research.

Bacterial cultures were isolated from a variety of samples, such as tropical fruits (alpuket - *Persea americana*; belimbing - *Averrhoa bilimbi;* jambu air - *Eugenia aquea*; jambu bol - *Eugenia malaccensis*; markisa - *Passiflora laurifolia*; papaya - *Carica papaya;* sawo - *Manilkara kauki;* sirsak/soursop - *Anona muricata*); different kinds of flowers; palm (*Arenga pinnata*) flower sap; traditional fermented products (dadih, tape singkong, tape ketan hitam, tempe, oncom); moromi; ragi; nata de coco; and tahu/tofu. These samples were collected from different locations in West Java; Central Java; Yogyakarta; East Java; Bali; Lombok; Riau (Sumatra), West Sumatra; Sanggau (Kalimantan); and Sulawesi.

Results

By the end of the study in 1999, over 342 bacterial cultures had been isolated. Preliminary identification of these cultures showed that 115 cultures belong to the acetic acid bacteria and the remaining 227 to the lactic acid bacteria. The majority of the acetic bacterial cultures are members of the *Acetobacter*, followed in descending order of abundance by those of *Gluconobacter* and *Gluconacetobacter*. Cultures of the lactic acid bacterial group sorted into 6 identified genera, i.e. *Enterococcus, Lactobacillus, Leuconostoc, Pediococcus, Staphylococcus,* and *Streptococcus*. The identity of a few cultures is still under study; tentatively they are put under *Enterococcus*, *Lactobacillus*, or *Streptococcus*. Regarding the remaining 131 cultures, their identity are unknown (Table 1). All these cultures are deposited in NODAI Research-Culture Collection Center (NRIC), Tokyo, Japan and in the Culture Collection of the Research & Development Center for Biotechnology - LIPI, Cibinong, Indonesia.

Table 1. Isolates of Acetic Acid and Lactic Acid Bacteria from Indonesia

Group	Species	Number of isolates	Source of isolate
Acetic acid bacteria	*Acetobacter* sp.	88	Bali; Bogor, Cibinong, Cigombong, Darmaga (West Java); Yogyakarta.
	Gluconacetobacter sp.	6	Bali, Bogor, Yogyakarta.
	Gluconobacter sp.	21	Bali; Bogor, Cibinong, Cigombong, Darmaga (West Java); Yogyakarta.
	Sub-total	115	
Lactic acid bacteria	*Enterococcus* sp.	6	Bogor, Cibinong (West Java); Dieng (Central Java).
	Lactobacillus sp.	66	Bogor (West Java); Bali; Dieng (Central Java); East Java; Lombok; Riau, West Sumatra (Sumatra); Sanggau (Kalimantan); Sulawesi.
	Leuconostoc sp.	2	Bogor (West Java); Pakanbaru (Riau).
	Pediococcus sp.	3	Cibinong (West Java); Dieng (Central Java); West Sumatra.
	Staphylococcus sp.	4	Cibinong (West Java); Dieng (Central Java);, Sulawesi.
	Streptococcus sp.	1	Lombok
Lactic acid bacteria	*Entero/Streptococcus* sp.	10	Cibinong (West Java); Riau; Sulawesi.
	Entero/Streptococcus sp. / *Lactobacillus* sp.	4	Dieng (Central Java)
	Unidentified cultures	131	Bogor, Cibinong (West Java); Dieng (Central Java); East Java; Lombok; Riau, West Sumatra; Sulawesi; West Kalimantan; Yogyakarta.
	Sub-total	227	
TOTAL		342	

Detailed taxonomical study was undertaken to identify the species of the acetic acid and lactic acid bacterial cultures. On the basis of the growth-, physiological-, biochemical characteristics, DNA base composition, and DNA relatedness, the genus *Acetobacter* had been proposed to be split into 7 homology groups. Three groups comprise the presently known species, i.e. *A. aceti, A. pasteurianus,* and *A. peroxydans.* Three groups had been proposed to be elevated from sub-species to species, i.e. *A. orleanensis, A. lovaniensis,* and *A. estunensis.* One group had been proposed as a new species, *A. indonesiensis* (Lisdiyanti *et al.*, 1998; 2000). In addition, detailed studies of the isolates resulted in the identification of 3 proposed new strains, respectively *A. roseisyzygii* sp. nov., *A. cibinongensis* sp. nov., and *A. orientalis* sp. nov. (Lisdiyanti *et al., in press*).

Results of the study also revealed, that 8 acetic acid bacterial strains located distantly from the members of the genera *Acetobacter, Gluconobacter, Acidomonas,* and *Gluconacetobacter.* For that reason a new genus and species, *Asaia bogorensis* gen. nov., sp. was proposed for the isolates, with isolate 71 (NRIC 0311 = JCM 10569) as the type strain (Yamada *et al.*,2000). Further studies on the 5 acetic acid bacterial strains isolated from tropical flowers collected in Thailand and Indonesia showed that they are closely similar to *A. bogorensis* strains. Hence, a new name *Asaia siamensis* sp. nov. is proposed for these isolates (Katsura *et al.*, 2001).

Other study on 64 strains of acetic acid bacteria isolated from various samples of Indonesian material showed that 45 were *Acetobacter,* 8 *Gluconacetobacter,* whereas the remaining 11 *Gluconobacter* strains. Analysis of the DNA base compositions showed that the *Gluconobacter* strains could be divided further into 2 groups, respectively 7 isolates as *Gluconobacter oxydans,* while the remaining 4 as *Gluconobacter frateurii* (Yamada, *et al.*, 1999).

Regarding the lactic acid bacteria, 50 strains comprising 30 of rod-shaped and 20 spherical-shaped cells, had been isolated from a variety of tropical fruits. Based on growth, morphological-, physiological-, and biochemical characteristics they were identified as *Enterococcus* sp., *E. avium, E. faecalis, E. faecium, E. flavescens, E. gallinarum, Lactobacillus* sp., *L. plantarum,* and *Streptococcus* sp. (Widyastuti *et al.*, 1998).

In addition to taxonomical study, attempt to improve the microbial culture collection system in Indonesia had been undertaken. In this connection a Communication Forum for Indonesian Culture Collection Curators (FORKOMIKRO) had been established in 1996 which serves as a medium for curators: (1) to exchange ideas and experiences, as well as to solve common problems in culture collection management, (2) on voluntary basis or upon request from interested clients, provide consultations and recommendations to solve culture collection management problems, and (3) to assist the authorities in the implementation of the Convention on Biodiversity dealing with microorganisms. The forum encourages the responsible authorities to speed up the establishment, if possible, a national culture collection of microorganisms or setting up a formal national network of culture collections. To facilitate the dissemination of information of its activities, FORKOMIKRO had published a "List of Indonesian Microorganisms", respectively in 1999 and 2000 (Saono *et al.*, 1998, 1999, 2000).

Conclusion

Indonesia represents one of the world megabiodiverties and at the same time a rapidly developing country utilizing its rich natural resources. Unless serious measures to rationalize the utilization of these resources are taken, destruction of the tropical ecosystem would eventually occur with serious consequences on the fate of the biodiversity and sustainable economic development.

To rationally use its rich biodiversity, Indonesia is constrained not only by the lack of facilities and funds, but more seriously by the inadequate number of well-qualified human resources. Hence, the need of international cooperation with developed countries to overcome these constraints.

In the context of collaboration with Japan, study on the biodiversity of 2 large important groups of economically potential microorganism, i.e. the lactic acid and acetic acid bacteria had been chosen. This is due to the paucity of information on their diversity, particularly their wild relatives. Results of the collaborative study revealed the high diversity of these 2 groups as evidenced by the identification of a new genus of acetic acid bacteria – *Asaia,* as well as the identification of 10 new species, respectively *Asaia bogorensis, A. siamensis, Acetobacter indonesiensis, A. tropicalis, A. orleanensis, A. lovaniensis, A. estunensis, A. roseisyzygii, A. cibinongensis,* and *A. orientalis.*

Because of the limited number of trained scientific personnel as well as the inadequate facilities and funding, for the time being the best alternative to maintain economically and scientifically important microorganisms *ex situ* is by setting up a network of independent culture collections where they could work together for common benefits.

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The National Survey on the Natural Environment in Japan

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Abstract

Since 1973, the Environment Agency of Japan has carried out the National Survey on the Natural Environment, which are specified in the Nature Conservation Law. These surveys are in operation by the Biodiversity Center of Japan (BiodiC-J), the Nature Conservation Bureau, the Environment Agency. The contents of the surveys are vegetation, flora and fauna distribution, wetlands, lakes and marshes, seaweed beds, tidal flats, coral reefs, the alteration of river and coastal line, the components of ecosystem and the genetic difference among species on all of Japan. The results of these surveys are provided by the reports and also the Japan Integrated Biodiversity Information System(J-IBIS). For the purpose of smooth enforcement of the flora and fauna survey, the inventory of the target species (8,118 plants, 3,687 animals) was prepared with the cooperation of the specialists. The goal of the inventory is to make a revised and enlarged database.

Key Words: biodiversity, The National Survey on the Natural Environment (Green Census), inventory, The Japan Integrated Biodiversity Information System (J-IBIS)

Introduction

The Environment Agency, the government of Japan, has been carried out the National Survey on the Natural Environment since 1973 in accordance with the Nature Conservation Law. This survey is called "Green Census". Its aims are to grasp the present status of Japan's natural environment and to keep watch on the changes in it.

The Biodiversity Center of Japan (BiodiC-J) is the organization authorized to carry out “Green Census”. The BiodiC-J was established in April 1998 at Fujiyoshida-city, Yamanashi Prefecture, as a branch of the Environment Agency, the Nature Conservation Bureau. Currently 14 staff members are working at the BiodiC-J.

The BiodiC-J has 4 main functions: surveys, information processing and offering, the collection and storage of specimen and documents and the publicity about the importance of biodiversity conservation.

1. Survey

List of surveys

Previously comprising the National Survey on the Natural Environment (the Green Census)

Object		Name of survey
Land	Plants	Vegetation Naturalness Survey Survey of Valuable Natural Areas (plants) Vegetation Survey Specific Plant Community Survey Big Trees Survey Species Diversity Survey Environmental Indicator Species Survey (Survey of Common Wildlife) Survey of Valuable Natural Areas (animals) Animal Distribution Survey (all species)
	Animals	
	Geography and landscape	Survey of Valuable Natural Areas (geography) Survey of Valuable Natural Areas (historic natural environment) Survey of Surface Ground Alterations Natural Landscape Resource Survey
Surface water	Rivers, lakes, marshes	Surface Water Naturalness Survey River Survey Lake and Marsh Survey Wetland Survey
Coastal areas	Coastline, tidal flats, seaweed beds, coral reefs	Coastal Area Naturalness Survey Survey of Valuable Natural Areas (marine environment) Coastline Survey Marine Organisms Biological Environment Survey Seashore Survey
	Marine life	Life in Coastal Areas Survey Survey of Valuable Natural Areas (Marine Environments) Marine Animal Survey
Ecosystems		Ecosystem Survey Typical Ecosystem Survey Ecosystem Survey for Regional Diversity
Genetic diversity		Genetic Diversity Survey

Fig.1. Table of the Green Census

1.1. Vegetation Survey

In the vegetation survey, an Actual Vegetation Map (scale: 1/50,000), consisting of 1,200 sheets all of Japan was made of using aerial photographs and field surveys with a legend of the plant sociology. An additional Actual Vegetation Map (scale: 1/2,500,000), showing all of Japan on one sheet, was made by computer processing each 1 square kilometer mesh.

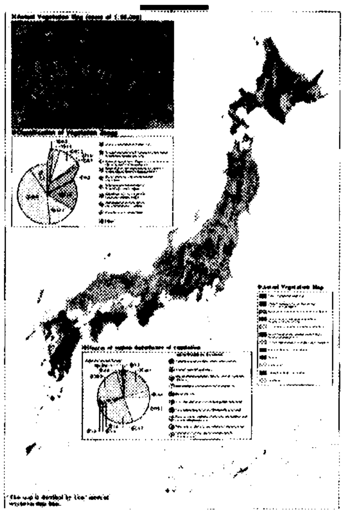

Fig.2. 1/50,000 Actual Vegetation Map

1.2. Species Diversity Survey

The Species Diversity Survey has been carried out and is aimed to make distribution maps of all species of fauna and flora in Japan. The survey's term is 5 years, but the results of the survey are not perfect, because the budget and the number of the researchers are insufficient and the inventory is not complete. The survey from 1994 to 1998 targets 8,118 plants and 3,687 animals, including subspecies. The actual number of species which are known in Japan are about 32,000 plants and 36,000 animals, including subspecies.

Species Diversity Survey(1994~1998) (*including sub species)

	Taxonomic Group	Number of target species*
Animals	Mammals	272
	Birds	577
	Amphibians	64
	Reptiles	100
	Brackish and fresh water fishes	345
	Insects	1,090
	Terrestrial and fresh water shells	1,239
(Subtotal)		3,687
Plants	Vascular plants	8,118
(Total)		12,805

Fig.3. Taxonomic Group and the Number of Target Species

The Environment Agency prepared the list of the target species, 8,118 plants and 3,687 animals, for the Species Diversity Survey in cooperation with specialists.

The researchers send the questionaire to the Environment Agency after writing the species' name and code number, the habitat place name (name of area) and the mesh code number of 1 square kilometer and the researched day.

From the results of this distribution survey, 10 square kilometer mesh distribution maps are made by computer processing and published.

The Following distribution map is that of the Asian black bear. The bear, which is distributed on Honsyu (the main island) to Kyusyu has a close relationship to the Beech forests. But the bear's local populations are getting smaller and smaller.

Each survey targets all of Japan, and valuable data has accumulated since the survey started in cooperation with the local government, the specialists and the volunteers. We recognize the importance of extending the human networks supporting the survey.

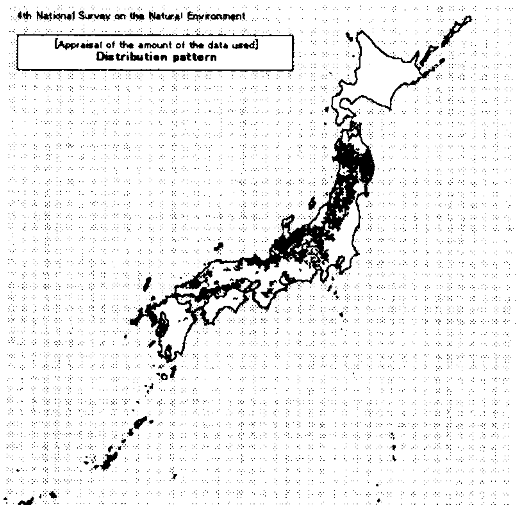

Fig. 4. Mesh Distribution Map (Asian black bear)

2. Information: Japan Integrated Biodiversity Information System

The results of the Green Census have been released to the public in reports and are available to the public by Japan Integrated Biodiversity Information System (J-IBIS). J-IBIS English version is also available to the public through the Internet from June 1999.

URL address http://www.biodic.go.jp/english/J-IBIS.html

J-IBIS(Japan Integrated Biodiversity Information System)

This system is a project of the Biodiversity Center and presents information based on data from the Environment Agency's "National Survey on the Natural Environment (the Green Census)" which the agency has been conducting for more than 20 years since 1973

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Fig.5. Japan Integrated Biodiversity Information System Top Page and URL

3. Collection and Storage: Documents and Specimen of Japanese Crested Ibis

The BiodiC-J collects the results of the Green Census, including reports and drawings, as well as other documents on the natural environment and biodiversity and holds them for safekeeping. The BiodiC-J also preserves specimens of rare wildlife, such as the Japanese Crested Ibis, the Iriomote Cat and so on, and other important specimens that might otherwise be lost if dispersed among universities and research institutes.

4. Publicity: Library and Exhibition Hall

To maintain biodiversity, the public must be enlightened in regards to its importance and encouraged to cooperate in whichever ways possible. With this in mind, the BiodiC-J has set up an exhibition hall demonstrating the importance of biodiversity. It is opens it to the public.

The Green Census reports and the other documents held by the BiodiC-J can be browsed in the library.

Conclusion
(The view for the future in connection with the contribution of Species 2000 project)

The Inventory for the Species Diversity Survey will be revised with the latest information. Now, the selected groups and the number of target species are limited, but otherwise, for example, the inventory of Insects in Japan, which has over 30,000 species, was completed in cooperation with specialists and the Environment Agency in 1990. And Dr.Tadauchi from Kyushu University completed putting this inventory to database system. The BiodiC-J is going to put the list of target species of the Green Census into a database system, such as J-IBIS, and modify the information (pictures, sounds, distribution maps, etc.) about each species. It is desirable to link with other inventory database systems in the near future.

The BiodiC-J is the only organization concerning itself with this inventory in the government of Japan, but now the target taxonomic groups are only higher animals and plants. The BiodiC-J will contribute to the Species 2000 project in cooperation with NIES and other research institutes and universities.

How the Biodiversity Issue is Handled in Taiwan

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Abstract

In order to conserve and protect the very rich biological resources that have evolved in a unique natural environment, the government in Taiwan has set up a special committee and assigned a government agency, both at the cabinet level, to be in charge of planning and implementing relevant programs, respectively. Convening symposia have been the main means of building the national consensus to identify issues to be studied, which have motivated scientists to initiate the challenging task with the help of research funding from the related agencies. Increase in the number of scientific publications and increased emphasis by news media show the increased concern of academicians and public on biodiversity issue. Besides, the material and information databases related to the biological resources of various categories have been established and revised regularly.

Keywords: ***Biodiversity, national park, public education, bioscience, conservation policy***

Introduction

Taiwan is a tobacco leaf shaped island located due east of Fu-Jian Province of the Mainland China across the Taiwan Strait. It has an area close to that of the Netherlands, or 36,000 km^2, and only about one-fourth of it are arable. The tropic of cancer dissects the center and the east-end of the monsoon belt reaches Taiwan. Thus it has a warm sub-tropic weather with abundant rainfall. The central mountain range, which has over one hundred peaks higher than 3,000 m, runs from the north to the south, and a temporal weather condition is prevalent at the elevated hilly areas. The balmy climate brings long springs and unfading green growth. Because of these geographic conditions, Taiwan enjoys a very rich fauna and an agricultural productivity of from the tropical to temporal crops.

Policy Formulating Committee for Climate Changes

The rapid economic and industrial growth and tripling of population in the past 50 years have put a heavy pressure on the natural environment. In order to cope with the global change problems, a cabinet level agency, the Policy Formulating Committee for Climate Changes (PFCCC), was established in 1995, and the Council of Agriculture (COA) has been charged with the responsibility of biodiversity preservation. The achievements of the government agencies are listed below (Lin, 1998a,b):

1. In order to help the formulation of working plans, three symposia were held on the biodiversity in the terrestrial and aquatic environments, since September 1998: Prospects of Biodiversity (Lin, 1998a), Biodiversity-1999 (Lin, 1999a) and Biodiversity in 21st Century: A Training Course in Biodiversity (Lin, 1999b,c).
2. There are 6 national parks, 18 natural reserves (Table 1), 13 wildlife protection areas (Table 2), and 24 natural protected areas, totally covering 12.2% of the land area. Kenting is the first national park established in January 1984; it gives an exclusive protection to 18,030.5 hectares of terrestrial lowland rainforest and 15,185.2 hectares of adjacent ocean. There are large coral reefs, mountain peaks, lakes, plants, sand dunes, beaches and volcanic rock formation (Fig. 1) (Yuan et al., 1999).

Table 1. Nature reserves in Taiwan

Name	Main protected features	Area(ha)	Location	Date established
Tamsui River mangrove nature reserve	Kandelia mangrove swamp	76.4	Taipei County	June 27, 1986
Kuantu nature reserve	Waterbirds	55.0	Taipei City	June 27, 1986
Pinglin Taiwan Keteleeria nature reserve	*Keteleeria davidiana*, rare plants & animals, ecosystems	34.6	Taipei County	June 27, 1986
Happen nature reserve	Broadleaved forest, birds, freshwater fish	332.7	Ilan County	June 27, 1986
Chatienshan nature reserve	Quercus zone, rare plants, animals & ecosystems	7759.2	Taoyuan & Taipei County	March 12, 1992
Yuanyang Lake nature reserve	Lake & wetlands, red cypress, *Sparganium falax*	374.0	Taoyuan,Hsinchu & Ilan County	June 27, 1986
Nanao broad-leaved forest nature reserve	Temperate broadleaved forest, pristine lake, rare plants & animals	200.0	Ilan County	March 12, 1992
Miaoli Sanyi Huoyenshan nature reserve	Nature cliff & Taiwan red pine	219.0	Miaoli County	June 27, 1986
Penghu columnar basalt nature reserve	Basalt landscape	*	Penghu County	March 12, 1992
Taiwan pleione nature reserve	Taiwan pleione & its environment	51.9	Chiayi County	March 12, 1992
Chuyunshan nature reserve	Broadleaved forest, coniferous forest, rare plants & animals, forest streams & fresh-water fish	6248	Kaohsiung County	March 12, 1992
Taitung hungyeh village Taitung cycas nature reserve	*Cycas taitungensis*	290.5	Taitung County	June 27, 1986
Wushanting mud volcano nature reserve	Mud volcano	4.89	Kaohsiung County	March 12, 1992
Tawushan nature reserve	Wildlife & habitat, virgin forest, mountain lakes	47000	Taitung County	January 13, 1988
Tawu Taiwan amentotaxus nature reserve	*Amentotaxus formosana*	86.4	Taitung County	June 27, 1986
Watzuwei nature reserve	Kandelia mangrove & wildlife	30	Taipei County	January 10, 1994
Wushihpi coastal nature reserve	Coastal forest & special landscape	347	Ilan County	January 10, 1994
Kenting uplifted coral reef nature reserve	Uplifted coral reefs & their ecosystems	137.6	Pintung County	January 10, 1994

* 19.13 high tidal zone and 30.87 low tidal zone.

3. The laws of conservation in enforcement are the acts of national park, wild animals conservation, forest, ethnic culture conservation, environmental impact assessment, soil and water conservation, and fisheries. The wildlife conservation law was enacted on June 23, 1989. Changes were made to the law on October 29, 1994. The law has been enacted to conserve wildlife, protect species diversity and maintain the balance of natural ecosystems.
4. The Taiwan Special Species Research and Preservation Center was established.
5. International Symposia on Terrestrial Ecology and Biodiversity (1994), Biodiversity, Biotechnology and Sustainable Agriculture (1997), Biodiversity

Survey and Monitoring of Western Pacific and Asia Areas (1997), Long-term Ecology and Biodiversity (1997) and Biodiversity of Pacific Area (1998) were held.

6. Academic researches on recovery of threatened species, taxonomy and life cycles of species were actively engaged. The Council of Agriculture actively promotes research for conservation of native wildlife and has established a wildlife databank. It also promotes conservation of rare species such as landlocked salmon, black bear, green turtle, Formosan serow, emerald tree frog and birdwing butterfly.

Table 2. Wildlife refuges in Taiwan

Name	Main protected features	Area (ha)	Location	Date established
Penghu County cat islet seabird refuge	Seabirds & their environment	30.204	Penghu County	May 24, 1991
Kaohsiung Nantzuhsien River wildlife refuge	Freshwater fish & their habitat	274.22	Kaohsiung County	May 26, 1993
Ilan County Wuwei Harbor waterbird refuge	Birds & their wetland habitat	101.62	Ilan County	September 24, 1993
Taipei City waterbird refuge	Waterbirds, rare plants & wildlife	245	Taipei City	November 19, 1993
Tainan City Ssutsao wildlife refuge	Wetland & birds	515.1	Tainan City	November 30, 1994
Penghu Wangan island green turtle refuge	Green turtle & its egg-laying grounds	23.33	Penghu County	January 17, 1995
Tatu rivermouth wildlife refuge	Rivermouth & coastal ecosystems, birds & wildlife	2669	Taichung & Changhu County	February 28, 1995
Mien Hua and Hua Ping islets wildlife refuge	Island ecosystems & birds, wildlife & volcanic landscape	226.4	Keelung City	March 18, 1996
Langyang rivermouth waterbird refuge	Rivermouth & coastal ecosystems, birds & wildlife	206	Ilan County	September 16, 1996
Formosan landlocked salmon refuge	Forman landlocked salmon & the environment	7124	Taichung County	October 1, 1997

Public Education and Research Programs

PFCCC has recommended the enforcement of public education on biodiversity, and has formulated the working plans on the national biodiversity preservation and bioresources survey. Each level of education on biodiversity is listed in the following:

1. Biology disciplines, local biology and diversity of species in elementary schools.
2. Effect of human activity on biodiversity, ecology of diversity, and maintenance of ecological environments in middle schools.
3. Genetics of diversity, developing process of biodiversity, and value of biodiversity in high schools.
4. Conservation of biodiversity, sustainable development and biodiversity, conservation of ethnic culture diversity, and research trend of biodiversity around the world in the general education of universities.
5. Measurement of biodiversity, conservation research of biodiversity, and recovery techniques of habitats in the related departments of universities.
6. Local animals, local plants, local ecosystems, forum of biodiversity, recognition of community, recognition of threatened species, conservation of biodiversity and personal action, culture, arts, and biodiversity, and conservation concepts in the social education (Wang and Chou, 1999).

The research programs in progress, supported by the national funding, include the following topics:

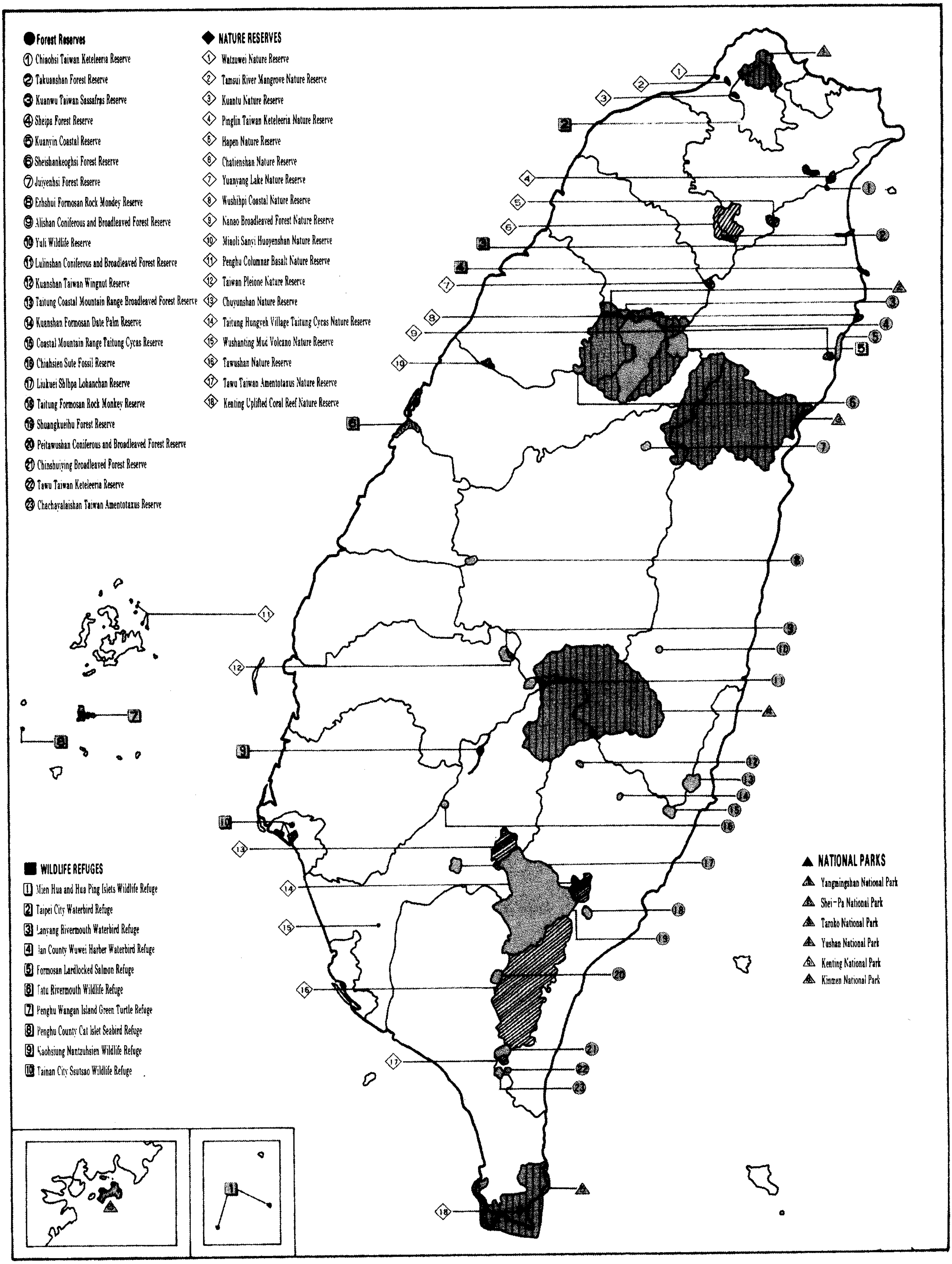

Fig. 1. Natural protection areas in Taiwan.

1. Surveys on species, habitats, ecosystems and genetic diversities (Hsu and Agoramoorthy, 1999; Liu, 1999).
2. Effect of human activity on biodiversity.
3. Biodiversity in the ecosystem maintenance.
4. Long-term monitoring of biodiversity (Yang et al., 1998a,b, 1999a,b,c).
5. Population kinetics of threatened species and conservation policy.
6. Sustainable bioresource utilization and biodiversity.
7. Effect of ecosystem fragmentation on biodiversity.
8. Biodiversity conservation.
9. Recovery of biodiversity.
10. Genetics of major crops, economic plants, and economic animals.
11. Flora of Taiwan.
12. Bioresources utilization:
    (a). Improvement of productivity by applying genetic engineering technology, such as increasing milk secretion of cow, increasing the number of cow embryo, preservation of species, asexual production of embryo, cell transformation, and gene transformation.
    (b). Enhancement of biological activities for biotechnology applications, such as organic wastes treatment, nitrogen-fixation, chemical pollutants removal, biological control of pests and disease, carbon dioxide assimilation, species improvement, and ecological tour.

The ratio of the number of biodiversity related papers to the total number of biology related papers published annually by the scientists in Taiwan increased from 0.52% in 1989 (70/13,379) to 1.27% in 1998 (722/56,975). During the same period, the number of news articles reporting the biodiversity related issues to the total number of news items also increased from 0.5% to 1.2%. Among the biodiversity related news items, the environmental issue had the highest share (55%), followed by ecology (18%), animals (15%), and plants (4%) (Shih and Cheng, 1999). In addition, the natural and scientific museums had 10 special exhibits on biodiversity, 15 permanent exhibition sites for biodiversity and conservation of species, 13 video-guide tapes, 20 DIY (do it yourself) biodiversity programs, 8 education programs, 9 studio classrooms programs, and 6 theater programs last year (Wang and Chou, 1999).

Database in Biosciences

The following bioscience databases have been established in Taiwan:

(1). National Plant Genetic Resources Information System.
(2). Multimedia Databank of Taiwan Wildlife.
(3). Taiwan Agricultural Institute Plant Information System.
(4). Distribution and Resources of Fishes in Taiwan.
(5). Herbaria at many sites.
(6). Cell Bank.
(7). Asian Vegetable Genetic Resources and Seeds.
(8). Database of Pig Production.
(9). Registry of Pure-Breed Swine.
(10). Mating, Furrowing, Performance and Transfer of Ownership of Pure-Breed Swine.
(11). Food Marketing Information System Database.

(12). Food Composition Table in Taiwan.
(13). Database on Heavy Metals in Taiwan Soils.
(14). Greenhouse Gases Emission from Agriculture.
(15). Global Change Database generated in Taiwan.

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Empowerment of Indonesian Biodiversity Information Resources

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Abstract

Indonesia is encumbered with the hefty tasks of managing its biological resources. Its economic development has been very dependent on utilizing its natural resources, where biological resources have been somewhat suffering from both political and intellectual negligence. The fact that existing biological data and information sources are disintegrated, has made it imposibble for planning and environmental consultants and private companies (*i.e.* private sectors) to develop their business on the basis of biodiversity conservation. At the national level, there has been widespread appreciation of the importance and value of Indonesia's biological diversity, but few systematic attempts have been made to organize and coordinate information about biological diversity across the country. In attempts to organize biological information, RDCB has been developing its biological specimen collections through the GEF-Biodiversity Collection Project, and the establishment of Biodiversity Information Center which has been sponsored by JICA-Biodiversity Conservation Project. RDCB has also been preparing the development of National Biodiversity Information Network whose sponsor was the Asian Development Bank. One component of the GEF-Biodiversity Collection Project has been the development of information system management, which is named as IBIS (Indonesian Biodiversity Information System). The details of all development measures concerning the empowerment of Indonesian biodiversity information resources are fully presented in the paper.

Key Words : GEF, IBIS, NCIC, NBIN, biodiversity information

Introduction

Indonesia is encumbered with the hefty tasks of managing its mega-biodiversity resources. Indeed, Indonesian economic development has traditionally been very dependent on utilizing its natural resources, but biological resources have been somewhat suffering from both political and intellectual negligence. The government has endorsed laws and regulation concerning the management of biological resources, but they have been lack of appropriate implementation.

The fact that existing biological data and information sources are disintegrated, has made it imposibble for both economic development and environmental plannings to be developed on the basis of biodiversity conservation. From the beginning this fact has created natural resource exploitation which has disregarded the sustainability of the existing biological diversity within the natural resources, yet human survival has always been dependent on our ability to recognize, understand and utilize biological diversity.

Despite nationally widespread appreciation towards the importance and value of biological diversity, very few systematic attempts have been made to organize and coordinate information about biological diversity across the country. At the international level, the Government of Indonesia (GOI) witnessed a growing interest from the multi-lateral and bilateral donors in funding projects to protect the country's biological diversity. The GOI responed such a growing interest with the formulation of a Biodiversity Action Plan, published in 1993, describing plans and strategies necessary for Indonesia to conserve its biodiversity (Ministry of National Development Planning, 1993). But for such plans and strategies to be effectively implemented, better information about the environment and biodiversity are needed to increase the range of policy options and allow more effective analyses of those options.

Current Status of Indonesian Biodiversity Information Resources

In Indonesia, traditionally, it has been government organizations that generate most of the biodiversity-related data and information. Despite the establishment of several committees and working groups, the linkages among different Government bodies in the area of biodiversity have always not been effective. Whenever possible, information sharing takes place only in an informal manner, yet the Government bodies have little experience in sharing information in a more systematic and transparent way. Furthermore, gaps, overlaps, and incompatibilities between data and information resources resulted from the fact that different Ministries, agencies, universities, and research institutes develop independent data and information resources. Concurrently additional data and information have emerged from a number of internationally-funded programs, non-governmental organizations (NGOs), and private sector initiatives in recent years.

Biodiversity-related data are currently held at, for example, the Indonesian Institute of Sciences (LIPI), the National Agency for Atomic Research (BATAN), the Agency for Assessment and Application of Technology (BPPT), the Agency for Space Development (LAPAN), the Central Bureau of Statistics (BPS), the Coordinating Agency for Land Survey and Mapping (BAKOSURTANAL), and the National Research Committee (DRN), and the Agency for Research & Development of Health, Dept. of Health; the Agency for Research & Development of Agriculture, Dept. of Agriculture; the Agency for Research & Development of Forestry, Dept. of Forestry and Plantation; the NCIC/National Conservation Information Center, Directorate General of Forest Protection & Natural Preservation, Dep. Forestry & Plantation; and amongst universities are the Bandung Institute of Technology (ITB), the Bogor Agricultural Institute (IPB), and the University of Padjadjaran Bandung (UNPAD). Several projects and NGOs which hold biodiversity-related data dan information are also potential resources, such as the EU-sponsored Forest Inventory and Monitoring Project, the Center for International Forestry Research (CIFOR), the Southeast Asian Regional Center for Tropical Biology (SEAMEO-BIOTROP), Wetlands International - Indonesia Programme (WI-IP), World Wide Fund for Nature (WWF), Birdlife International, and PT Mapindo are representative of the growing accumulation of data and information resources from all sectors related to biodiversity.

Despite a number of institutions generating biodiversity-related data and information existing in the country, the availability of biodiversity information has always been troublesome, especially when biodiversity information is categorized further such as follows. Since biodiversity can be categorized into three levels, *i.e.* ecosystem, species, and genetic, the biodiversity information should accordingly encompass these three levels. Ecosystem information may contain all data and comprehensive information about existing ecosystem within the Indonesian archipelago. Bioregional division may be applied in this category, but for those thousands of small islands such division system may not be appropriate.

Unfortunately, information about Indonesian ecosystem is far from comprehensiveness and integrity. The existing ecosystem information is merely about the forest coverages and structures at a regional scale (at the scale 1:1,000,000), but lack of local scale (at the scale of 1:20,000). This has been worsened when all existing maps containing such ecosystem information have been disintegrated. Even the maps of national parks containing ecosystem information are not all available, let alone all Indonesian regions.

Those institutions which are reported to generate ecosystem information are, for example, the Indonesian Institute of Sciences (LIPI), the Agency for Assessment and Application of Technology (BPPT), the Agency for Space Development (LAPAN), the Coordinating Agency for Land Survey and Mapping (BAKOSURTANAL), the Dir. Gen. of Inventory and Forest Use (INTAG)-Dep. Forestry & Plantation, and PT Mapindo. But each of them generate their own and independent data format and platforms, which can not be integrated into and accessed by each other.

Species information may be found in a number of organizations, such as the Indonesian Institute of Sciences (LIPI), the Agency for Research & Development of Agriculture-Dept. of Agriculture, the Agency for Research & Development of Forestry-Dept. of Forestry and Plantation, the NCIC-Directorate General of Forest Protection & Nature Preservation-Dep. Forestry & Plantation, the Bandung Institute of Technology (ITB), the Bogor Agricultural Institute (IPB), the University of Padjadjaran Bandung (UNPAD), the Southeast Asian Regional Center for Tropical Biology (SEAMEO-BIOTROP), Wetlands International-Indonesia Programme (WI-IP), World Wide Fund for Nature (WWF), and Birdlife International.

At the species information level, each organization also generate their own and independent data and information through a series of researches and surveys. Such research and survey works have only resulted in scattered and disintegrated data and information. These data and information are generally put in tabular or textual format, and not catalogued in computerized formats. During an NBIN study (ARD, 1999), it was found at least 23 governmental and non-governmental organizations in Indonesia work on all aspects of biological diversity. None of them has been electronically linked to each other, and this has made it impossible for sharing information through an internet. Some of them have biological data and information in textual formats, and some of them do not even understand how valuable their data are. Each of them has their respective data and information stored in their respective shelves.

The main institution for species information in Indonesia is the Research and Development Center for Biology (RDCB), which manages the Bogor Herbarium (Herbarium Bogoriense) and Bogor Zoological Museum (Museum Zoologicum Bogoriense). RDCB has always dealt with a quite wide range of biological sciences from the development of biosystematics to industrial microbiology. Those major herbarium and museum are in Bogor, a town near Jakarta, the capital city. The Bogor Herbarium holds about 2 million specimens of plants, seeds, fungi, and mosses, and the Bogor Zoological Museum held about 780,000 specimens of animals. It is only recently the scientific collections of plants and animals in RDCB being managed in computerized formats, with the supports from international projects, such as GEF-Biodiversity Collections Project and JICA-Biodiversity Conservation Project. The information network for biodiversity is going to be materialized with NBIN (National Biodiversity Information Network) which will be sponsored by the Asian Development Bank (ARD, 1999).

At the genetic level, information may be in a very poor condition, where none of existing information is stored in computerized formats. Yet a number of organizations work on genetic level information, such as the Indonesian Institute of Sciences (LIPI), the National Agency for Atomic Research (BATAN), the Agency for Assessment and Application of Technology (BPPT), the Agency for Research & Development of Health-Dept. of Health, the Agency for Research & Development of Agriculture-Dept. of Agriculture, the Bandung Institute of

Technology (ITB), the Bogor Agricultural Institute (IPB), and the University of Padjadjaran Bandung (UNPAD).

The RDCB-LIPI which has scientific collections of microbes, has not started yet the genetic exploration of all available specimens. The RDCApplied Chemistry-LIPI which generates genetic data and information has neither started tranferring all available data and information into computerized formats. The other institutions may just be as not ready as LIPI in providing computerized genetic data and information.

Incomprehensive data and information about all levels of biodiversity stems from lack of coordination between existing organizations. This actually stems further from political and intellectual negligence shown by the government and all parties involved in biodiversity works. This has created disintegrated biodiversity-related data and information, and also generated scattered data and information. Such scattered data and information are not yet organized and communicated with other stakeholders (data/information holders). This reflects lack of data/information flow amongst data holders. Such lack of information flow has made potential users such as researchers, government agencies, and private sectors suffer from comprehensiveness and integrity. It has even generated research duplication, and redundancy, that has actually made the government spend a lot of money for wasteful efforts. Incomprehensiveness and disintegrity of research and survey works resulted from lack of information flow has created nothing but a failure to promote public awareness about biodiversity conservation and its sustainable use. Available data and information which are scattered and disintegrated cannot be linked into geo-spatial data to produce a comprehensive analysis vital for decision planning and making, as well as for private sectors in developing their business plans.

Researches on biological resources have indeed been encouraged amongst Indonesian intellectuals, but those money spending researches have also been suffering from both comprehensiveness and integrity. This is perhaps why there has rarely been any discovery and/or invention generated from biological studies that was recognized internationally. Another major problem in biological researches which can be identified, has been research duplication, where several research institutions conducted the same studies. Such duplication has indeed forced the government to spend inefficient fundings for researches. The main identified explanation for such duplication has been the lack of information flows between Indonesian scientists. Such a lag on information flow could only be overcome when an information network is established and promoted, by which any information can be accessed by anybody concerned with biological research.

By cataloguing biodiversity data and sharing data across organizations, redundant data collection can be minimized. Organizations can make better use of their limited resources by concentrating on collecting new data sets where none exist or updating and upgrading previously collected data. By making data sets more accessible and thereby increasing their use, incentives are created for storing and maintaining them. As organizations gain improved access to a wider variety of data and information, they will gain a more secure basis for planning, management, and decision making. Improved access to information will also facilitate cross-disciplinary, cross-organizational cooperation and generation of revenue.

It is therefore concluded that biodiversity data and information have been available in an invaluable amount, but scattered under the custodian of various owners, be it governmental agencies or non-geovernmental institutions, and almost all data and information are inaccessible. Such inaccessibility might have been incited by the fact that there was no compatibility in data/information structures, yet each institution may have sophisticated information facilities. Such incompatibility and inaccessibility has made it impossible for decision planning and decision making are based upon appropriate data and information.

Current Management of Indonesian Biodiversity Information

In early days the main mission of taxonomic institutions such as museums and herbaria housing biological collections, is to collect, document, and store safely in readily accessible form specimens of the local, national, regional, and global diversity of living organisms from which the records of morphological variation and geographical distribution are available. Today such records are demanded more than just such information, but to include other biological information such as genetic maps, local knowledge, and local utilization of specimens. Genetic information from specimens collected in early days could be analysed today with applying modern technology, but information about local values has been rarely recorded. A series of collected specimen could be used in analysing the past and present geographical distribution, and when this information is combined with landscape changes a conclusion on what to do with such a species could be generated. In all, demanded data and information should today cover all levels of biodiversity.

However, the commonest constraint across all organizations has been lack of computerized data management, about which RDCB-LIPI has started to systematically organize its scientific specimen collections through international projects, such as GEF-Collections Project, JICA-Biodiversity Conservation Project, and NBIN Project.

* GEF-Collections Project

The project is aimed at strengthening the institutional capacity of the Bogor Herbarium and Bogor Zoological Museum, both under RDCB-LIPI, to support systematic biological collections as a basic reference tools for biodiversity inventory and monitoring, and to make information from the collections available to external clients. One of the main objectives of the project is to design and establish a computerized database of specimen-based data for collections management, collection plans and development, and external use.

One component of the project is Information Systems Management, which sets up a computer database and a local area network capable of basic specimen data entry, automated label production, collections management functions, and information dissemination. This comprises inputs of technical assistance, an overseas work-study program, computer and network equipment and installation, software development and support, and the establishment of a new sub-division with redeployed and newly recruited staff. IBIS, or the Indonesian Biodiversity Information System, is an application program developed by the project for developing a computerised specimen-based database which is easily accessible by any institution needing information within the biological collections held by RDCB.

* JICA-Biodiversity Conservation Project

Under the component of GEF Biodiversity Collections Project, JICA has supported an establishment of a new building for Bogor Zoological Museum equipped with research facilities. Along with this component, JICA has also set up a JICA Conservation project to implement the Japanese Technical Cooperation Program of the Biodiversity Conservation Project. This project encompassed three main components: (a) information processing and network; (b) research and survey; (c) national park planning and management; and (d) data/information sharing between research institutions and park management.

The output of Information Processing and Network Component is an increase in the institutional capability of RDCB to manage biodiversity information in the field of botany and zoology. To achieve this the following activities are carried out: (a) to survey the potential organizations which will be the data providers and/or data users for the future nationwide network of biodiversity information; (b) to examine the utilization purpose of biodiversity information; and (c) to develop a standard database for biodiversity information and collection management and other associated programs. The establishment of BIC, or the Biodiversity Information Center and NCIC, or the Nature Conservation Information Center, have been the achievement of the project.

The BIC is to develop institutional capacity in the management of data/information of biodiversity, of which the main activity has been to established facilities, such as building, computer and GIS equipments needed for the BIC development. On the other hand, NCIC is aimed at increasing the capability of national park administration (i.e. PHPA, or the Dir.Gen. Forest Protection and Nature Preservation) in the management of data and information collected in Indonesian national parks. The establishment of NCIC has started with the construction of a building for NCIC equipped with computers and GIS facilities. This NCIC is supposed to manage all information about Indonesian national parks making it accessible by external clients. The link between BIC and NCIC is to be established for data and information collected in Gunung Halimun National Park to promote effective data/information sharing between institutions.

* NBIN (ADB)

NBIN's primary goal is precisely targeted at improving information exchange among agencies. The institutional strengthening, the largest component of the proposed investment project, would provide NBIN member organizations with the tools and skills required for them to contribute to, participate in, and benefit from NBIN. The legal arrangements, marketing activities, and other mechanisms proposed for generating and retaining revenue among NBIN member organizations are intended to provide an incentive to agencies and organizations to participate in NBIN.

The establishment of NBIN is also emphasized in the Biodiversity Action Plan for Indonesia (BAPI) which urges that Indonesia should start implementing the development of biodiversity information to make such information accessible to users. The NBIN should play a role as a media for strengthening cooperation between associated institutions, by which biodiversity information is made available and accessible by public at large. The very existence of NBIN as a national biodiversity information center could become a node in the international network, which is considered to be very vital for effective benefit-sharing between nations involving biodiversity. This has been outlined under the Global Biodiversity Strategy (WRI *et al.* 1992).

In a long-term, the NBIN should be capable of achieveing the following objectives:

* the establishment of national a reference center for conservation, research and development, and sustainable utilization of biodiversity.
* the acceleration of the flows of biodiversity information at the local, national, regional, and global scales.
* leading all national network members through transition processes of the transformation from traditional scientific communication to electronically scientific communication in a global network.

The NBIN Project is to provide biodiversity information in a format, quality, and accessibility that promotes planning and decision making for wise use of natural resources in Indonesia. Associated objectives are to (i) establish a practical mechanism for sharing biodiversity data and information, *i.e.*, establish NBIN; (ii) improve responsiveness to user demands; and (iii) secure NBIN's long-term viability.

The NBIN will therefore require (i) motivation and capability to develop and maintain data and information of sufficient interest, relevance, and quality to justify the cost incurred;

(ii) mutual trust and agreement of all participants to share that data and information; (iii) a sense of responsibility for protecting against the abuse or misuse of the privileges which come with that trust and agreement; (iv) technical mechanisms for maintaining, updating, and exchanging that data and information; and (v) the capacity to contribute to and benefit from the wider range of resources that will become available through such a network.

This ambitious goal can only be achieved by simultaneously addressing the technical, legal, institutional, and financial aspects of establishing a operational data and information sharing network. NBIN's success will be determined by the skills, knowledge, and abilities of member organizations' staff in developing, maintaining, and managing their data, communications, and network resources, and in their willingness to share their data and information resources with others. Ideally, each NBIN member organization should have useful, high-quality data, and reliable databases and network resources under their control and at their disposal.

In addition, NBIN member organization should have a good sense of how to make their data and information useful and relevant to external as well as internal users, have a willingness to share that data and information, and have a sense of how to protect their shared data and information products from misuse. The majority of the proposed loan package will therefore go toward assistance in developing strong beneficiary organizations capable of contributing to, participating in, and benefiting from NBIN. This will include both institutional strengthening of the individual NBIN member organizations and strengthening in establishing connections among them.

The NBIN should link existing organizational databases, programs, and initiatives, in a comprehensive nationwide system for sharing, upgrading, integrating, using, and communicating information about biological diversity. NBIN would encompass data and information about genetic variability, species diversity, and ecosystem diversity. The types and forms of data and information used to record, study, and understand biodiversity could extend from tabular data about individual collected specimens to spatially-referenced maps of geographic regions having specific characteristics to bibliographic information describing everything from research findings to treaties, laws, and regulations covering biodiversity. The uses of these data and information resources would be similarly wide-ranging, and might include many types of planning and management, policy making, investment, and pure and applied scientific research.

Application of Biodiversity Information System and Network

* IBIS Application

The IBIS, which stands for Indonesian Biodiversity Information System, has been developed under the GEF-Biodiversity Collection Project. The structure of this application consists of Collection Tables, Determination Tables, Locality Tables, and Reference Tables. The latter consists of scientific name, habitat classification, substrates, collection methods, disturbances, slope, geology, abundance, and local name. Two versions of IBIS have been developed, mainly related to zoological and botanical scientific collections.

Until recently, the IBIS has been applied to store 228,000 records of botanical collections, from about 2,000,000 records available at the herbarium of RDCB, and 60,000 records of zoological collection from about 300,000 records available at the zoological museum of RDCB. A long way to go to complete cimputerizing all available data at the RDCB-LIPI. The IBIS is currently being revised from Version 1.10 into Version 2.00 where the application should be made relational into other applications.

* **BIC/NCIC Development**

The BIC, or Biodiversity Information Center, should act as a core for all biodiversity information available at the RDCB (JICA-Biodiversity Conservation Project, 1998). For this purpose, the BIC will manage databases on bibliography, field records, and specimen records resulted from IBIS application. On the other hand, the NCIC or Nature Conservation Information Center, will manage databases on management activities of national parks in the country. At this period of development, data utilized for databases at the NCIC come from the Gunung Halimun National Park. This development will be extended further into other national parks in Indonesia.

At both development, GIS is heavily applied in order to produce maps of existing ecosystem components within the national park. Having all data relationalized into GIS, the application of analyzing environmental conditions is also developed further. With this development, environmental sensitivity analysis could be carried out to fulfill public demand for sustainable development planning.

* **NBIN Implementation**

The following issues are the common objectives of any biodiversity information network establishment:

(a) Biodiversity is to become nature capital for developing agriculture, forestry, industry, and services sectors;
(b) Supporting the involvement of nations in international activities and resolutions;
(c) Implementing national legislation concerning biodiversity;
(d) Supporting the GCHM of CBD through the development of a 'national focal point'; and
(e) Implementing National Strategy, Plans, and Programs concerning biodiversity issues.

The following steps of NBIN development will have to be carried out:

* To initiate the development of biodiversity information infrastructure (*i.e.* a basic tools for development of packaged value-added information to an extent, quality, and availability required for planning and decision-making, and private sectors). This basic tools could consist of geo-referenced biodiversity data and its distribution maps produced by utilizing existing specimen-base databases.

* To develop a mechanism which could bring about partnership. NBIN partners constitute registered members (as providers), unregistered providers, and users. Such a mechanism should incorporate 'formal/legal arrangements' for sharing and/or utilizing data/information. This will enable NBIN to establish cooperation with other related institutions in order to initiate the development of information systems infrastructure, and also to initiate the consolidation of a national network.

* To utilize the web as the backbone of a distribution network, with which a network of distributed biological information and swift user access to the available information sources can be developed.

* To develop metadata systems and applications.

* To develop appropriate applications of selected tools or techniques for serving, accessing, retrieving, and applying biodiversity information.

- To develop the distribution maps of data/information sources on biological resources, using metadata format obtained from NBIN members/providers/partners.

- To develop analyses on information gaps which should then be distributed across network members/partners, so that they could interact with each other to promote programs for fulfilling the gaps. This will enable NBIN to identify priority information needs and address the gaps accordingly.

- To support and encourage NBIN members/partners in fulfilling such information gaps as biodiversity distribution and status, landcover monitoring, ecological landscape information, catalogues of Indonesian biodiversity, and acessibly integrated geo-referenced data sets.

- To use information for producing biological information packages in its attempt to promote public appreciation towards the value of biological resources.

- To develop 'value-added packages' of biodiversity information using analysis and modelling tools which are applied to shared-data/information, for an extent, quality, and availability required for planning and decision-making, and private sectors. Such 'value-added information' could be presented in the forms of hard-copy (*e.g.* species distribution maps or environmental models and predictions), soft-copy (*e.g.* application tools), and multi-media (*e.g.* CDRoms). With this development, NBIN can corporate explicitly the value of biodiversity as the national capital within the constellation of forestry, agricultural, industrial, and service sector outputs.

- To promote the value of biological reources as the prime national capital using its network mechanism.

- To develop cooperative efforts with those interested in biodiversity information and effective decision making.

- To assess the accessibility of NBIN members/providers/partners to information technology. This will identify those capable of tranferring technology to the others.

- To create directories, dictionaries, and vocabularies of data/information sources on biodiversity and its ecosystems.

- To provide a leadership role in the development of national biodiversity information network.

- To undertake pilot projects such as populating the NBIN meta-database system and creating a distribution network system.

- To create a vigorous marketing strategy.

NBIN USERS or those who utilize data/information about biodiversity are targetted from all types of communities, ranging from policy and/or decision makers (from all sectors whose programs are related to biodiversity and its ecosystem), scientific communities (from all government research institutes and/or non-governmental institutions), business communities (states' companies, private companies, industrialists, or consulting companies), to public at large. In order to achieve a better synergy as well as a sustainability of an information network, the existence of a User Working Group will be urgently needed. This working group should represent all information network users.

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Developing Natural Resource Information Network for Prioritizing Biodiversity Conservation: An Avian Database Perspective

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Abstract

The current trend in natural resource conservation in the wake of new developmental initiatives focuses on sustainable use. To cope with the pace of dvelopmental activities in most of the developing countries, natural resource manager and policy makers need to be well equipped with latest and accurate information on the biological resources. Development of information resources in form of database hence assumes special significance in many countries for two simple reasons. The first is presence of basic information on different taxa at few selected places so that research community can use the information available for a variety of scientific purposes. The second is its instant use in policy making and planning for sustainable development. This paper describes how such information centres can be developed as a first step followed by development of resource banks in selected areas. Urgent efforts are needed to collate, collect such data which at present is patchy, unorganized and often not on a widely accepted format. Such efforts will also augment the Global Species Database besides providing numerous benefits at local and regional levels for making informed decisions.

Key Words: Birds, Biodiversity conservation, Database, GIS, Information Network, Sustainable development

Introduction

The new paradigm in resource conservation in the wake of current developmental initiatives focuses on sustainable use of natural resources. Under this shifting paradigm it has become increasingly important to develop mechanisms through which information can be quickly acquired to make wise decisions. It has become more important since the signing of Convention on Biological Diversity (CBD). The CBD places high premium on sustainable use of biological resources and equitable sharing of the benefits derived from the use of genetic resources. The convention stresses on the national action (Burhenne-Guilmin & Glowka 1994) in identifying a party's biological capital, developing and implementing a national biodiversity strategy.

To achieve this, biodiversity concerns need to be included into national decision making. And to do this the first step would be to acquire information essential for making such decisions. Researchers and scientific community can use the acquired information for conservation action and also for policy and decision making at the highest level. Through this paper, I have attempted to highlight importance of database on birds for biodiversity conservation and also integration of such database in a biodiversity information network for making informed decisions.

Perspective

To protect the rich biodiversity of the country efforts were initiated nearly four decades back by declaring key areas as protected areas. The real impetus came after the enactment of

Wildlife (Protection) Act of 1972. India is also signatory to major international conventions including the Convention on Biological Diversity (CBD), which indicate the country's commitment towards biodiversity. A network of more than 600 protected areas exist today. These areas are not only meant to save tigers, elephants or rhinos but the overall biodiversity.

Saving biodiversity means taking steps to protect genes, species, habitat and ecosystems. To save biodiversity is to document its composition, distribution structure and function and to understand various links to support sustainable development (WRI 1992). One of the weakest links in biodiversity conservation today stands out due to lack of baseline information in form of databases. This is a major handicap in developing and prioritizing areas for immediate conservation actions and hence initiation of reliable database activity should be first step toward respecting CBD and achieving sustainable development.

Why Birds?

Bird data has been used to highlight conservation issues worldwide. The knowledge and distribution of tropical forest birds while woefully inadequate, is often greater than that of other groups (Diamond 1985). Like many tropical regions birds in India are better studied than many other groups and there are more ornithologists and amateur bird watchers. This is due to the fact that birds are easy to observe, can be seen even in small patches of forest, gardens and urban landscape. Birds are also fascinating to watch by virtue of their colourful plumage, display and calls. Birds have also found place in history, paintings, and folklore and are more easily associated with humans than any other group.

With 2100 species and subspecies Indian subcontinent accounts for nearly 24% of the global avifauna. The avifauna of the country constitutes a significant portion of the country's biodiversity as India figures among the top 12 'megadiversity nations' of the world. The avifauna of Indian subcontinent has been well studied and properly documented by Ali and Ripley (1987). Of the 2100 species and subspecies occur in Indian subcontinent, India alone has 1200 species and 1500 including subspecies. With new Sibley & Monroe classification the number of species may well be 1300 (13% of world's birds). The Indian subcontinent also supports 142 endemic bird species, which is 10% of the region's avifauna.

Using Birds to Assess and Monitor Biodiversity

Birds by virtue of being mobile are better indicators of changes unlike sessile species. They have been characterized as "supertramps" by Fjeldsa (1994). Birds, being ecologically diverse and sensitive to various biotic and abiotic perturbations are one of the most suitable biological subjects for monitoring biodiversity. The diversity and richness of avian species in a community also mirrors the diversity and richness of the habitat and hence act as predictors of the quality and health of a habitat (Javed 1996). Avian endemism is correlated with endemism of other life forms. Bird data is very useful for large-scale habitat changes (Diamond 1985).

The sensitivity of avian communities to various changes makes them an ideal subject for assigning conservation value to sites (Fuller and Langslow 1986, Daniels *et al.*, 1991) and for monitoring environmental and ecosystem health (Jarvinen and Vaisaunen 1979). The patterns of diversity and richness of avian taxa have been found to be correlated with patterns of diversity of other taxa (Pearson and Cassola 1992). Fragmentation and disturbance causes decline in raptor density (Thiollay 1993; Julien and Thiollay 1996). Decline in species diversity as a consequence of habitat loss, fragmentation and degradation may alter the ecosystem processes (Naeem *et al.,* 1995), lower the resilience of ecosystem (Fjeldsa 1994) and has great implications for conservation.

Development of Bird Database

The preceding section has made it amply clear that birds are very important component of ecosystem, constitute significant portion of earth's biodiversity and are one of the most reliable indicators of biodiversity for rapid assessment of areas and initiating conservation activities. Existing quality baseline information on Indian birds prompted the development of a bird database. The baseline information is from Ali & Ripley (1987) and is being supplemented with new information. The database has been structured to input information on status, distribution, habitat types, biogeographical zones, coordinates, grid reference, threat types, sighting records, museum holdings and bibliographical information. For each record, information on sites, vegetation type, habitat, its extent, status of the area will also be entered. Existing database, such as Birdlife International's RDB database will also be utilized. Any other information that exists in India or elsewhere will be used. Active collaboration of the various national and international institutes and museum will be sought.

The Database Structure

Efforts are underway to procure funds to move the existing database to other platforms such as Oracle or Visual Basic. The database will contain the above mentioned fields in forms of the tables. Each field would be querriable. The layout of the database would be in form of basic tables. The first table will contain the list of the species, followed by another table containing detail information on species, population status, habitat type, bio-geographic zone, photo, call, information on food items. The third table will contain information on the distribution of species, both old, current and museum holdings. This would be used to allow users to plot distribution maps of species both old and current and also species occurring in a particular habitat type. This would be done using ESRI Map Object Internet map server along with a web server. Another table will provide access to this database for classification and ordination. Bibliographic information will be contained in a separate table for all the published information on the species. The database will be modular so that it could be regularly updated. The database would also be linked to other relevant databases and will serve as a Global Species Database (GSD) for birds.

Making Informed Decisions Using Bird Database

The use of various kind of data pertaining to different aspect of distribution of taxa has been used to accurately map the distribution and assess the gaps in information using Geographical Information Systems (GIS). Kemp *et. al.,* (1998) have used random bird sightings for geographical analysis of vegetation structure using GIS. The database can be used to identify and prioritize areas for immediate conservation needs and also to plan studies in those areas for which the present knowledge is inadequate. The existing bird database would also linkup and standardized database as per the requirement of the Species 2000 effort so that this database is just not used regionally and nationally but globally too (Fig. 1) and can act as GSD for Species 2000. The Bird Life International (BLI) has used such information in prioritizing areas for conservation, identifying threatened species. They have been able to chart centres of endemism using such a database. Similarly database with information on old and new species of birds can be used for comparing biogeographical patterns (Fjeldsa 1994). Prioritizing and conserving areas not only protects the birds but whole variety of life forms, many of them either endangered, threatened or endemic to the region.

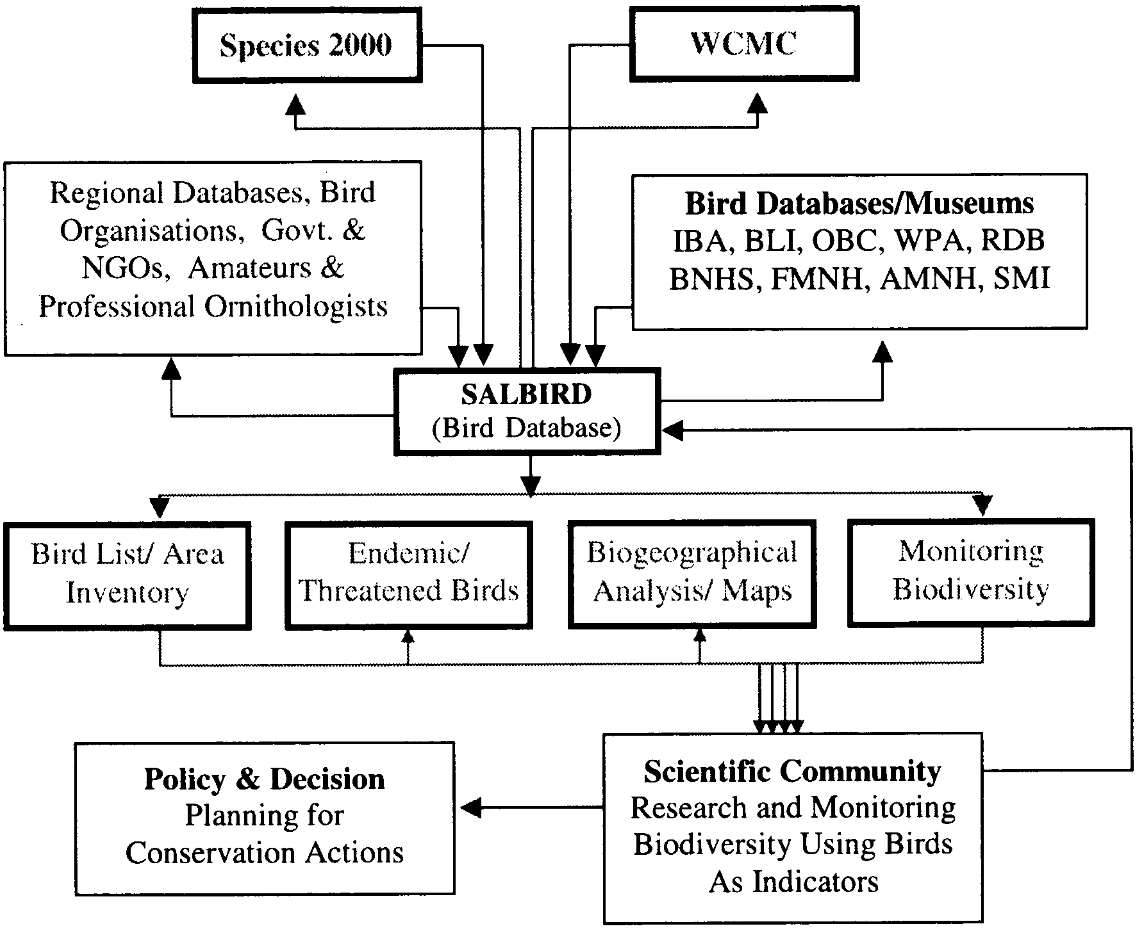

Fig. 1. Bird database and its prospective uses

Development of Biodiversity Information Network

Development of a natural resource information centre network is a key requirement for planning biodiversity conservation. To initiate action in this direction an autonomuos "National Biodiversity Conservation Monitoring Centre (NBCMC)" needs to be setup. The Centre would be within the Ministry of Environment and Forests of Government of India and will work very closely with other relevant programs and organizations such as Wildlife Institute of India, WWF's Indira Gandhi Conservation Monitoring Centre (IGCMC), M S Swaminathan Research Foundation (MSSRF), Lifescape Project of Nehru Centre, Bangalore and Department of Biotechnology (DBT). Subsequent to this regional centres atleast in four regions could be established. Regional centres would source information in their region from different agencies and individuals and will feed to NBCMC. NBCMC will process and analyze information in chalking out priorities for biodiversity conservation and provide such information to planners, policy makers and lobbyist (Fig.2). The information can also be made available to World Conservation Monitoring Centre, World Resources Institute, World Conservation Union, Species 2000 and other globally active organizations and databases.

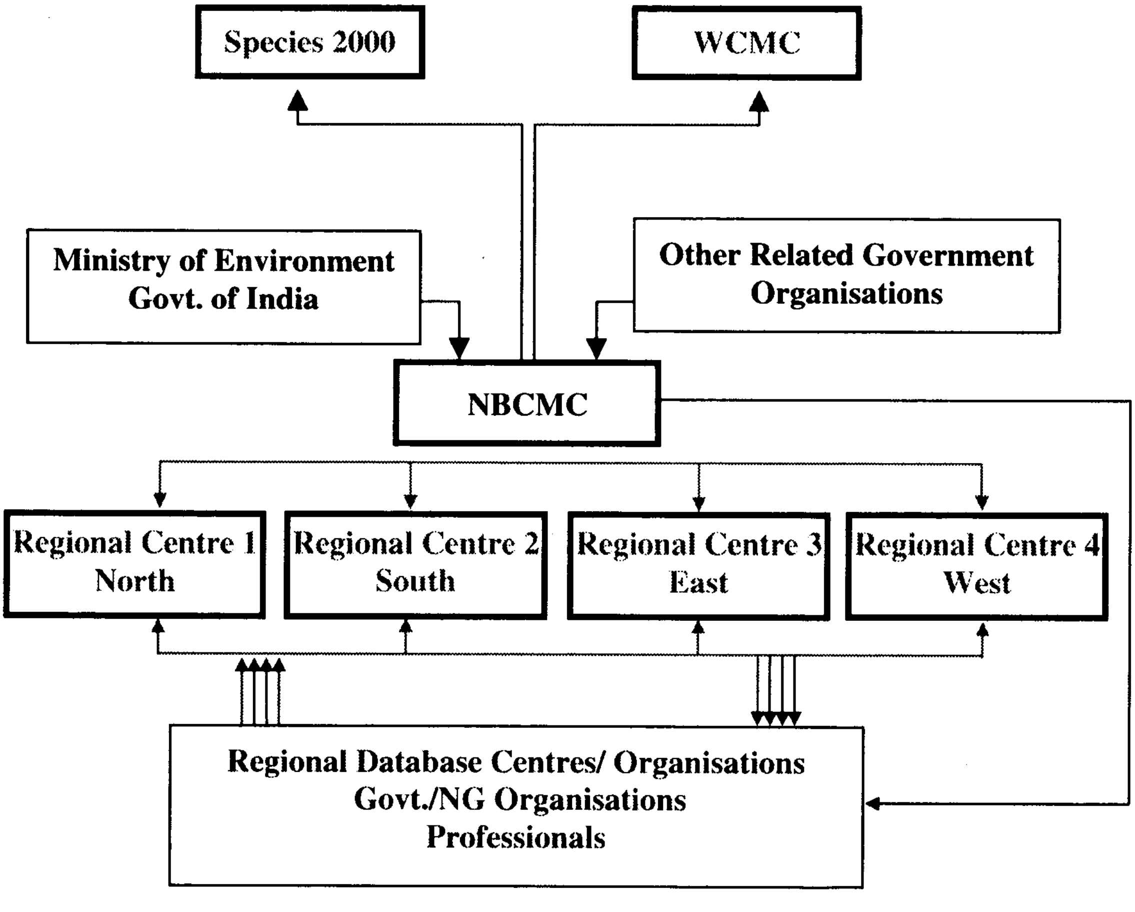

Fig. 2. Proposed plan for the development of biodiversity information network

Given lack of information, there is an urgent need to develop information centres. Subsequent to this other centres, capable of doing such work can be identified and networked with the established centres (Fig. 2). These centres would not only be working towards collection of information and database development but also towards use of this information for initiating conservation actions through public participation, involvement of non-government and government organizations. Information on different taxa at few selected places can also be used by the research community for scientific purposes. Such an approach would require a fully functional information system on our biological resources.

Indian Bird Conservation Network (IBCN) has been recently setup in India to conserve birds and their habitat as part of biodiversity in India. To monitor and initiate conservation action, the first step would be to build a database. In such a situation the existing database would be useful to begin with and this could be further strengthened with the proposed development of network for access and retrieval of information by network partners and those outside the network. The Nature Conservancy in USA has created nearly 87 biodiversity information centres. Known as Conservation Data Centres, these centres provide a computerized inventory on biological resources of the region.

The Birdlife Internationals, formerly ICBP's project "Putting Biodiversity on Map" (ICBP 1992) followed by "Endemic Bird Areas Project (EBA)" (Stattersfield *et al.,* 1998) and recently launched "Important Bird Areas (IBA) Project are an effort in this direction. The first two projects have been able to highlight areas for conservation using birds as tools and indicators of biodiversity and endemism. The EBA project has documented that conservation of a major part of the earth's terrestrial biodiversity can be ensured by focussing conservation resources and actions within a relatively small total area, identified as EBA's (Stattersfield *et al.,* 1998). These efforts not only have helped in prioritizing conservation of birds and their habitats but more importantly the total biodiversity.

Conclusion

Looking at the state of information that at present is patchy, unorganized and often not on a standard and widely accepted format development of databases on various components of biodiversity is top priority for any nation. It is all the more significant and immediate concern in the tropics, the major centres of biological diversity. Tropical regions in spite of high diversity are information poor. Adding to this is the new development initiatives under the garb of globalisation in new and emerging market economies. The total impact of all these combined would be catastrophic if urgent conservation initiative is not undertaken. One such initiative would be to develop a national level centre (NBCMC) for monitoring and conservation of biological diversity. This autonomous centre would cater to developing conservation priorities based on systematic and scientific accumulation of information, its processing and analyses. The centre would use various component of biodiversity i.e. birds, plants etc. on which information is more easily available to draw such priorities and initiate and strengthen reliable database activities amenable to Species 2000.

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DWNP Conservation Programmes under the National Policy on Biological Diversity

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Abstract

After signing the Convention on Biological Diversity, Malaysia has taken the necessary steps to conserve its Biological Diversity. It has conducted country study on Biological Diversity consistent with the UNEP guidelines. Knowing the status of Biological Diversity (as base line information) Malaysia formulated a National Policy to be used as guidelines to manage its Biological Diversity. DWNP which is responsible for conserving terrestrial wild fauna and protected areas, is playing a major role in line with the policy guidelines. Though DWNP is bogged down with limited resources of qualified personnel and financial constraint, it has been able to contribute considerably towards fulfilling the Biological Diversity conservation.

Key Words: ***National Policy, strategy and programmes on Biodiversity.***

Introduction

Malaysia is a signatory to the Convention on Biological Diversity (CBD) which was generated from the United Nations Conference on Environment and Development (UNCED) in Rio de Janeiro in 1992. Malaysia has incorporating it into national policies, and has a set of commitments under the treaty (Anon.,1992) At national level, Malaysia's efforts to implement the convention was coordinated by the National Committee on Biological Diversity and led by the Ministry of Science, Technology and the Environment (MOSTE). The National Biological Diversity Committee, chaired by the Secretary-General of MOSTE, has been formed to coordinate the formulation and implementation of the National Policy on Biological Diversity. Under the National Committee is the Technical Committee on Biological Diversity with three task forces working on specific issues such as national policy on Biological Diversity (BD), country study on BD and access to genetic resources. A national Advisory Committee on Genetic Manipulation was also established. Malaysia drafted a national policy on BD which was launched in October 1997 and has since became the reference guidelines for the implementation of the National Biological Diversity conservation programmes.

MOSTE commissioned a Country Study on Biological Diversity leading to the formulation of the assessment of Biological Diversity in Malaysia and Background Documents. Financial assistance to undertake the Country Study and preparation of the documents was provided by the United Nations Environment Programme (UNEP).

As we all know biological diversity covers a very wide range of subjects, from genetic to species and habitat variations, domestic as well as wild matters. With such broad subjects it cannot naturally be managed by a single agency because there are already in existence agencies designated to a particular task. On the other hand, it is difficult to reorganise different agencies into one as it might involve legal and constitutional implication involving federal and state interests.

Apart from the National and Technical Committee on BD, administratively BD matters are legally looked after by at least five authorities. The Forestry Department is basically looking after the forestry while Agricultural Department is on the agricultural related plant and insects. Department of Veterinary Services concentrates more on domestic animals while Department of Fishery covers aquatic life in both sea and fresh water. Wildlife in animal kingdom from mammals to insects are covered under the jurisdiction of the DWNP.

This paper highlights steps taken by the Department of Wildlife and National Parks Malaysia (DWNP) in its effort to protect the national biological diversity in compliance with the international convention and the national policy. It also indicates the status of biological diversity in the country but confining only to those related with the DWNP jurisdiction.

Components in the Biological Diversity Policy

The policy outlined the country's vision, principles and objectives of conserving biological diversity. It rationalizes the reasons for the need to protect the Biological Diversity. The present status of conservation and management are gathered as a basis for formulating strategies in the policy and followed by outlining strategies for effective management and action plan of programmes to be implemented.

DWNP Roles

DWNP is the Federal government agency entrusted to conserve and manage wildlife species and to manage protected areas in the form of National Parks, wildlife reserve and wildlife sanctuaries for the preservation and conservation of flora, fauna and natural habitats. Outside protected areas, DWNP has no jurisdiction over the land or habitat but instead, protects the species that are listed under the Protection of Wildlife Act 1972.

Legislative amendment. Initially, under the Wildlife Protection Act 1972 only indigenous species were protected; include 51 large and small mammals, 7 reptiles, over 700 birds and 10 insects. None of the amphibian are listed under protection. Malaysia signed the CITES Convention on 20th October 1977 and rectified on 18 Jan 1978. Only in 1994 Malaysia was able to incorporate CITES lists into the local wildlife protection legislation. At present all species under CITES lists are listed under the Schedule Two of the Protection of Wildlife Act 1972. This move has enabled the authority to take legal action against offenders of related CITES species.

The DWNP with the assistance of MOSTE is seriously looking into the possibilities in ammending the list of protected species in the Protection of Wildlife Act to cover all wild fauna species ranging from invertebrates to large mammals.

Conservation Programmes

Translocation. Apart from applying legal instrument as a management tool, from early 70's to late 80,s at the era of agricultural development, DWNP concentrated on capture and translocation of elephants from forest fragments to a more promising area. This was carried out in order to reduce damage to agricultural plantation as well as to protect elephant from being poisoned, killed or injured by plantation owners. The translocation programme is still going on but at a scaled down pace and as a last resort.

Captive breeding. Rapid progress in the agricultural development had sacrificed vast track of natural forest of prime wildlife habitat. It was even worse when logging roads which were constructed for transporting timber have provided easy access to poachers to carry out their activities. As a result, popular game animals such as deer and gaur had dwindled very rapidly.

Realising the dwindling population of these two species, DWNP has carried out a pilot study on captive breeding and followed by setting up semi wild farms at different localities. For deer, captive breeding was started with few pairs taken from different zoos within the country and from confiscated individuals kept illegally. The gaur breeding stock was taken from the wild since there was not any of it in captivity at that time.

Besides deer and gaur, DWNP has not forgotten birds especially the breeding of galliforms, which are found in the lowland forest. These birds were also seriously threatened with extinction and habitat loss. At present DWNP has in its captivity all its eight indigenous species of pheasants. Some of them are breeding successfully while others need indepth studies to improve the breeding technique.

Inventory. In line with the national policy requirements, DWNP began inventory works in protected areas under its jurisdiction and other BD rich areas of special interest. The main objective is to know the species diversity in these areas. The inventory however did not include lower plant and animal species. DWNP hopes to carry out inventory in all its protected areas over the next few years. The information will be documented and kept as its database and will be used in drawing up management plans for the concerned areas.

Wildlife Plan

DWNP has drafted a wildlife plan (Anon., 1992) for conservation of wildlife in Malaysia. It outlined actions needed for species depending on their conservation status. It includes all species of large mammals which are more vulnerable than the smaller relatives. Small mammals and certain groups of birds which play important roles in ecosystem equilibrium are all in the plan.

Conservation Strategy

Creation of Ecotourism Division at DWNP. Ecotourism seem to be a new paradigm in tourism industry in Malaysia. The interest has been overwhelming in the local arena within the business circles of tourism related ventures. Any programme with ecotourism tag would get support from the government. The creation of the Ecotourisn Division in DWNP was partly the result of eagerness in promoting ecotourism in the country. The function of this division is to promote ecotourism and at the same time provides guidelines on development of environmental-friendly eco tourism site.

In a way promoting ecotourism would give advantage to wildlife protection. It will open the eyes of many that forest can bring in revenue without it being destroyed. Although to a certain extend ecotourism would have a negative affect on wildlife, it is a far better alternative, rather than destroying the habitat by extracting timber from it. Protecting forest means protecting wildlife habitat and its contents.

Strengthening DWNP Capacity. At one time, in the era of rapid agricultural development DWNP was only a small neglected government agency. It was known as an agency nothing more than that of issuing hunting licenses, preventing illegal hunting and shooting rouge elephants and wild boar. This perception was due to the over emphasis on development and thus forgetting the importance of wildlife to man and the environment. It was also partly due to the failure of the DWNP to portray its importance in the development limelight. The failure of the DWNP to shine was the results of weak institutional capacity and the low profile approach it undertook.

At the begining of this decade, with the environmental and biological diversity issues becoming high on priority list, DWNP managed to catch the limelight and gradually becoming more important. With financial and technical assistance from external sources like the Danish Government's DANCED Programmes, the DWNP prepared its strategic plan to build up its institutional capacity. Emphasis on additional staffing, proper training, aggressive awareness programmes, human resource development and appropriate priority programming are some of the plans toward capacity strengthening.

Strengthening Protected Area System. Malaysia has about 6 percent of the total area reserved under protected areas (PA) known as either national parks, wildlife reserves and wildlife sanctuaries. This figure does not include permanent forest and virgin jungle reserves (as they do not comply with UNEP's defination of PA) under the jurisdiction of Forestry Department.

In the early days of its establishment DWNP had never thought of managing PAs in intensive manner because by leaving it undisturbed the habitat and the BD resources found within would be protected. Later, such assumption was however misunderstood as neglecting the PAs. Some of the PAs were encroached and DWNP realised the pressures mounted forcing the DWNP to prepare comprehensive plans for its PAs. Again, with the combined government and external and financial and technical assistance the DWNP is preparing a Management Plan for Krau Wildlife Reserve (one of the bigget PAs). This plan is being implemented and will set as a model for the rest of the PAs in the country. In addition with some assumption NIES, Japan GAP analysis method is being utilised to map out the habitats of the Merapoh section of Taman Negara National Park.

Enchancing Research Activity. One of the setback in the DWNP progress (feedback from clients) was the shortfall in its research. Very limited research works were conducted eventhough a lot of things need to be uncovered. The classic reasons for this were the lack of qualified personnels and financial constraints.

The situation has remarkably changed in recent years when additional graduate officers were recruited and deployed under the research division. This change however is inadequate to accommodate to the previous setback and the increasing demand for scientific data and information. To cope with the demand, the DWNP will have to intensify cooperation with universities, NGOs and other agencies both local and international in the future research programmes.

Public Awareness. Awareness among the general public on biological diversity conservation and environmental issues such as global warming, green house effect, ozone layer depletion etc. is still at minimal level. Some changes have been felt to take place at high level of government officials and intelectual circles. The general public need to be educated on the related subjects in order to gain their support to conserve biological diversity and support in other environmental related programmes.

Awareness programme is a long term process. The result could not possibly be realised overnight. Therefore the DWNP has developed and has been conducting environmental awareness with the priority target groups are students at secondary school and institutes of higher learning. Young pupil at primary schools are also being instilled with conservation knowledge hoping that the early age exposure will be more effective. The awareness programmes include talks in class room, camping in the jungle, slide and video documentary show, jungle tacking and expedition.

Constraints

The tempo of progress in BD conservation programmes is hindered by the complexity in species diversity and the difficulty to access into the densely covered tropical forest, especially related to population survey. Low density in individual species on the other hand, made it difficult to conduct behavioural study of the animals. Advance technology could possibly resolved the said constraints. Application of satellite telemetry to study elephant movement, and camera trapping to study tiger population have shown some fairly successful results. Financial constraint and shortage of expertise in related fields however limit the application of advance technology in the third world countries.

Conclusion

Malaysia has benefitted very much in terms of economic development through financial assistance from various resources, particularly Japan. Presently DWNP plays a major role in implementing the National Policy on Biological Diversity in Malaysia. Japanese institutions like NIES are welcome to collaborate with DWNP. This will assist in institutional strengthening of DWNP conservation of Biological Diversity reserves for the benefit of the nation and also for the whole mankind.

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Abstrek

Selepas menandatangani konvensen kepelbagaian biologi, Malaysia telah mengambil langkah-langkah yang perlu untuk melindungi kepelbagaian tersebut. Malaysia telah menjalankan kajian negara ke atas kepelbagaian biologi untuk menilai status perlindungan kepelbagaian biologi selaras dengan garispanduan UNEP (Program Alam Sekitar Bangsa-Bangsa Bersatu). Dengan mengetahui status kepelbagaian biologi negara (sebagai maklumat dasar), Malaysia telah mengubal satu Dasar Kepelbagaian Biologi Negara untuk digunapakai sebagai garispanduan untuk menguruskan kepelbagaian ini. Sebagai satu badan yang bertanggungjawab untuk pemuliharaan fauna liar daratan, Jabatan PERHILITAN telah memainkan peranannya sejajar dengan dasar yang digubal. Walaupun Jabatan PERHILITAN dibelengu dengan tekanan kekurangan kewangan dan pegawai yang berkelayakan, ianya telah berupaya untuk memberi sumbangan besar dalam memulihara kepelbagaian biologi negara ini.

Constructing Informational Infrastructure for Bio-Resources – A Prototype Bio-Resource Database

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Abstract

JST has been conducting a project "Promotion System for Intellectual Infrastructure of Research and Development FY1999", supported by the Science and Technology Agency (STA) of Japan. The project aims to develop a Bio-Resource database, a directory database comprising information on various kinds of biological research materials, such as microorganisms, plant cells, and animal cells. The database is intended to promote biological resource sharing among researchers in Japan. In the first phase of the project JST developed a prototype Bio-Resource database, comprising actinomycetes selected by the International Streptomyces Project (ISP).

Key Words : Bio-Resource, Directory database, Microorganism

Introduction

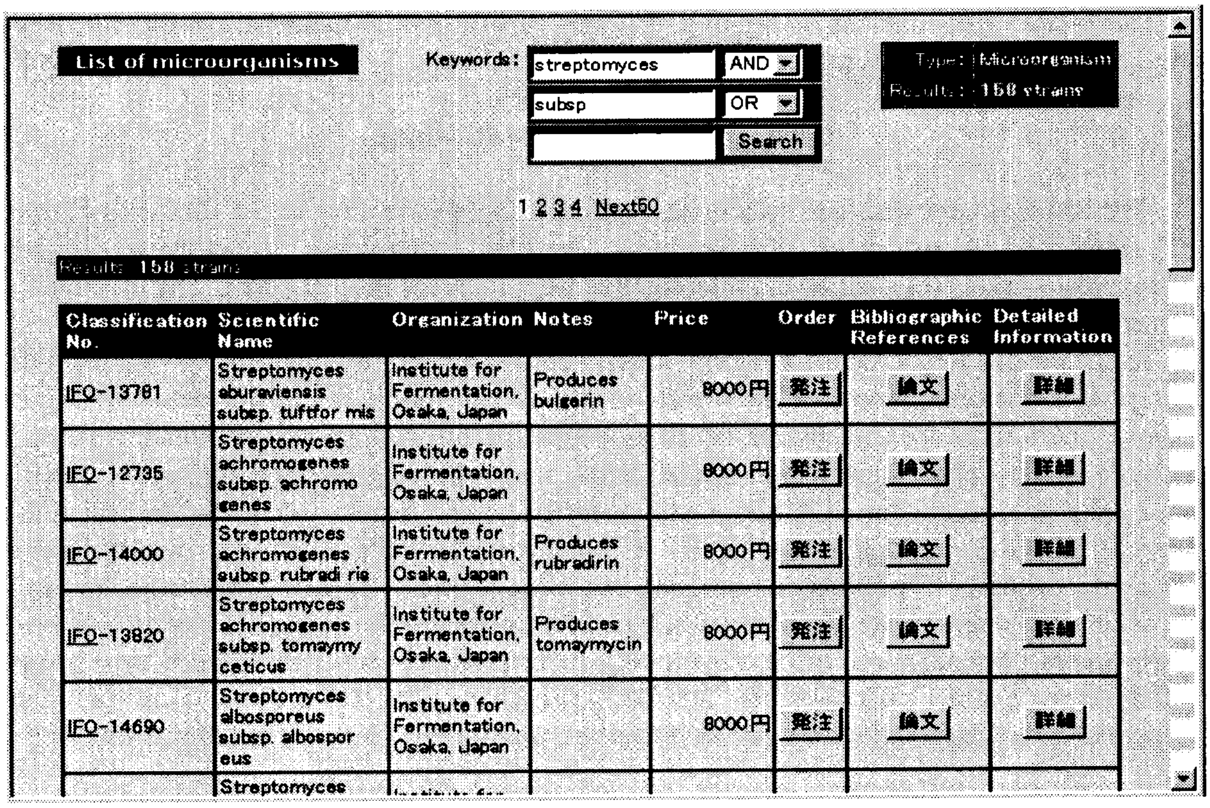
To promote biological resource sharing in Japan, JST has been conducting a project for developing Bio-Resource databases. This project was carried out using Special Coordination Funds of the Science and Technology Agency (STA) of the Japanese Government. Bio-Resource databases are directory databases that help researchers locate and obtain the biological research materials they need. Major biological banks and culture collections in Japan have joined the project.

In order to express adequately the variety of biological research materials available, we have coined the term "Bio-Resource", here defined as various kinds of biological resources useful for research in biology and related fields. Biological resources include microorganisms, yeasts, bacteria, protozoans, animal cells, plant cells, genes, and so on.

The national information infrastructure is not well established, making it difficult to promote biological resource sharing among researchers. The major biological banks and culture collections in Japan are generally small in size and don't have enough human and financial resources to organize and provide information about their Bio-Resource collections. According to a JST survey of Bio-Resource distribution in Japan, some small research groups share Bio-Resources while others have difficulty locating and obtaining the research materials they need. In these circumstances, many researchers have to contact each biological bank to obtain necessary research materials.

Goals of the Project

The project will develop an information system that collects a range of Bio-Resource information from as many biological banks and culture collections as possible. The project will create Bio-Resource databases, provide access to them and, as a result, promote Bio-Resource sharing among researchers in Japan. Each Bio-Resource database record contains a variety of data elements characterizing a biological material including the names of the owner.



List of microorganisms

Keywords: streptomyces AND / subsp OR / Search

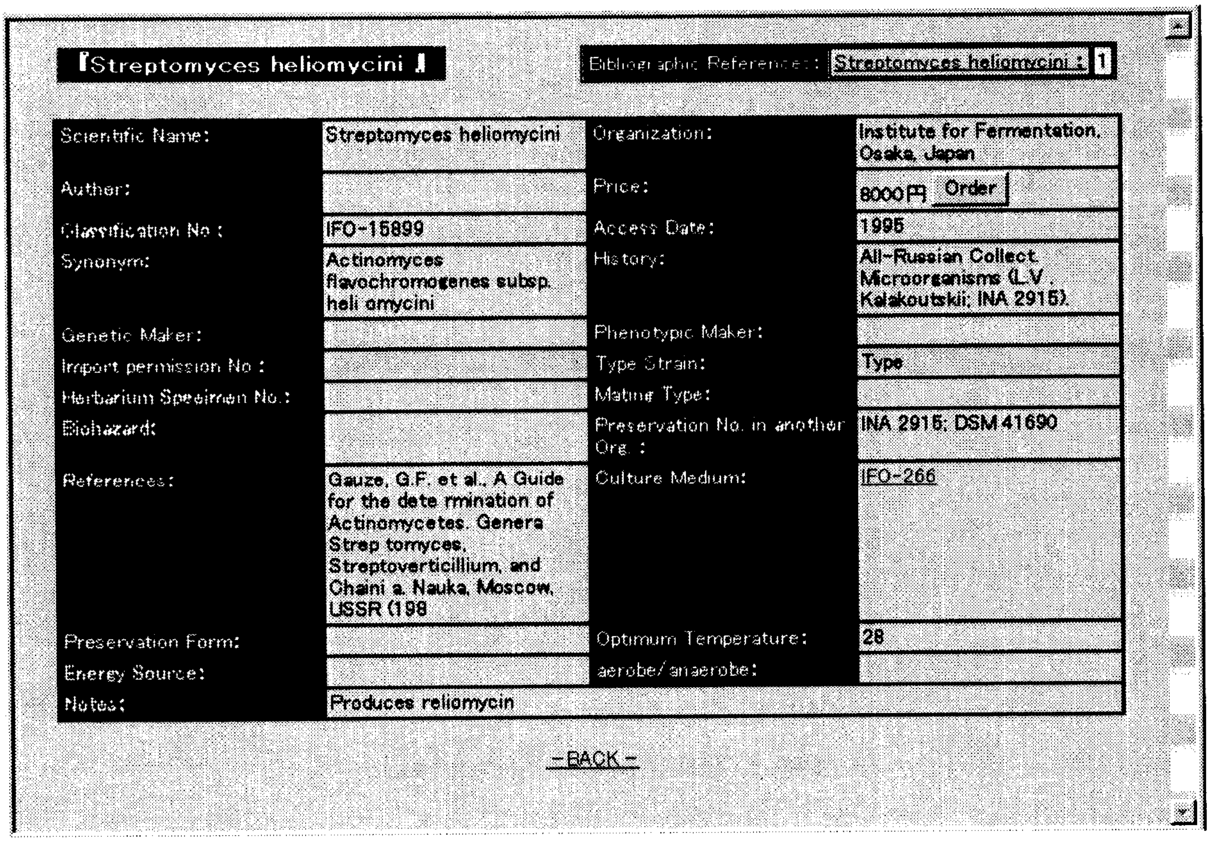
Type: Microorganism
Results: 158 strains

1 2 3 4 Next50

Results: 158 strains

Classification No.	Scientific Name	Organization	Notes	Price	Order	Bibliographic References	Detailed Information
IFO-13781	Streptomyces aburaviensis subsp. tuftfor mis	Institute for Fermentation, Osaka, Japan	Produces bulgerin	8000円	発注	論文	詳細
IFO-12735	Streptomyces achromogenes subsp. achromogenes	Institute for Fermentation, Osaka, Japan		8000円	発注	論文	詳細
IFO-14000	Streptomyces achromogenes subsp. rubradi ris	Institute for Fermentation, Osaka, Japan	Produces rubradirin	8000円	発注	論文	詳細
IFO-13820	Streptomyces achromogenes subsp. tomaymyceticus	Institute for Fermentation, Osaka, Japan	Produces tomaymycin	8000円	発注	論文	詳細
IFO-14690	Streptomyces albosporeus subsp. albosporeus	Institute for Fermentation, Osaka, Japan		8000円	発注	論文	詳細
	Streptomyces						

Fig. 1. Search Results (Simple).



『Streptomyces heliomycini』

Bibliographic Reference: Streptomyces heliomycini : 1

Scientific Name:	Streptomyces heliomycini	Organization:	Institute for Fermentation, Osaka, Japan
Auther:		Price:	8000円 Order
Classification No.:	IFO-15899	Access Date:	1995
Synonym:	Actinomyces flavochromogenes subsp. heli omycini	History:	All-Russian Collect. Microorganisms (L.V. Kalakoutskii; INA 2915).
Genetic Maker:		Phenotypic Maker:	
Import permission No.:		Type Strain:	Type
Herbarium Specimen No.:		Mating Type:	
Biohazard:		Preservation No. in another Org.:	INA 2915; DSM 41690
References:	Gauze, G.F. et al., A Guide for the dete rmination of Actinomycetes. Genera Strep tomyces, Streptoverticillium, and Chaini a. Nauka, Moscow, USSR (198	Culture Medium:	IFO-266
Preservation Form:		Optimum Temperature:	28
Energy Source:		aerobe/anaerobe:	
Notes:	Produces reliomycin		

-BACK-

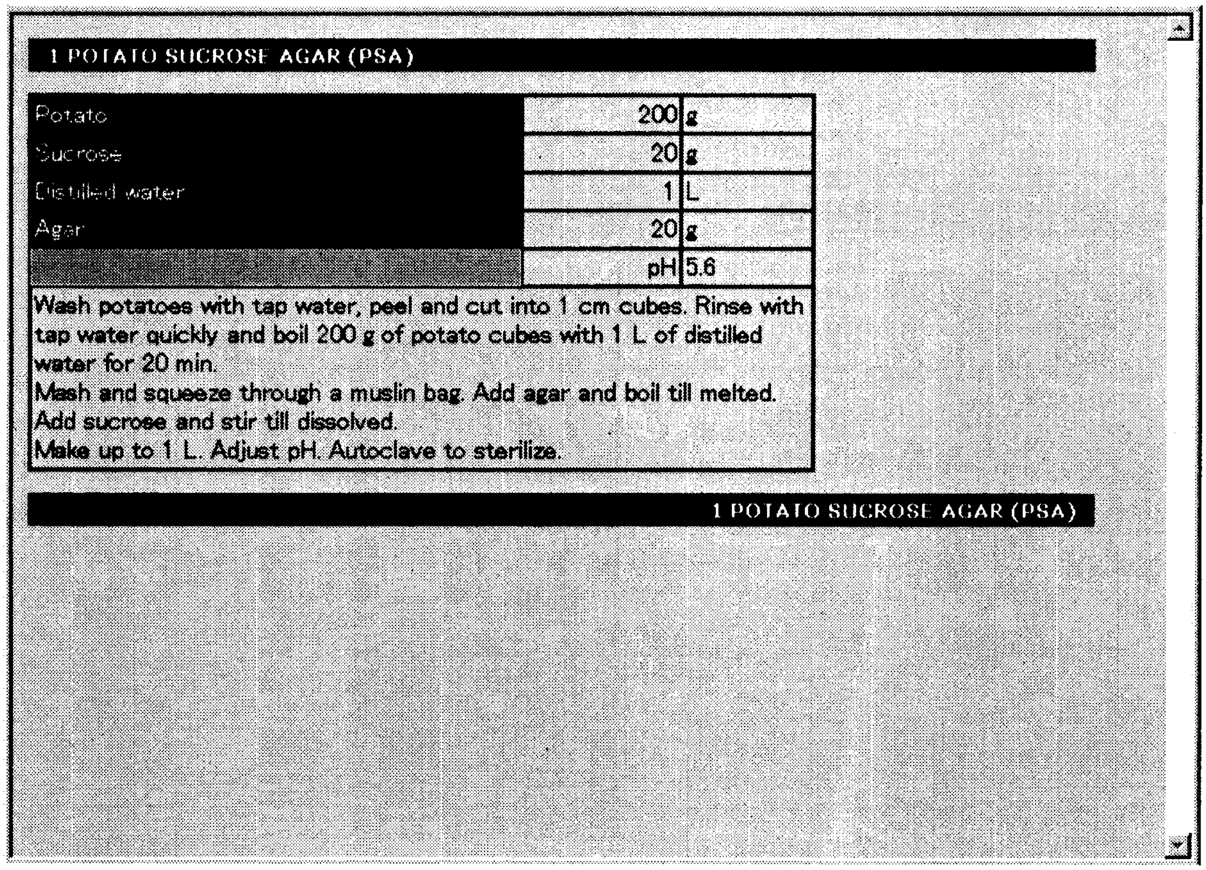
Fig. 2. Search Results (Detailed).

There are also databases relating to the Bio-Resource Database, each including bibliographic references, culture media information, and so on.

Prototype Bio-Resource Database

The Bio-Resource database system has been developed in several stages. In the first stage, JST developed a prototype Bio-Resource database comprising information on 500 actinomycete strains selected by the International Streptomyces Project (ISP). The Institute for Fermentation, Osaka (IFO), owns these strains.

To search Bio-Resource information, a user submits a query by inputting keywords in the dialog box of the search screen. The search result is in two forms, simple and detailed. Figure 1 shows the simple form, a list of microorganisms. Each row shows information about a microorganism – classification number, scientific name, holding organization, notes, pricing (with links to an order form), bibliographic references, and ancillary 'detailed information'. Figure 2 shows an example of the latter. It contains the following items: a scientific name, synonymy, author, classification number, genetic marker, import permission number, herbarium specimen number, biohazard status, bibliographic references, preservational form, notes, holding organization, price, registration date, origin, phenotypic marker, type strain, mating type, preservation number in another organization, culture medium, optimum temperature, oxygen relationship: aerobe/anaerobe, and finally a link to the order form.



1 POTATO SUCROSE AGAR (PSA)

Potato	200	g
Sucrose	20	g
Distilled water	1	L
Agar	20	g
	pH	5.6

Wash potatoes with tap water, peel and cut into 1 cm cubes. Rinse with tap water quickly and boil 200 g of potato cubes with 1 L of distilled water for 20 min.
Mash and squeeze through a muslin bag. Add agar and boil till melted.
Add sucrose and stir till dissolved.
Make up to 1 L. Adjust pH. Autoclave to sterilize.

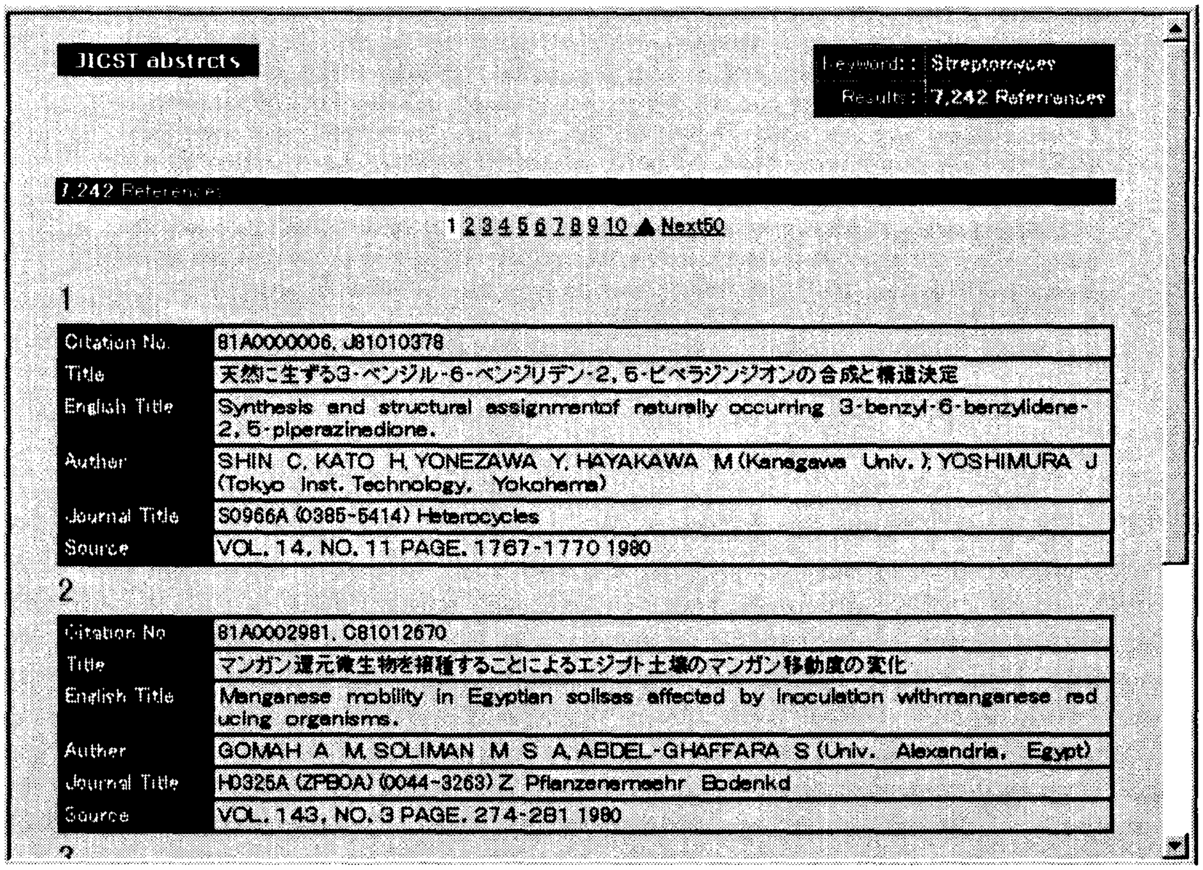
1 POTATO SUCROSE AGAR (PSA)

Fig. 3. Culture-medium Database.

In the prototype system, three databases related to the Bio-Resource database are also available. They contain culture media information, bibliographic references, and the biological bank (IFO)'s guidelines for deposition and distribution of research materials, respectively, and are searchable independently as well as simultaneously.

The culture-medium database can be used to find the most appropriate medium for a strain and the method for preparing it (Fig. 3).

JST's bibliographic databases in the field of science, technology, and medicine will facilitate finding bibliographic reference data related to your inquiry (Fig. 4). Anyone who wishes to deposit or purchase biological research materials can refer to the guidelines of the corresponding biological bank or culture collection. IFO also provides the guidelines in its homepage.



1

Citation No.	81A0000006, J81010378
Title	天然に生ずる3-ベンジル-6-ベンジリデン-2, 5-ピペラジンジオンの合成と構造決定
English Title	Synthesis and structural assignmentof naturally occurring 3-benzyl-6-benzylidene-2, 5-piperazinedione.
Auther	SHIN C, KATO H, YONEZAWA Y, HAYAKAWA M (Kanagawa Univ.), YOSHIMURA J (Tokyo Inst. Technology, Yokohama)
Journal Title	S0966A (0385-5414) Heterocycles
Source	VOL. 14, NO. 11 PAGE. 1767-1770 1980

2

Citation No	81A0002981, C81012670
Title	マンガン還元微生物を接種することによるエジプト土壌のマンガン移動度の変化
English Title	Manganese mobility in Egyptian soilses affected by inoculation withmanganese red ucing organisms.
Auther	GOMAH A M, SOLIMAN M S A, ABDEL-GHAFFARA S (Univ. Alexandria, Egypt)
Journal Title	H0325A (ZPBOA) (0044-3263) Z Pflanzenernaehr Bodenkd
Source	VOL. 143, NO. 3 PAGE. 274-281 1980

Fig. 4. Bibliographic References Database

Future Plans

As mentioned earlier, the project intends to expand the Bio-Resource database in terms of the kind and the number of biological research materials. The number of biological banks and biological collections that provide Bio-Resource information is expected to increase.

We also hope to make the Bio-Resource database system available worldwide. Although the database content is mostly written in English, graphic user interface is Japanese oriented. Internationalization is one of the challenges in this era.

Medicinal Plant Information on Some International Databases

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Abstract

Medicinal plant is one of the most valuable natural resources. It is said that more than 10,000 plant species are used for medicinal purposes mainly as traditional medicines and at least 25 percent of drugs used in modern pharmacopoeia are derived from plants. As strong interest in natural-healing and alternative medicine grows, more and more people are turning to traditional herbal treatment. In order to develop new drugs for helpless diseases and to obtain scientific research result for safety and efficacy, to organize usable and reliable medicinal plants information is great concern by researchers and clinicians. One of the issues to provide reliable medicinal plant information is that it is not always possible to identify some species. This may be due to the fact that same plant might be known by different local names, or widely differing species are known by the same name in different cultures. In this paper the author does not attempt to reach a solution, rather the aim is to present the issues associated with medicinal plant information on some international databases.

Key Words: Database, Headings, Information, Medicinal plant, Thesaurus

Introduction

Medicinal plant information is much more concerned in the world today. In developed countries, chronic disease and lifestyle related diseases are increasing as growing number of the aged, and some of the diseases cannot be coped with only by modern medicine. Medical cost is another aspect. Modern medicine usually cost lots in using high-tech machines for examination. Under these conditions, complementary remedies and natural healings are growing world widely. Herbal treatment is remarkably noticed with a strong interest as complimentary and alternative medicine. In developing countries, where medical supplies and medical care system have not been fully covered yet, medicinal plants still play a very important roll of medical resources. Medicinal plants in local area are commonly used by herbal doctors and for domestic care in primary care.

Medicinal plants have a great potential value for new drug development. Medicinal plants are staple new drug resources and traditional knowledge offers an idea of development strategy for new drugs. It is said that more than 10,000 plants are used for medicinal purposes mainly as traditional medicines and at least 25 percent of drugs used in modern medicine are derived from medicinal plants. But most of the plants are not completely studied yet, and some species of them are on the verge of extinction before the studies have been done.

Therefore, not only for protection of plant resources but also for preserving traditional knowledge of plant usage, systematization of medicinal plant information are essentially needed. Sustainable utilization of medicinal plant resources and good service of medicinal plant information will bring health for all in the world.

Materials and Methods

Some international databases were investigated on the information about medicinal plants.

The databases, which were investigated, were as follows.

AGRIS, the international information system for the agricultural sciences and technology, created by the Food and Agriculture Organization of the United Nations (FAO) in 1974, in order to facilitate information exchange and to identify world literature dealing with all aspect of agriculture. (http://www.fao.org/agris)

IBIDS, the International Bibliographic Information on Dietary Supplements database is one of international scientific literature database on dietary supplements, including vitamins, minerals, and botanicals. It is produced by the Office of Dietary Supplements (ODS) at the National Institutes of Health (NIH) in the US, in order to assist the public, health care providers, and researchers in locating credible, scientific literature on dietary supplements. (http://odp.od.nih.gov/ods/databases)

JICST database is one of the world's most comprehensive and largest databases with about 11.7 million citations (March, 1998) in the field of science and technology, including unique literatures published in Japan. It is organized by the Information Center for Science and Technology in the Japan Science and Technology Corporation (JST). The JISCT-E is English language database, which contains citations published in Japan and extracted from the JICST file published in the world. (http://www.jst.go.jp/EN/JICST)

MEDLINE is provided by the US National Library of Medicine at the NIH. It covers 3700 primary journals and monographs on virtually every subject in the field of biomedicine. (http://www.nlm.nih.gov/databases/databases_medline.html)

These databases were examined to check terms about medicinal plants. The heading terms related to ‘medicinal plants’ were searched on the web pages of the databases through the Internet on 12 July 1999, except the JICST database. The heading terms were used for searching descriptors under the terms.

The Multilingual Agricultural Thesaurus (AGROVOC) of the AGRIS database was directly accessed through the Internet and offered descriptors under the term ‘Drug Plants’. On the IBIDS database, they have keyword list classified with 5 categories; General Search Terms, Vitamins, Minerals, Amino Acids, and Herbal and Botanical Supplements, and descriptors under the Herbal and Botanical Supplements were obtained from the list. The JICST database was accessible through the Internet with password but they did not offer their thesaurus on the web. The JICST Science and Technological Thesaurus 1993 (English and Japanese versions) was looked through to find heading term equivalent to medicinal plants and picked up narrower terms of the term ‘medical plant’. On the MEDLINE, the MeSH (Medical Subject Headings) Browser was used for finding descriptors under the term ‘Plants, Medicinal’.

Results

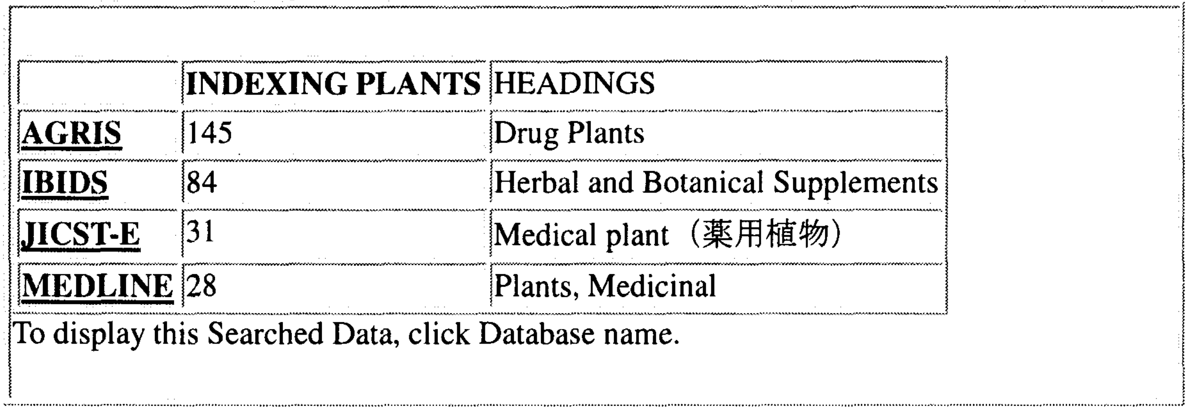
On the AGROVOC of the AGRIS database, the term of ‘Drug Plants’ was a heading term to equivalent to ‘medicinal plant’, and 145 plants were listed as narrower terms of ‘Drug Plants’. All of the plants were given with botanical name. The keyword list of Herbal and Botanical Supplements on the IBIDS database had 84 plants with their botanical names and common names. The term of ‘medical plants’ was used for ‘medicinal plants’ as a heading term in the JICST Science and Technological Thesaurus 1993. As narrower terms of ‘medical plant’, 31 plants were listed with botanical names on the thesaurus as shown in Table 1. The term ‘Plants, Medicinal’ was heading on the MeSH of the MEDLINE, and 28 plants were listed with common names. A summary of results was shown in Table 2.

Table 1. List of 'medical plant' on the JICST Science and Technological Thesaurus 1993.

medical plant

- Aconitum
- Aloe
- Angelica acutlloba
- Artemisia vulgaris indIca
- Bupleurum
- Cassia glauca
- Coix lacryma-joli frumentacea
- Coptis
- Curcuma longa
- Datura
- Digitalis
- Elettaria cardamomum
- Ephedra
- Foeniculum
- Glycyrrhiza
- Hyoscyamus
- Linum usitatissimun
- Matricaria chamomilla
- Myristica
- Paeonia lactlflora
- Panax schinseng
- Papaver
- Pinellia
- Plantago
- Rauwolfla
- Rheum
- Rictnus
- Strychnos
- Syzygium aromaticum
- Thailictrum
- Trigonella

Table 2. Medicinal plant information on the international databases.



	INDEXING PLANTS	HEADINGS
AGRIS	145	Drug Plants
IBIDS	84	Herbal and Botanical Supplements
JICST-E	31	Medical plant（薬用植物）
MEDLINE	28	Plants, Medicinal

To display this Searched Data, click Database name.

Discussion

There are different headings used for 'medicinal plants' on the 4 major international databases. The term 'medical plant' on the JICST thesaurus should be substituted for 'medicinal plant'. The heading of 'Drug Plant' on the AGROVOC in the AGRIS is so simple and clear that it may be useful for lay people. It is not easy to choose one of the terms, however standardization of terms should be needed. Another issue is category of plant name. Botanical names and common names are miscellaneously used in the lists. We need more research for checking up other thesauri of major database, and united catalogue of thesauri in the field of medicinal plant is to be developed in near future. Finally, there are some technical issues for using non-alphabetical languages and fonts on the Internet, however the database providers should concern and study of the use of those languages and fonts. We often find valuable information of medicinal plant in Chinese character. Some might be political issues, but we should take into account the issues for harmonious and continuous utilization of plant resources.

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Eskinazi, D. *el al.* (1998) CAMed Digital Library Project (on the information resources in alternative and traditional medicine), by Rosenthal Center for Complementary and Alternative Medicine, at the International Conference on Medicinal Plants, Bangalore, India, 16-20 February.

TaxonBank, Proposal for a New Online Database for Taxonomic Research on Type Specimens

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Abstract

Current taxonomic process is very slow. It is difficult to retrieve information on type specimens, and access to the actual specimens in museums is expensive or prohibitive from remote areas or developing countries. A new online database, *TaxonBank*, is proposed as a central depository for data on type specimens. This database will simplify locating specimens, original descriptions, and experts. It will also offer tools for species identification and enable the user to check the identification with digital vouchers of type specimens, biogeographic maps, lists of description statements, etc. Webpages for each species will be produced from an online database. The ultimate goal of *TaxonBank* is to expedite the taxonomic process and to empower researchers around the world to actively participate in taxonomic research via the Internet.

Key Words: Taxonomic databases, type specimens, digital vouchers, original descriptions, webpages

Introduction

The typical chain of events in current alpha taxonomic research in zoology remains similar to that Mayr (1969) described 30 years ago: 1) scan *Zoological Records* for literature; 2) search for a monograph or original descriptions; 3) obtain a copy of the original paper and look for the type depository (some type specimens end up in collections other than that of the author), making it difficult to locate them); 4) contact the curator/collection manager; 5) visit the collection to study the type and/or borrow additional specimens for study; 6) compare study specimens with types (ideally) or with descriptions and illustrations in the literature to confirm identifications, to describe new species, or for a monographic revision.

Taxonomic research is slow and can be expensive. In New Zealand, an intensive effort to sample benthic deep water invertebrates generated thousands of undescribed species now awaiting description. At the current rate of new species descriptions in New Zealand, taxonomists will take some 100 years to describe the unnamed species of research collection (Gordon, 1999). While deep water biodiversity may not be immediately threatened, biological diversity in other habitats such as tropical rain forest and coral reefs, which contain countless species unknown to science, is being lost at an ever accelerated rate (e.g. Heywood and Stuart, 1992; Whitmore and Sayer, 1992). As a result, we are starting to lose biodiversity in some locations faster than we can document it (Solem, 1990; Bouchet, 1997).

Current taxonomic practices are tied to type specimens. Therefore, these specimens are valuable and special: seldom are they allowed to leave the museum, particularly by mail (in contrast with non-type specimens). This difficulty makes it mandatory for many taxonomists, especially in malacology, to visit museums, an especially onerous requirement for researchers in developing countries or in remote locations.

One way to accelerate the cataloging of biodiversity is to take advantage of the Internet for fast information exchange and biotic databases to centralize and synthesize the data that is already known. Many independent biodiversity and specimen databases are currently being produced. Unfortunately, they are not yet fully compatible (Rosenberg, 1997, Rumble, 1999). Several large international projects are aimed at interconnecting these databases (e.g. Species 2000, GIBF) (Bisby, 1999, Nielsen, 1999), but molecular biologists are well ahead of taxonomists in the field of databasing. GenBank is a highly successful example as the standard resource for molecular sequences. In fact, a number of journals (e.g. *Nucleic Acids Research, Cell*) now require DNA sequences to be deposited at GenBank (or other databases) and accession numbers given prior to acceptance of a manuscript. GenBank inspired the idea for *TaxonBank*.

TaxonBank Outline

Goals: The primary goals of the *TaxonBank* expert system are the following: 1) to become a central depository for data on primary type specimen data; and 2) to offer tools for alpha taxonomists. These tools include location of type specimens, original literature and experts, an expert system to aid in identifications, links to other databases, etc. The database will automatically output one webpage per species from the database. Within each webpage there will be links to pertinent data in other databases (e.g. molecular data on the species or closely related group). The database should be user-friendly, and the webpages should be printer-friendly, with images embedded, or with an option for text-only). Some of the necessary and desirable information that should be part of the database are shown in Table 1.

Table 1. *TaxonBank*: necessary and desirable information for the database:

Necessary	Desirable
• Basic data on primary types, such as species name, author and year; host collection name and catalog number • Description or redescription (if available, in DELTA language) • Type locality and geographic distribution for GIS-based distribution maps • Facsimile (an exact copy) of original description paper in PDF format • Digital vouchers of type specimens • Higher taxonomic ranks • List of synonyms and current taxonomic status (valid taxon, synonym, etc.) • Links to other databases (e.g. GenBank, biodiversity databases, etc.)	• Accurate measurements/counts on type • Recent references (especially systematic monographs) • Data on additional specimens, including images, showing diagnostic features • List of loanable specimens (at host collection and other museums) • Pictorial keys to closest taxa • Phylogenetic information • Video or audio recording of live specimens (e.g. for insects or birds) • Remarks or additional data on the species, such as ecological, life history, paleontological, conservation, etc.

Data to be included in the database will be collected from museum catalogs and taxonomic databases. Morphometric data will be measured directly from specimens, with additional data from the literature. Published descriptions as well as those generated by DELTA upon study of specimens will be used to populate the database. Data for GIS-based studies will be obtained from the locality in the specimen record, and the coordinates will be obtained from a gazeteer such as the Getty Thesaurus of Geographical names (http://shiva.pub.getty.edu/tgn_browser/).

Facsimile of original paper: It is fundamentally important to refer to the original description (Mayr, 1969) but many papers with original species descriptions are difficult to find (e.g. they were published in obscure journals, old publications, etc.). Hardcopy originals can be scanned and saved as facsimiles in Adobe Acrobat's PDF (Portable Document Format), which works across computer platforms, and has become the standard for web publication because it maintains the exact formatting of the original. While there may be copyright issues for recent publications, the most difficult to find papers are generally older and less likely to involve active copyrights. In the case of more recent papers, copyright laws can be complex and vary in different countries. The U.S. Copyright Act of 1976 (Bielefield and Cheeseman 1993; Gasaway and Wiant, 1994: 21) sets the term of copyright protection to the life of author plus 50 years, and "for anonymous works 75 years from year of first publication or a term of 100 years from year of work's creation, whichever expires first." (Bielefield and Cheeseman 1993: 45). Therefore, it is safe to assume that works published in the 19th century or earlier are in the public domain. I follow Kohn's strategy (Kohn, 1963, and references in Kohn, 1992), beginning with species described by early taxonomists (1758) and will work my way to the more recently described species. This strategy has two objectives: 1) older publications are usually more difficult to obtain than recent publications; and 2) old publications (pre-20th century) are certainly in the public domain (i.e., no copyright issues). Discussion with legal experts is needed to clarify potential copyright problems. To avoid copyright problems, in the case of recent works, there will be a link to the copyright owner's website where a copy can be purchased.

Digital vouchering of type specimens: Type specimens are the underpinning of the current biological taxonomic system. They are the name-bearers that provide the connection between a physical object (the holotype) and a concept (the species name), hence taxonomists must use types to verify identifications. However, types of species, even within one family or genus, may be distributed in many different collections and often in different countries. This makes it impractical for most researchers to visit all museums to check their specimens against the types.

One of the reasons for the sluggishness of taxonomic research is the use of physical objects that are not readily available. Even when electronic databases are available, they may not be fully compatible, as for example, when different names are used for the same species (Rosenberg, 1997). With the advent of computers, and more recently the Internet, information is becoming increasingly more accessible. To take full advantage of the digital era and the Information Superhighway, type specimens will be digitized, producing "digital vouchers." The physical object will remain in a museum, but its digital voucher will be made available via Internet or disks.

There are many advantages for digital vouchering, including: 1) once digitized the specimen can be reproduced or copied many times without loss of quality; 2) the specimen can be displayed on a computer screen, printed, sent to other researchers via email, etc.; 3) for most cases of identification, there will be no need to consult the actual type specimen, thus avoiding unnecessary handling and sparing the type from wear and possible contamination (e.g. extraneous DNA, for molecular studies); 4) the specimen has theoretically eternal life; 5) the specimen is more easily archived and retrieved than are physical specimens, etc.

Digital vouchering may be achieved by digital photography, video or audio recording, laser scanning or by using other technologies that transform analog information into digital data. Models can be reconstructed with intricate details (e.g. in 2D or 3D), and hence the models are amenable to different types of studies (e.g. identification, morphometrics, etc.)

The specimens should be digitized at the highest possible resolution for archival purposes, but not necessarily be displayed at full resolution. The current standard for Internet graphic formats are JPEG (for continuous tone, as in photographs), and GIF (for line drawings or color drawings). Both of these formats offer significant reduction in file size relative to native TIF, which is recommended for image editing, but not for web publishing. The new format PNG has been hailed by some as the ideal graphics format, with several advantages over most current formats (e.g. lossless compression scheme, gamma correction, 8-bit to 48-bit color, etc.), but most web browsers do not yet support this format (Niederst, 1999).

The ideal system for the *TaxonBank* would be one that supports multiple resolutions or magnifications of part of the image, without the need to download the whole image. The *TaxonBank* will have options for both low- and high-resolution image displays; therefore, casual users may access the system even with a slow Internet access. In most cases, images at VGA resolution (640 x 480 pixels) should be sufficient. For more serious users, images will be available at full resolution.

Another feature that will be developed is the "CD-cache" (name borrowed from disk-cache, which saves frequently accessed files for increased performance) in which images are stored in a CD (F. Moretzsohn and R. Kinzie, unpublished data). When the user accesses the *TaxonBank*, the system would point to images on the disk in the local CD drive. This would empower researchers in developing countries such as Thailand (S. Fucharoen, pers. comm., 1999), where the bottleneck is a very slow Internet connection, to actively participate in taxonomic and biodiversity research. Since image data are less likely to change as fast as text data, the expert system would always be current, and text-only connections would be sufficient. Prices for CD-Rs are dropping fast, and currently one disk costs about the same as two color copies (under US$1 in bulk). One such CD-R could pack thousands of low-resolution images, adequate for most users.

Expert systems for identification: One of the most important contributions of taxonomists to the scientific community is the reliable identification of species. Scientists in other areas of biology are dependent on proper identifications; misidentifications can lead to disastrous consequences (e.g. flawed conservation management plans, wrong medical treatment, etc.) However, accurate identifications are not readily available because species descriptions, diagnoses, keys, etc. are buried in the literature, difficult to access and not always interpretable to the untrained researcher or lay person. Because of a worldwide decline in taxonomic training (Gaston and May, 1992), there is a dearth of taxonomic expertise. In some areas of high biological diversity (e.g. Costa Rica, Papua New Guinea), research centers are resorting to fast training of lay people ('parataxonomists' *sensu* Janzen et al., 1993) to help and/or support field researchers.

With Internet's fast growth, and digital vouchering becoming reality (e.g. NY Botanical Garden type specimen catalog http://www.nybg.org/bsci/hcol/vasc/), the development of expert systems will be a major step towards correct identification of organisms. Interactive systems that guide the user through pictorial keys (e.g. katydid insects in La Selva, Costa Rica http://viceroy.eeb.uconn.edu/interkey/Titlepg), or systems that evaluate the best overall fit of a list of statements (e.g., number of scales on the lateral line, position of pectoral fins, etc.) enable the user to make accurate identifications unassisted by a professional taxonomist. With the resources and tools envisioned for the *TaxonBank* expert system, the user will be able to verify the identification by checking images of digital type vouchers, those of closely related species, species that may look alike, or by reading the description of the taxon. Additional data such as GIS-based distributional maps may further verify the identification.

Perspectives: The *TaxonBank* can become part of a wider effort such as Species 2000. Similar to the GenBank, registration of new taxa could be required for publication (Bouchet, 1999; Howcroft and Thorne, 1999). The new International Code for Zoological Nomenclature, which will be operational January 1, 2000 will not yet accept online descriptions of new taxa, but the situation is likely to change in the future (once stable libraries for electronic publications become available). Even though the amount of data involved with this database will be enormous, computer technology advances faster than taxonomic research, and storage space and computer, as well as Internet access speed will likely not become a problem. If successful, the *TaxonBank* will help accelerate the currently slow taxonomic process.

Acknowledgements

This paper is dedicated to the late C.M. "Pat" Burgess, M.D., of Honolulu, Hawaii, a cowrie expert and my mentor. Many people contributed to the development of the ideas presented here. Among them, I thank E. Alison Kay, my academic advisor, and Robert Kinzie III (Univ. Hawaii), Gary Rosenberg (ANSP, Philadelphia), Robert Ricklefs (Univ. Missouri), Philippe Bouchet (MNHN, Paris), and my wife, Heather Stanton for ideas and helpful suggestions on the manuscript. Financial support from the University of Hawaii Graduate Student Organization to attend the Species 2000 workshop, an Edmondson Research Fund grant (Univ. Hawaii), and a Graduate Research Assistantship from the University of Hawaii were greatly appreciated as well.

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Species Information Database KONCHU on Japanese, East Asian and Pacific Insects on INTERNET

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Abstract

A publically available entomology database KONCHU is a general database name which includes various files of bibliographical and image databases. The former is a taxon-based entomology database based on main Japanese entomological journals (12 journals (= files) at present). Therefore it includes many records of East Asian and Pacific insects including spiders and mites as well as Japanese ones. It has a taxonomical feature as well as a bibliographical one because it treats one taxon, *e.g.* species, genus, family, as one record. The records of KONCHU are written mainly in English, and in Japanese with katakana and kanji characters. Each record of the database is composed of 13 items, such as bibliographical (author, title, journal, volume, page and year), taxonomical (order, family, synonymy), distributional data, key words (taxonomy, morphology, ecology, biology, etc) and notes including usuful information such as the type locality and the type depository of new species, and host record of parasite. The KONCHU is managed by a text database management system SIGMA. The KONCHU has been opened to the public on INTERNET as well as at Computer Center of Kyushu University, Fukuoka, Japan. A user can access to the KONCHU by retrieving the following URL: http://konchudb. agr.agr. kyushu-u. ac.jp/. Outline, usage and examples of use of the KONCHU are presented.

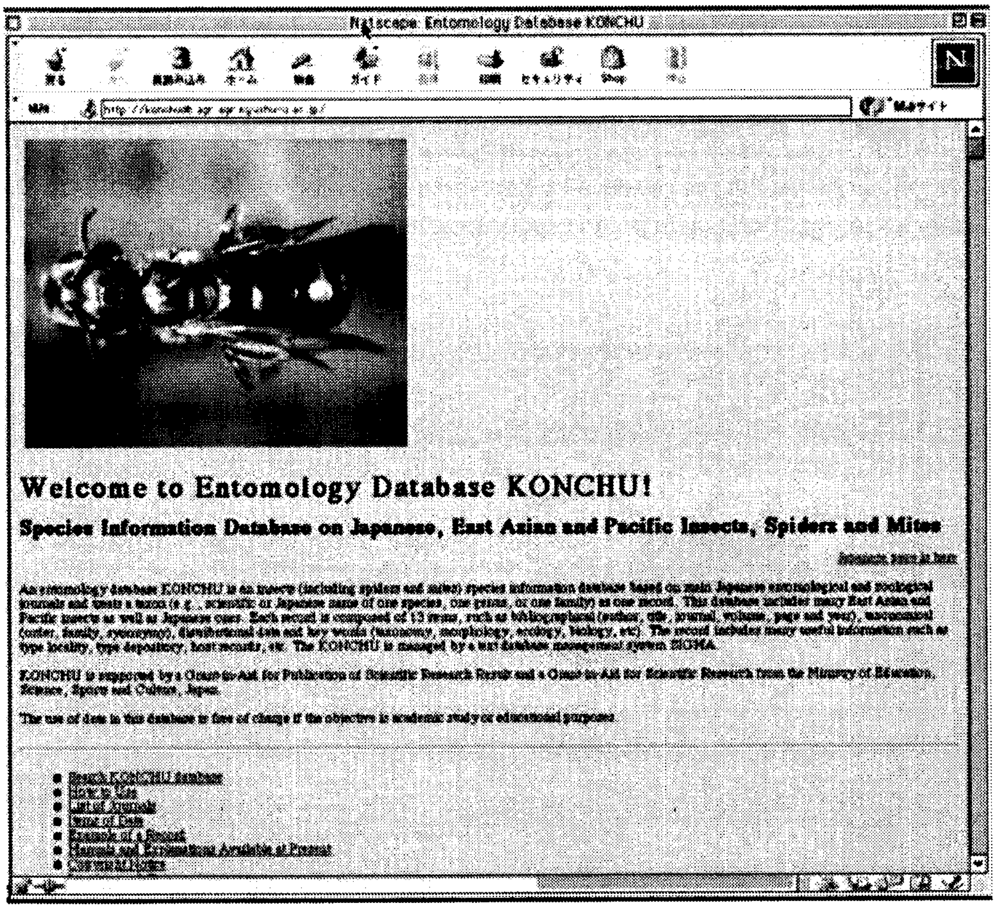
Key Words: Biodiversity, species information, database, Japan, East Asia, Pacific Area, insects, spiders, mites, KONCHU, INTERNET

An entomology database KONCHU (= insects in Japanese) is a general database name which includes various files of bibliographical and image databases. The former is a taxon-based entomology database based on main Japanese entomological journals (12 journals (= files) at present) and treats a taxon as one record, i. e., species, genus, family, etc. The KONCHU includes many records of East Asian and Pacific insects, spiders and mites as well as Japanese ones. Each record is written mainly in English, and in Japanese with katakana and kanji characters and composed of 13 items, such as bibliographical (author, title, journal, volume, page and year), taxonomical (order, family, synonymy), distributional data, key words (taxonomy, morphology, phylogeny, ecology, biology, physiology, genetics, cell biology, biogeography, etc) and notes including useful information such as the type locality, and the type depository of new species, and host record of parasite. It has been open to the public at Computer Center of Kyushu University, Fukuoka, Japan since 1987 (Tadauchi, 1987). The files of database KONCHU are managed by a text database management system SIGMA (Arikawa et al., 1987, 1988) working at the Computer Center of Kyushu University. The system SIGMA had recently modified for use on a work station. The KONCHU was also reproduced on a work station in the Entomological Laboratory, Kyushu University and was open to the public on INTERNET as well as from the Computer Center of Kyushu University.

A user can access to the KONCHU by retrieving the following URL: http://konchudb. agr.agr.kyushu-u.ac.jp/ and can register from a registration form on the homepage. Outline and usage of the KONCHU are shown in Tadauchi (1987, 1994, 1996) and Tadauchi et al.

(1999). A user can also get information about the KONCHU including its usage on the homepage. Some files in the KONCHU are summarized in Tadauchi (1985: MUSHI file), Tadauchi (1994, ESAKIA file), Tadauchi & Takematsu (1995: AKITU & TMU files), Tadauchi et al. (1997: INMS file), and Takematsu et al. (1996: SHIKOKU file) and usage of the SIGMA system is explained in Arikawa et al. (1987, 1988).

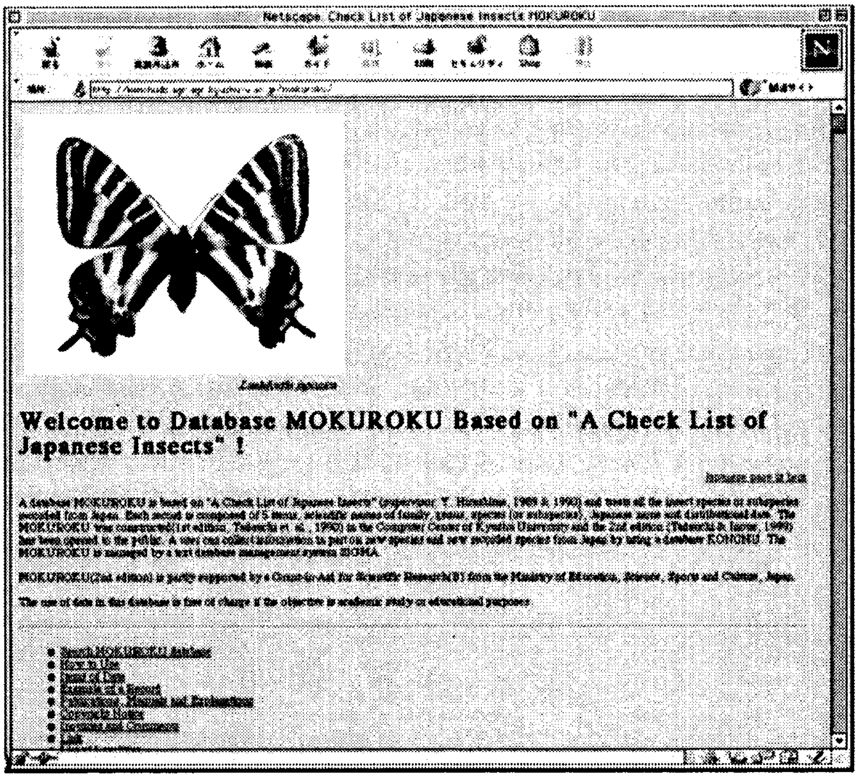
Contents of the home page are as follows: 1) Search KONCHU database (for registrant), 2) How to use, 3) List of journals, 4) Items of data, 5) Example of a record, 6) Manuals and explanations available at present, 7) Copyright notice, 8) Registration system, 9) Inquiries and comments, and 10) Link. We have two searches, simple and advanced modes in our KONCHU. A user can retrieve taxa by any key words in the 13 items, such as bibliographical, taxonomical, distributional words, key words and notes. The home page and examples of the use of the KONCHU are presented in Figs. 1-3 with another homepage of our database MOKUROKU based on "A Check List of Japanese Insects"(Fig. 4), which includes all the Japanese insects and is the most related to biodiversity databases. Both databases are useful for applied entomologists as well as taxonomists interested in Japanese, East Asian and Pacific insects.



Welcome to Entomology Database KONCHU!

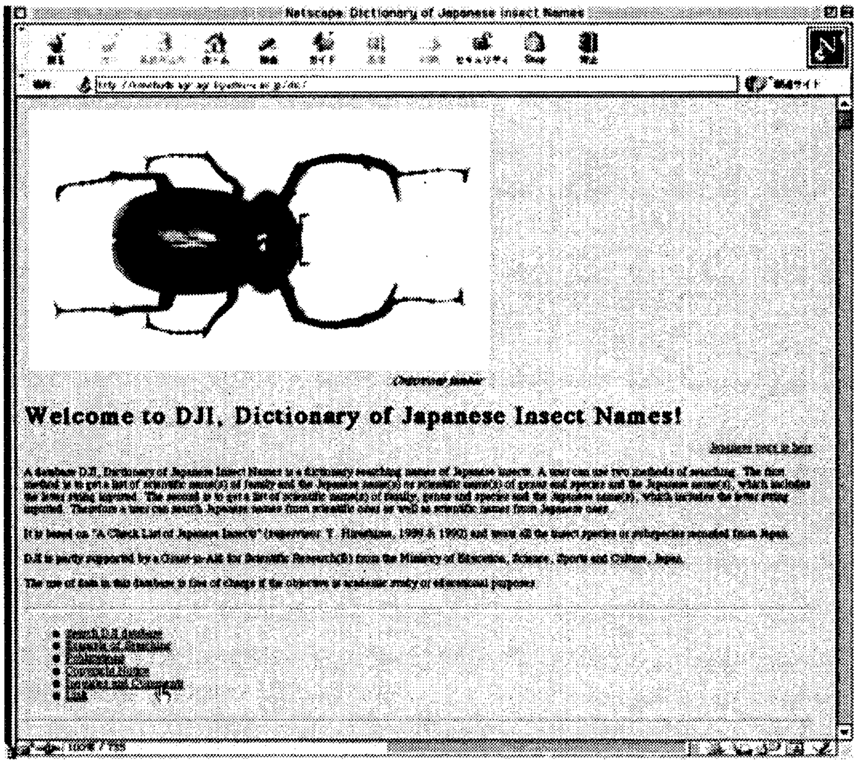
Species Information Database on Japanese, East Asian and Pacific Insects, Spiders and Mites

Fig. 1. A homepage of a taxon-based entomology database KONCHU treating species information on Japanese, east Asian and Pacific insects, spiders and mites. The URL is http://konchudb. agr.agr.kyushu-u.ac.jp/



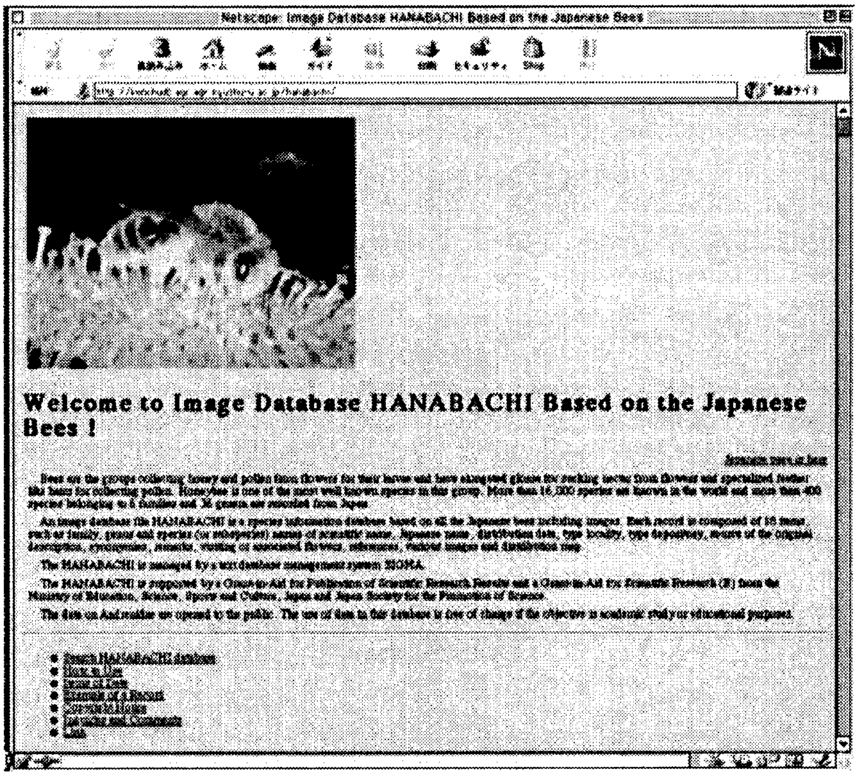
Welcome to Database MOKUROKU Based on "A Check List of Japanese Insects" !

Fig. 2. The KONCHU is based on main Japanese entomological and zoological journals and treats one taxon as one record including 13 items, such as bibliographical, taxonomical, distributional data, key words and notes.



Welcome to DJI, Dictionary of Japanese Insect Names!

Fig. 3. A user can get information how to use entomology database KONCHU on the homepage. It shows the first page of the usage.



Netscape: Image Database HANABACHI Based on the Japanese Bees

Welcome to Image Database HANABACHI Based on the Japanese Bees !

Fig. 4. A homepage of a database MOKUROKU based on "A Check List of Japanese Insects" treating all the Japanese insects with distributional data. The URL is http://konchudb. agr.agr.kyushu-u.ac.jp/mokuroku/index-e.html/.

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J-IBIS (Japan Integrated Biodiversity Information System)

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Abstract

The Biodiversity Center of Japan (Biodic-J) has developed the Japan Integrated Biodiversity Information System (J-IBIS), a database of Japan's natural environment and biodiversity. The information held, which includes the Green Census results, is available to the public through the Internet and other means.

Key Word: GIS, Natural environment, Biodiversity

Introduction

The Biodiversity Center (Biodic-J) has developed the Japan Integrated Biodiversity Information System (J-IBIS) to hold an extensive database of biodiversity information. It includes the Green Census results, information on the center's animal and plant collection, and other relevant documents. The database is accessible through the Internet as well as by other means. Computer networks are also used to monitor the natural environment and to gather information from animal and plant experts. Geographic information system (GIS) and digital mapping techniques are employed to analyze and utilize the stored information as basic data for projects to conserve biodiversity.

The Biodic-J is Japan's center for biodiversity information, and it also serves as the national focal point of the Clearing-House Mechanism as prescribed by the Convention on Biological Diversity.

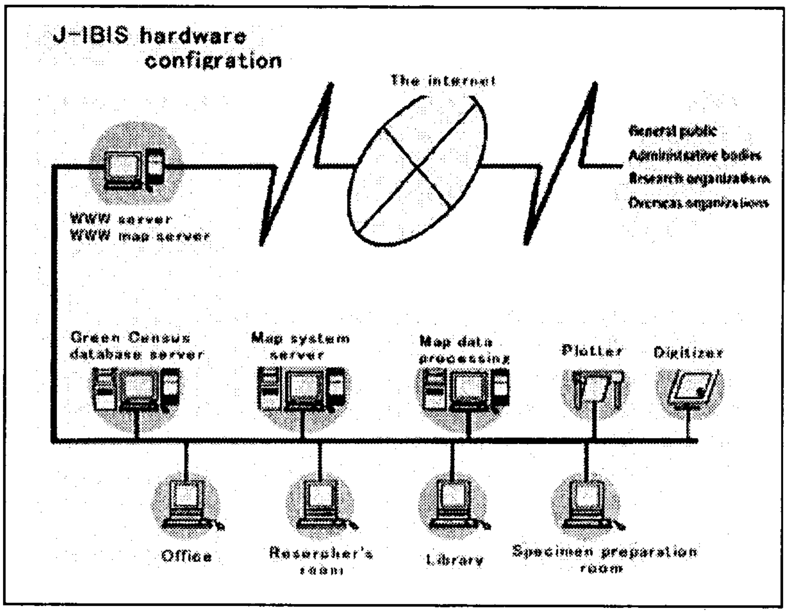


Fig. 1. J-IBIS hardware configuration

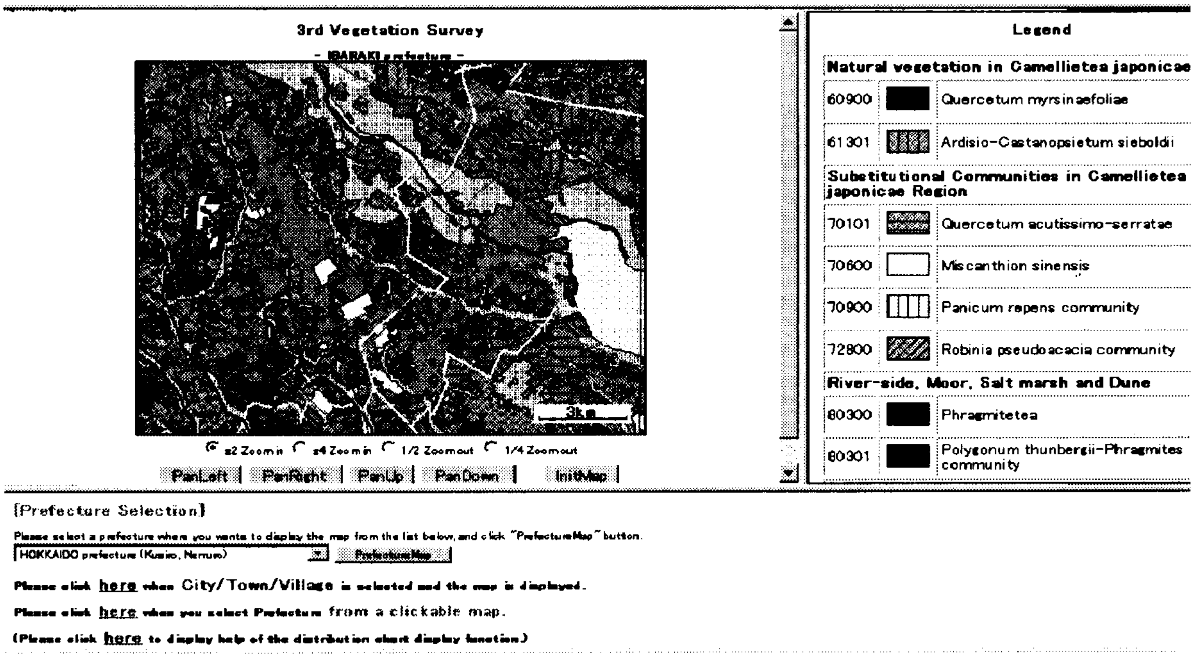
Contents

The Japan Integrated Biodiversity Information System (J-IBIS) manages the data of the National Survey on the Natural Environment, Threatened Species, Laws and Treaties for Nature Conservation and National Parks.

By using the Internet, everyone can search the Japanese vegetation map, distribution of mammals, birds, amphibians, reptiles, freshwater fishes, insects, and so on.

We started an English web page in June 1999.

The data of the National Survey on the Natural Environment shows only the points where living beings were confirmed. No point areas include out of research areas.



3rd Vegetation Survey

- IBARAKI prefecture -

Legend

Natural vegetation in Camellietea japonicae		
60900	■	Quercetum myrsinaefoliae
61301	▥	Ardisio-Castanopsietum sieboldii
Substitutional Communities in Camellietea japonicae Region		
70101	▩	Quercetum acutissimo-serratae
70600	□	Miscanthion sinensis
70900	▥	Panicum repens community
72800	▨	Robinia pseudoacacia community
River-side, Moor, Salt marsh and Dune		
80300	■	Phragmitetea
80301	■	Polygonum thunbergii-Phragmites community

[Prefecture Selection]

Please select a prefecture where you wants to display the map from the list below, and click "PrefectureMap" button.

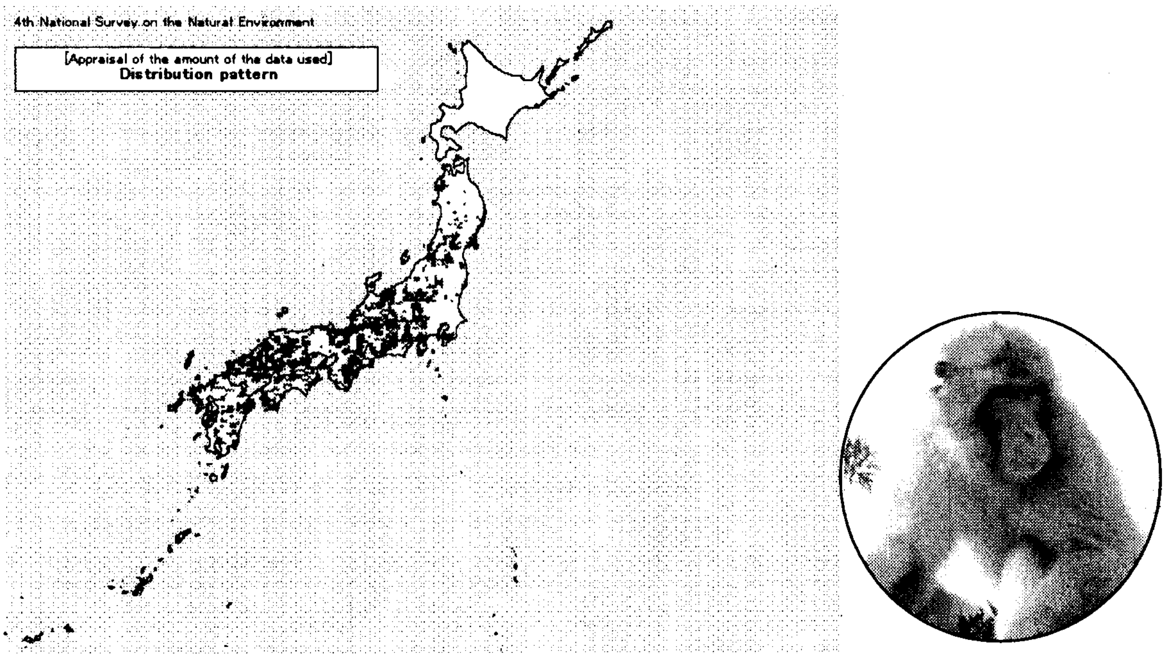
HOKKAIDO prefecture (Kusiro, Nemuro)

Please click here when City/Town/Village is selected and the map is displayed.

Please click here when you select Prefecture from a clickable map.

(Please click here to display help of the distribution chart display function)

Fig. 2. Vegetation map of Tsukuba city



4th National Survey on the Natural Environment

[Appraisal of the amount of the data used]
Distribution pattern

Fig. 3. The distribution of the Japanese Macaque

[Red List of Threatened Mammals of Japan]

Extinct (EX)

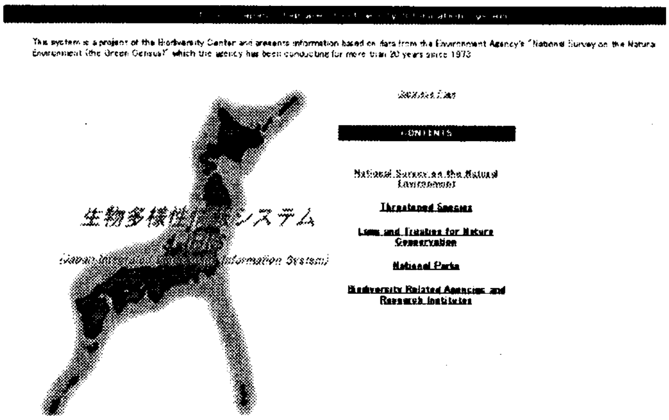
Pteropus loochoensis
Pipistrellus sturdeei
Canis lupus hattai
Canis lupus hodophilax

Critically Endangered (CR)

Nesoscaptor uchidai
Pteropus dasymallus daitoensis
Pteropus dasymallus dasymallus
Pteropus pselaphon
Rhinolophus pumilus miyakonis
Myctis yanbarensis
Felis bengalensis euptilura
Lutra lutra nippon
Lutra lutra whiteleyi
Zalophus californianus japonicus
Apodemus agrarius
Tokudaia osimensis muenninki

Endangered (EN)

Crocidura orii
Rhinolophus pumilus pumilus
Rhinolophus perditus perditus
Hipposideros turpis
Myotis ikonnikovi hosonoi
Myotis ikonnikovi ikonnikovi
Myotis ikonnikovi yesoensis



This system is a project of the Biodiversity Center and presents information based on data from the Environment Agency's "National Survey on the Natural Environment (the Green Census)" which the agency has been conducting for more than 20 years since 1973

Fig. 4. Top page of J-IBIS

Conclusion

We will improve this system step by step. Please visit the J-IBIS webpage at least once. The URL address is http://www.biodic.go.jp/english/J-IBIS.html

Data on Biodiversity in West Africa – The Senegalese Case

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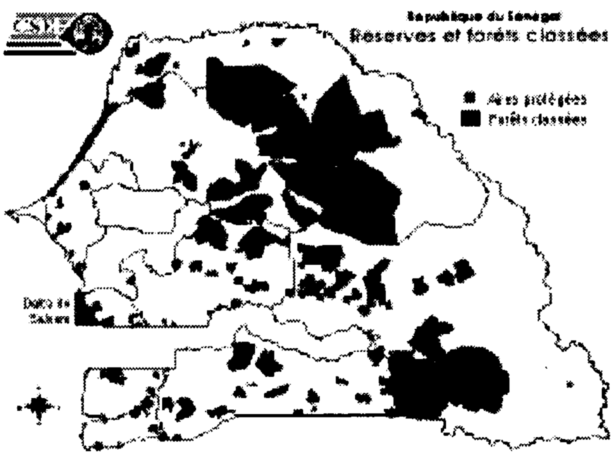
Chairman of CODATA Sénégal

Introduction

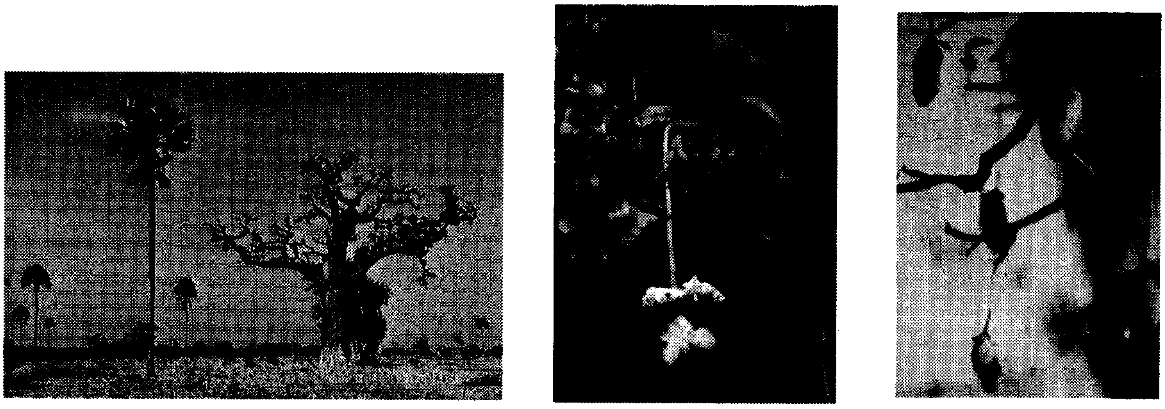
It was formally stated in the Species 2000 Project Plan that one of its aims is to « initiate and fund a major worldwide programme of new taxonomic databases, many of them in developing countries, to fill the gaps in current knowledge. While recognizing that the lack of a widely accessible index is a significant impediment to all nations wishing to fulfill their obligations under the Convention on Biological Diversity highlighted in the UNEP Global Biodiversity Assessment (1995), this up most important project has kept African scientists aside. Nonetheless, we keep supporting it even by enthusiastic votes during the CODATA General Assemblies.

That enormous task is as stated «a vital for the easy comparison or exchange of biodiversity information and related matters between different organizations and countries. » One of our aims is to bring together existing scattered data and information that will help reduce duplication and enhance efficiency specially in agriculture, environment, health and education.

Taxonomy Background in Senegal



Senegal, the most westerly country in Africa, has had opportunities for centuries to be visited by the very first phytogeography specialists from France and England : e.g. Adamsonia digitata, Guiera senegalensis, Combretum senegalensis and thousands others from fungi to angiosperms, a being at the cross-roads of Europe, the Americas and on the marine junction to the Indian peninsula and Asia, it has experienced several introductions of both animal and vegetal species and varieties. Research on these fields began almost 350 years ago with the beginning of colonization and much of laboratories and institutions began their works in Senegal , long before doing so elsewhere in Africa. This geopolitical situation and position must be used by the Species 2000 Project in order to fulfill one of its aim and get the numerous local or international research institutions, centers, laboratories and sponsors in the process of verifying the existence, spelling and current status of the names used for each species, and the classification of that species and participate in creating an index made easily accessible through a Common Access System of Databases on the World Wide Web. In the case of african countries, still traditional means of information dissemination will continue to be used at least for the next ten years. As mentioned previously by experts, capital technologies with biological effects serve as strong substitutes for land for the future.



Adamsonia digitata flower § fruits

Biodiversity and Environment Database Activities

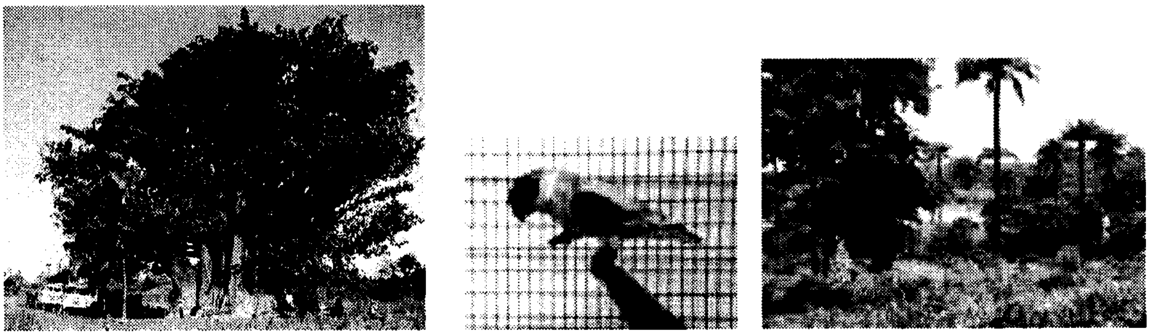
About 20 databases systems (some dealing with environment, biodiversity and drought) have been identified in our recent survey of questionnaires. They include the following:

- National Research Results Valorization System
- National Center for Scientific and Technical Documentation which has no less than 10 well designed databases.
- Senegalese Institute for Agricultural Research (15 research centers and stations), one of the most important research institutes of West Africa since 1933.
- University Cheikh Anta DIOP and its numerous Institutes and Laboratories in DAKAR
- University Gaston BERGER and its components in Saint Louis
- Food and Alimentation Technology Institute
- ORSTOM & Institut Pasteur (Dakar-based French Institutes for Medicine and tropical research for these last 55 years)
- OMVS a regional governmental organization in charge of the Senegal River Basin covering 4 countries (Guinea, Mali, Mauritania and Senegal).
- Databases of the Senegalese Army
- Various databases of the Ministry of Agriculture.

- Databases of the Direction of Statistics (Ministry of Economy and Finance)
- Databases related to Meteorology and Weather: 29 stations.
- Database on Scientific and Technical Potential (P.S.T.) initiated by UNESCO and the Senegalese Ministry for Science and Technology.

Interdisciplinary Projects and Joint Programmes

Currently, we are setting a new task group entitled *"Reliable Scientific Data Sources in West Africa"* expandable to the whole continent. CODATA members will begin by a survey of the Scientific and Technical Potential of Senegal namely *PST* (Potentiel Scientifique et Technique au Senegal) in order to obtain information on senegalese factual and numerical data collections with directories and summaries of current research projects, centers of expertise and individual scientific qualifications and experiences.). OMVS is considering some ecological problems related to the new dams (Diama and Manantaly) on the Senegal River, natural boundary of 4 countries (Mauritania, Mali, Guinea and Senegal): estimation of biodiversity and health-related consequences on human health and on ecosystems (geobiocenoze).



This problem-oriented database will include soon a thesaurus of terms and key words. By the end of year 2000 formats for the data and the general structure of the *'CO-SCIENCES" integrated multidisciplinary database* will be developed. This database is assumed to satisfy the following minimum requirements for working as effective research-support tool: step-by-step development of small-sized single discipline databases before their integration, clarification of data sources, reliability of systematically covered data within a specific area, and user-friendliness in search, analysis, estimation, simulation, presentation and visualization interfaces. Several *CODATA* members are database modeling specialists who are willing to develop a practical multidisciplinary database prototype that will help us to move to a short to long time-scale advanced database with functions for data analysis and estimation as well as for data validation, presentation and visualization.

The Senegalese Scientific Community and the Web

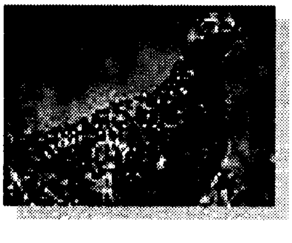
The senegalese scientific community is increasingly interested and involved in ongoing CODATA activities on the Web for networking and electronic publishing of their valuable work without having to depend upon foreign publishers. The advent of the Internet and networking technology provides an extraordinary opportunity to african scientists and effect major changes in worldwide scientific and technical communication. Yet, whilst recognizing and applauding all these marvels, we are too well aware of present realities in developing countries.

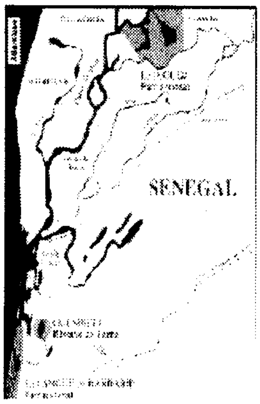
There is evidence of significant losses in efficiency in agriculture, transportation, commerce, banking, government, tourism and other sectors due to the lack or inadequacy of telecommunications services. Telecommunications also contribute to quality of life, by facilitating access to emerging services. In aggregate, these benefits accrue mostly to middle income urban families, although some basic telecommunications services are also extended to rural and low income urban areas tied to the development of rural solar energy technologies.

Linking Africa to the Species 2000 Project

It is obviously quite impossible, in a short paper such as this, to address the needs of each individual african country and the level of accomplishment and capabilities in data gathering and exchange in biodiversity particularly tied to stage of development of its telecommunications system. Our objective, therefore, is to consider some of the lessons being learnt by the countries concerned by Species 2000 within Europe, North America and Asia and to offer some of those experiences for consideration by developing countries in Africa.

Our first objective must be to establish a framework, in order to establish reliable biodiversity databases, and then to fully participate in this useful multifunctional data sharing. Perhaps, learning from the Japanese, North American and European experiences, companies within a particular country (or, better still, within a group of countries like the Asian-Oceanic which is our model by its long and successful experience in data management on a regional basis) should be encouraged to cooperate with each other in their evolution so that everyone will benefit from sharing activities rationally. Global and national infrastructure systems will transmit huge amount of data at a low cost, stimulating the development of hundreds of new types of applications, all geared towards instant and efficient data exchanges.





The Benefits of International Data Networks

If we do not want to stay behind in the coming millennium, our developing nations must get the right links to data networks that are so essential in agriculture, biodiversity, health and environment, industries, banking, manufacturing, transport, retailing and services. The developed world, for its part, tends to support free trade in information, except when it doesn't suit. There are countless instances of governments and private corporations intervening themselves to prevent the free movement of data when it runs counter to political or commercial convenience.

The considerable success and resulting high profile of international data communications has thrown into sharp relief the unequal distribution of facilities for information collection, processing and dissemination which currently exists between the developed countries and their developing counterparts. In this context there is a great suspicion that the developed world contrives to control and limit developing countries' access to information resources. This can take a variety of forms, ranging from restrictions on access to scientific and technical data held in the North even if these data were collected in the South (80% of species known to date). Depending upon the type of cooperation, to local agents of the northern commercial enterprises conspiring to arrange the unregulated removal of personnel details, information about manufacturing processes, research developments, and data relating to a developing country's natural resources and biodiversity etc.

Hope and Actions for a Better Future

Having said all that, though, it obviously, remains difficult to persuade nations whose people do not have enough to eat that a high priority should be given to expanding and modernizing their telecommunications infrastructures. Scientists and economists can help to a better understanding of this very high priority in their own countries.

Development, progress, improving the condition of the people – whatever we may call it – the basic requirement is knowledge. Without reliable data and information men and women in our continent, industry and economy as a whole will fail to cope with the obstacles that lie in their way. Fortunately, ICSU and CODATA are trying to change the trend respectively by the "Freedom in the Conduct of Science" ; "Capacity Building" , "Bits of Power" and the very beneficial work of the ICSU-CODATA Joint Commission on Data Access which develops positions, policies and procedures that can impact on data access for scientific research including governmental, commercial, and legal constraints. There are much more to do for scientists and engineers of developing nations. ICSU and it's Interdisciplinary Committee CODATA are on the forefront of international efforts to find solutions to unequal Transborder Data Flow. It is hoped that ICSU and other bodies like International Bureau for Informatics (I.B.I), succeed in their endeavours. We hope that Species 2000 will do the same. The consequences of failure to do so could lead to a data trade war with potentially disastrous consequences for all concerned, and for african countries in particular.

We strongly believe in the spirit, philosophy and guidelines of the International Council for Science. We believe and will fulfill our commitment to act in order to support CODATA and its Species 2000 Project to be a real force multiplier for biodiversity and environment in Africa and elsewhere.

Dakar, February 29, 2000

Biodiversity of Insects at Ton-Nga-Chang Wildlife Sanctuary, Southern Thailand

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Abstract

The purpose of this project is to study diversity and fluctuation of insects at Ton-Nga-Chang Wildlife Sanctuary. The study involves the selection of the primary rain forest area and establishment of the permanent site of 100x100m^2. The area has been divided into small quadrats of 10x10 m^2 for long-term ecological study. Light traps were set up to collect insects for three consecutive nights. Malaise traps, flight intercept traps, pitfall traps and yellow pan traps were left for five days whereas litter samples were taken at one time. Insects monitoring during dry and wet seasons for two years period at the permanent plot revealed a total of 113 families in 14 orders. Although Collembola, Coleoptera, Diptera, Hymenoptera and Lepidoptera comprised the majority of insects caught (~90%) for both seasons, there was a seasonal change in their abundance. A total of 59 species in 31 genera of 7 subfamilies are listed for ants (Hymenoptera:Formicidae). Six species of the geometrids (Lepidoptera:Geometridae) in the genera *Achrosis, Biston, Ourapterx* and *Xeropteryx* are confirmed to be new to science.

Key Words: Biodiversity of insects, Tropical rain forest, Formicidae, Geometridae

Introduction

It has been generally recognized that the knowledge on biodiversity is served as an important aspect for management objective. Stork (1987a,b) presented data on arthropod structure from Bornean rain forest trees and long term study of insects in Australian rain forest canopy has been conducted since 1983 (Kitching and Arthur, 1993; Kitching et al., 1993). The insects from Thai rain forest received little attention to date. Although Hutacharern and Tubtim (1995) published a book on Checklist of Forest Insects in Thailand, it represents only a fraction of all-insect species known and unknown in Southeast Asian countries.

Ton-Nga-Chang Wildlife Sanctuary is one of the most mature tropical rain forest in Bantad Mountain Range of Southern Thailand (15°33′-16°23′ N and 98°33′-99°7′ E). It covers the area of approximately 182 km^2. The elevation of the wildlife sanctuary ranges between 100-932 m. above mean sea level. Like most of the tropical rain forests, it is comprised of a diverse range of plants and animals species. It is now becoming one of the important tourist destination in Songkhla Province. Various developments have taken place for the convenience of tourists. These will ultimately have an environmental impact on the ecosystem of this locality. The purpose of this project is to study diversity and fluctuation of insects at Ton-Nga-Chang Wildlife Sanctuary. The results from this study will form an important addition database to be used for purpose of rain forest conservation and management in the future.

Materials and Methods

Permanent plot of 100x100m^2 was established at about 250 m above mean sea level in the primary forest at Ton-Nga-Chang Wildlife sanctuary (Figure 1). The area was subdivided into small quadrats of 10x10m^2. Different types of trap were used for insect collection. Two collections were carried out for each season year.

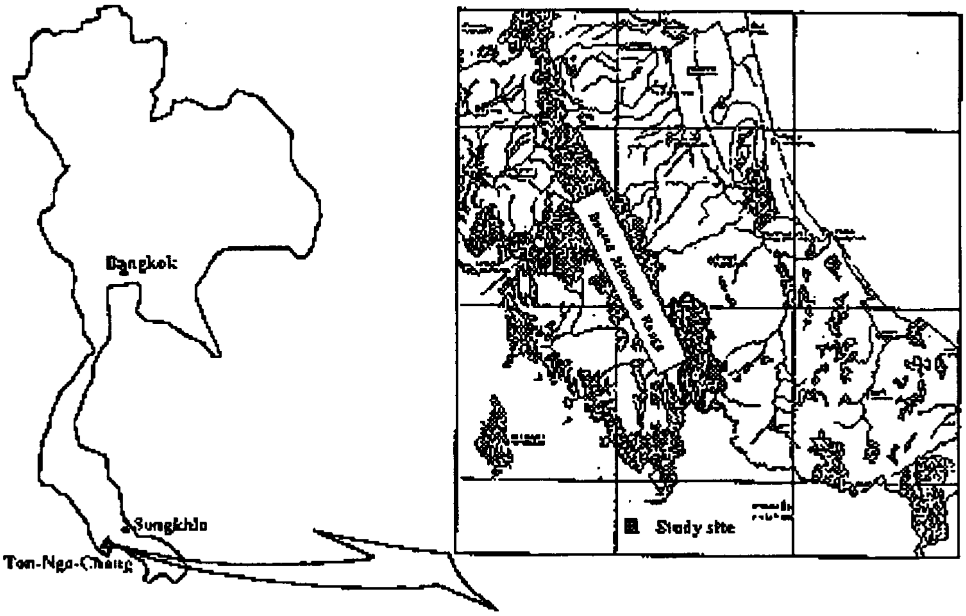

Fig. 1. The study area, Ton-Nga Chang Wildlife Sanctuary, Songkhla, Thailand

Table 1. Mean percentages of insects caught in each season of the study period (n=2)

Orders	Dry (1997) (%)*	Wet (1997) (%) X ± S.E.	Dry (1998) (%) X ± S.E.	Wet (1998) (%) X ± S.E.
Collembola	16.73	2.33 ± 0.01	13.44 ± 1.37	15.00 ± 3.11
Coleoptera	19.23	2.12 ± 0.04	4.49 ± 0.16	7.38 ± 2.38
Diptera	12.89	2.66 ± 0.06	3.98 ± 1.10	2.96 ± 1.82
Hymenoptera	21.29	89.08 ± 1.85	64.57 ± 4.70	61.78 ± 10.49
Lepidoptera	22.32	2.12 ± 1.66	7.46 ± 1.06	9.41 ± 2.17
Others	7.54	1.69 ± 0.15	4.06 ± 1.02	3.47 ± 0.98

*n=1

Ground Insects

Pitfall trapping: random sampling from 3 quadrats, 25 baited traps were placed in each subplot and the traps were left for 5 days.

Flight intercept trapping: random sampling from 2 subplots, the traps were left for 5 days.

Leaf litter sampling: samples were collected from 9 subplots

Lower canopy insects

Light trapping: random sampling from 2 quadrats, light traps were set up to collect insects for 3 consecutive nights, insects were hand-picked from 6.00 p.m. until midnight.

Malaise trapping: random sampling from 2 subplots, the traps were left for 5 days.

Yellow pan trapping: random sampling from 3 subplots, the traps were left for 5 days

Results and Discussion

During the 2 years period, 14 orders of insects were collected. Five orders comprised the major group of insect found. They were Collembola, Coleoptera, Diptera, Hymenoptera and Lepidoptera. Table 1 and Figure 2 represented an average percentage of insects collected during the two years study. In the dry season of 1997 and 1998, the amount of Collembola remained unchanged and was approximately similar to the wet season of 1998 (~16%). However, this number reduced greatly to ~2% in the wet season of 1997. In contrast, the amount of hymenopterans were high in both seasons of 1998 (~62-64%). Nevertheless, the figure was still lower than in the wet season of 1997 in which the number rose to ~89%. It is noticeable that ants were the major group of insects found in the order Hymenoptera, and was the dominant family observed in this study. The numbers of insects in the other three orders were not much different in the two years excepted for the dry season of 1997 where the amount of these insects were relatively high. Accidentally, during the wet season of 1997 and continuing to the dry season of the following year, southern part of Thailand was influenced greatly from the forest fire in Indonesia. This severe impact might be one of the reasons for the insect decline in the wet season of 1997. However, its effect could not be confirmed scientifically.

Statistical analyses of the difference in insects abundance will be further analyzed in relation to some environmental factors.

Taxonomic study was carried out with the families Formicidae (Hymenoptera) and Geometridae (Lepidoptera). A total of 59 species in 31 genera of the 7 subfamilies were listed for ants (Table 2). The books by Chey (1996) and Hollaway (1993,1996) were used for the purpose of moth identification. In the family Geometridae, 118 species of 32 genera were recorded. Six species of the geometrid moths were confirmed to be new to science (Figure 3) and the descriptive information will be published elsewhere.

The study suggested that long term monitoring is required in order to explain fluctuation and community structure of these forest insects.

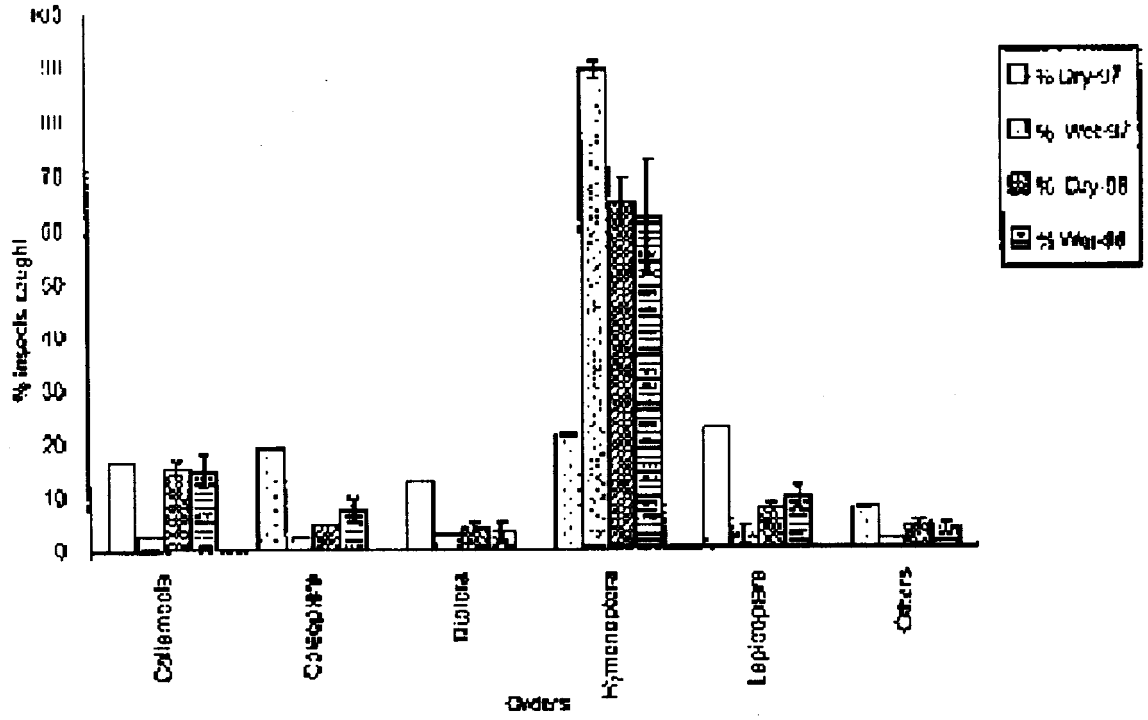

Fig. 2. Percentages of insects collected during dry and wet seasons of 1997 and 1998

Table 2. List of ants found at Ton-Nga-Chang Wildlife Sanctuary

Subfamily Formicinae

Camponotus sp.1
Camponotus sp.2
Camponotus sp.3
Camponotus sp.4
Camponotus sp.5
Camponotus sp.6
Calomyrmex sp.
Euprenolepis sp.1
Euprenolepis sp.2
Gesomyrmex sp.
Oecophylla sp.
Polyrhachis sp.1
Polyrhachis sp.2

Subfamily Dolichoderinae

Hypoclinea sp.1
Hypoclinea sp.2
Tapinoma sp.1
Tapinoma sp.2

Subfamily Dorylinae

Aenictus sp.1
Aenictus sp.2

Subfamily Myrmicinae

Crematogaster sp.1
Crematogaster sp.2
Kyidris sp.
Liomyrmex sp.
Lophomyrmex sp.
Monomorium sp.1
Monomorium sp.2
Paedalgus sp.
Paratopula sp.1
Paratopula sp.2
Paratopula sp.3
Paratopula sp.4
Pheidole sp.1
Pheidole sp.2
Pheidole sp.3
Pheidole sp.4
Pheidole sp.5
Pheidole sp.6
Pheidologeton sp.1
Pheidologeton sp.2
Pheidologeton sp.3
Pheidologeton sp.4
Pheidologeton sp.5
Proatta sp.
Strumigenys sp.

Subfamily Ponerinae

Diacamma sp.
Discothyrea sp.1
Discothyrea sp.2
Hypoponera sp.
Myopopone sp.
Mystrium sp.
Odontomachus sp.
Odontoponera sp.
Pachycondyla sp.1
Pachycondyla sp.2
Pachycondyla sp.3
Prionopelta sp.

Subfamily Pseudomyrmicinae

Tetraponera sp.1
Tetraponera sp.2

Subfamily Leptanillinae

Leptanilla sp.

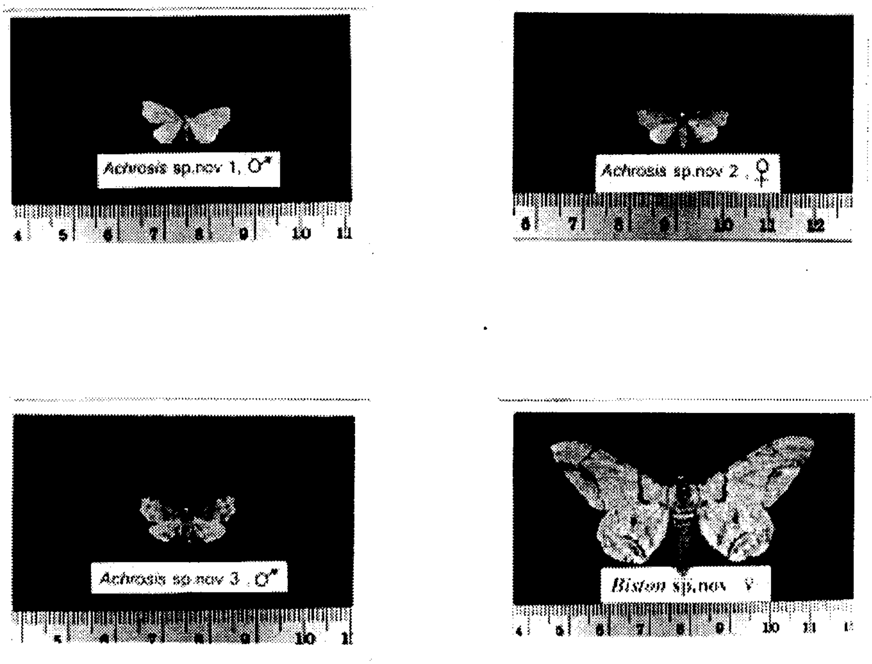

Fig. 3. Six new species of the Family Geometridae

Acknowledgement

We are grateful to Dr. Chey Vun Khen, Sabah Forestry department, for his assistance in the geometrid identifications. This work was supported by TRF/BIOTEC Special program for Biodiversity Research and Training grant BRT 139022.

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Biodiversity of Freshwater Hyphomycetes at Ton-Nga-Chang Wildlife Sanctuary, Southern Thailand

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Abstract

A survey of freshwater hyphomycetes was conducted at Ton-Nga-Chang Wildlife Sanctuary, Songkhla, Thailand. The objective was to study fungal diversity in the stream of tropical rain forest, southern Thailand. Samples were collected from foam that persistently accumulated below the waterfall. The foam samples were examined and identified to fungal genera based on the shapes of conidia under a compound microscope. Sixty-two genera of fungi (mainly hyphomycetes) were found in the foams. The common genera were Anguillospora, Articulospora, Beltrania, Brachiosphaera, Campylospora, Clavariopsis, Condylospora, Diplocladiella, Dwayaangam, Flabellospora, Helicomyces, Helicosporium, Isthmotricladia, Laridospora, Phalangispora, Tricladium, Triscelophorus and Varicosporium. The viability of the fungal conidia trapped in foam was estimated with tetrazolium bromide. In fresh foam, 44-77 % of all conidia had at least one viable cell; in old foam, these values were 42-69%. The numbers of conidia in foams estimated by total plate count were 2.7×10^3 to 1.4×10^5 cfu/ml. Sixty-five strains were isolated from the fresh foams. Forty-four percent of these sporulate on cornmeal agar.

***Key Words:** Biodiversity, freshwater hyphomycetes, southern Thailand, conidial viability, tetrazolium bromide*

Introduction

Freshwater hyphomycetes are a very specialised group of mitosporic fungi that play an important role in the degradation of leaf litters or submerged substrates in aquatic habitats (Singh, 1982). This group of fungi also acts as intermediaries in energy and food webs in aquatic ecosystem. Their distribution is worldwide. In Thailand, only a few studies have been investigated (Tabaki et al., 1983, Hywel-Jones, 1991, Sivichai et al., 1998). The tropical rain forest at Ton-Nga-Chang Wildlife Sanctuary is one of the primary forests in southern Thailand. It habors diverse varieties of plants, animals and microorganisms, including fungi. Our objective was to determine the diversity of freshwater hyphomycetes in foams that accumulated below Ton-Nga-Chang waterfall. The viability of fungal conidia in foam was revealed by tetrazolium staining. Many fungal species were isolated and identified.

Materials and Methods

Collection of foam samples

Two types of foams were distinguished: fresh foam (colour and consistency similar to whipped egg white) and old foam (yellow-brown, partly dried up) as shown in Fig.1. Foam was scooped into plastic bottles in an icebox and returned to the laboratory within an hour. Eight samples of fresh and old foam, each at 4 different stream sites below Ton-Nga-Chang waterfall were collected during June to September 1998.

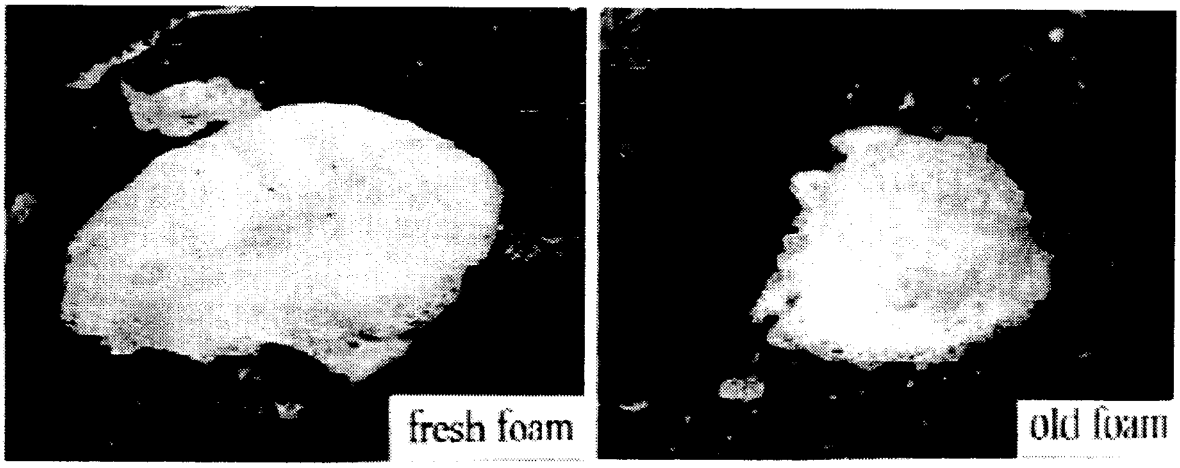

Fig. 1. Appearance of foam sample

Fungal identification

Fungal diversity was examined directly from the foam samples under a microscope according to the conidial morphology as described by Carmichael et al. (1980), Ingold (1975) and Janardhanan et al. (1997).

Viability Test

The viability of conidial cells was tested with tetrazolium bromide (MTT, Sigma 2128). A few drops of foam diluted with sterile distilled water were transferred to clean slides in Petri dishes, mixed with an equal quantity of MTT (0.5 mg/ml), and incubated in darkness for 3 h at 25 °C. A total of 200 conidia per sample were then examined under a microscope. Conidia were considered to be viable when at least one cell had reduced the stain and formed the red-coloured formazan product. Non-living conidia or cells were colourless (Sridhar and Barlocher, 1994).

Fungal isolation

The diluted foam samples were spread onto antibiotic-cornmeal agar, incubated at 25 °C for 24 h, and scanned for germinated conidia. The total viable plate count was then calculated. The germinated conidia from the fresh foam were transferred onto new cornmeal agar plates.

Results and Discussion

Diversity of freshwater fungi

Sixty-two genera of fungi, mainly hyphomycetes were found in the foams. The common genera are listed in Table 1. The results clearly demonstrated that foam is an important inoculum reservoir of aquatic fungi. Most of the conidia found in foam were branched or multiradiate (Fig. 2) that were effectively trapped by air bubbles (Iqbal and Webster, 1973) and accumulated in persistent foam.

Table 1. Alphabetical list of freshwater hyphomycetes found in foam.

Genus, species	Conidial shape
Anguillospora sp.	• unbranched, long and threadlike
Articulospora sp.	• conidia hyaline, stalk not capitate, branches apical
Beltrania sp.	• conidia biconic, 1-celled, brown with a paler middle band
Brachiosphaera tropicalis	• conidial body globose, branches long, radiating
Campylospora chaetocladia	• conidia large, branches longer than conidial body, integrated, straight
C. filicladia	• conidia small, conidial apices rounded, branches hair-like, mostly longer than the conidial body, subapical
Clavariopsis sp.	• conidial body clavate, branches 3, filiform
Condylospora spumigena	• conidia septate, 1-2 times strongly bent near the middle, 72-104 μm long
Diplocladiella appendiculata	• conidia brownish, distoseptate, primary branches conical, 2 filiform secondary branches at each end
D. scalaroides	• one filiform branch at each end
Dwayaangam cornuta	• conidia hyaline, euseptate, primary branches very short, secondary branches hornlike
D. dichotoma	• primary branches distinct, secondary branches long-fusoid
Flabellospora crassa	• conidia branches 4-5, stalk very short, capitate
F. multiradiata	• branches typically 18-19, 90-140 μm long, stalk indistinctly capitate
F. verticillata	• branches typically 5-7, 50-90 μm long, stalk narrow-clavate
Helicomyces sp.	• conidia hyaline to subhyaline, septate, conidial filament thin, tightly coiled
Helocosporium sp.	• conidia hyaline to pigmented, septate, coiled
Isthmotricladia gombakiensis	• conidia scopiform, with a narrow-clavate stalk 20-27 μm, branches 3-5, 70-100 μm long
Laridospora appendiculata	• conidial body obclavate, basally slightly curved and rostrate, branches typically 2
Phalangispora constricta	• conidia pale fuscous, of more than 5 cells, conidial axis 84-140 μm, single cell 18-23x3-4 μm
Tricladium aciculum	• conidial axis up to 100 μm long, branches, conidia hyaline, ends acute
Triscelophorus acuminatus	• conidia multiseptate, axis 40-70 μm long
T. monosporus	• conidial axis obclavate, uniseptate, branches cylindrical, aseptate or indistinctly septate
Varicosporium macrosporum	• conidial axis typically long, mostly strongly curved, branch ends subulate or conidial elements cylindrical, primary branches 2-4

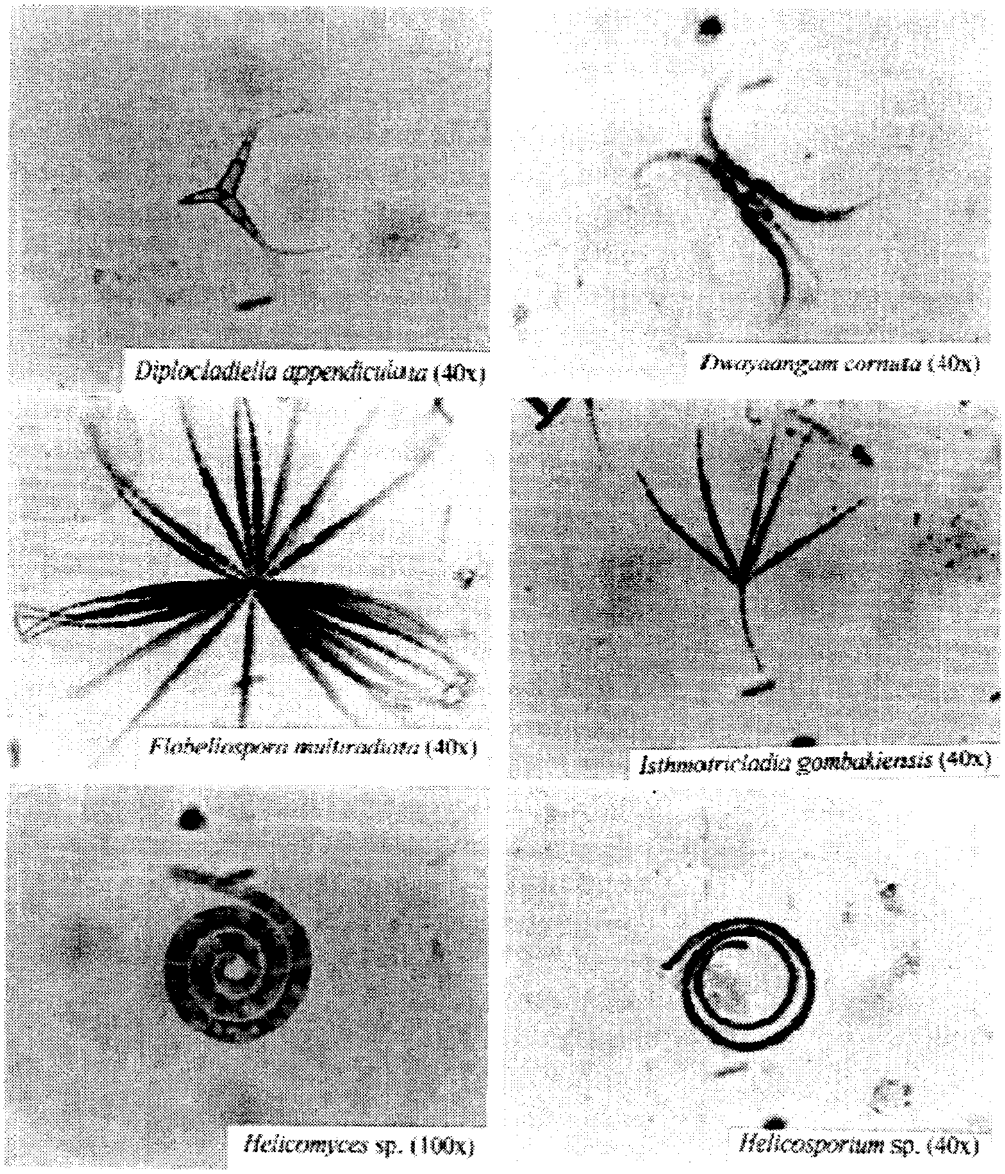

Fig. 2. Conidia of some freshwater hyphomycetes.

Viability of conidia in foam

The viable cells of conidia stained with MTT initially turned bright red and later became deep blues that could easily be distinguished from non-viable cells (Fig. 3). The percentage of conidia with at least one viable cell varied between 44 to 77 % and 42 to 69 % in fresh and old foams, respectively (Fig 3).

Fungal isolation

The numbers of viable conidia estimated by total plate count were between 2.7×10^3 and 9.2×10^4 cfu/ml in fresh foam and 6×10^3 and 1.4×10^5 cfu/ml in old foam. Sixty-five pure isolates were isolated from the fresh foam. Forty-four percent of these sporulate on cornmeal agar, including *Helicosporium* spp., *Varicosporium* spp. and *Anguillospora* spp.

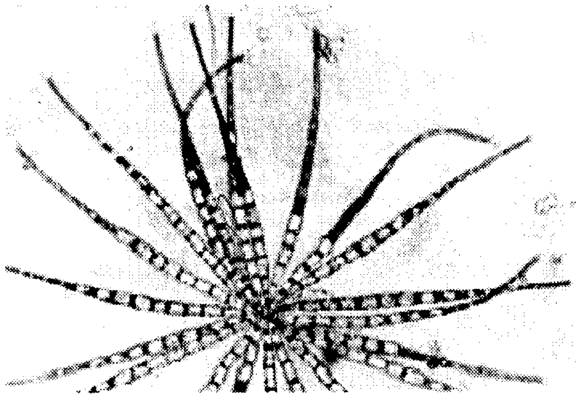

Fig. 3. Conidiun of *Flabellospora multiradiata* in foam treated with tetrazolium bromide (MTT) The living cells stained purple or deep blue. The non- living cells were colourless.

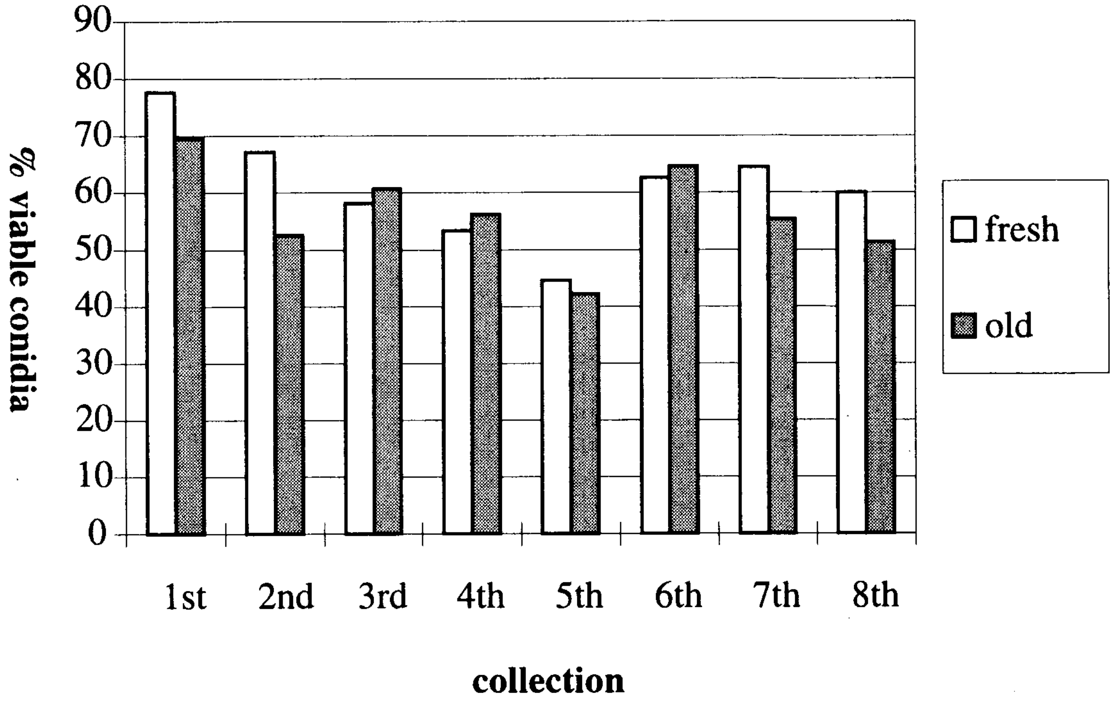

Fig. 4. Percentages of viable conidia in fresh and old foam.

Acknowledgements

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Molecular Phylogeny of Drosophilidae Based on the *Adh* Gene Sequences

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Abstract

The family Drosophilidae is one of the most popular materials in biology. Nevertheless, the phylogenetic relationship of Drosophilidae, which should provide a basis for the various studies using drosophilids, has not yet been established. In this workshop, we mainly present our phylogenetic study for Drosophilidae based on the alcohol dehydrogenase (*Adh*) gene sequences. Our phylogenetic study on the whole supports Throckmorton's (1975) classical study rather than Grimaldi's (1990) recent study, although additional findings, which are also different from Throckmorton's study, are obtained for several taxa. Furthermore, we are now developing a database for compiling the comprehensive biological information of East to Southeast Asian drosophilid species, which have the highest level of biodiversity of drosophilid flies in the world. Our database is attempting to help taxonomically untrained researchers and/or students in species identification with the aid of matrix-style key system using plentiful image information, and further to facilitate the comprehensive inventory of Asian drosophilids, which are still far from well known especially in tropical countries.

Key Words: Phylogenetic tree, Drosophilidae, Adh

Introduction

The family Drosophilidae is one of the most popular materials in biology. Since *D. melanogaster* was used as a material for the study of genetics, it has widely been used as an experimental organism in various fields, including genetics, ecology, behavior, development, and so on. Nevertheless, the phylogenetic relationship of Drosophilidae, which should provide a basis for the various studies using drosophilids, has not yet been established.

One of the most remarkable studies for the drosophilid phylogeny is Throckmorton's (1975), which is mainly based on internal morphology and biogeography. His hypothesis has widely been accepted by many evolutionary biologists. On the other hand, using a cladistic analysis of external morphology, Grimaldi (1990) recently put forward another hypothesis, that is substantially different from Throckmorton's. Since then, several molecular approaches have been made to elucidate the phylogeny of drosophilids. The results from molecular data on the whole agree with Throckmorton's hypothesis rather than Grimaldi's hypothesis. However, some inconsistencies has also been shown among these studies, and therefore the consensus for the phylogeny of drosophilid species has not been attained.

In this workshop, we mainly present our phylogenetic study for Drosophilidae based on the nucleotide sequences of alcohol dehydrogenase (*Adh*) gene. The phylogenetic studies for the drosophilid *Adh* have been already made by Thomas and Hunt (1993), Russo et al. (1995), and Tamura et al. (1996). In these studies, *Adh* has been shown to have an appropriate substitution rate for reconstructing the phylogenetic tree of drosophilid species. Therefore, to clarify the phylogeny of Drosophilidae, we determined the *Adh* sequences for 21 species in Drosophilidae. Together with homologous sequences already determined for 60 species, we reconstructed the phylogenetic tree of Drosophilidae based on the *Adh* sequences.

Furthermore, we are now developing a database for compiling the comprehensive biological information of Asian drosophilid species. East to Southeast Asia is endowed with the highest level of biodiversity of drosophilid flies in the world, retaining major lineages forming the skeleton of drosophilid phylogeny. Up to the present, a total of 1175 drosophilid species have been recorded from this region, corresponding about 34% of the world total: 145 spp. from Siberia and Russian Far East, 113 spp. from Korea, 281 spp. from Japan, 230 spp. from Taiwan, 454 spp. from mainland China, and 622 spp. from Southeast Asian countries.

Our database is attempting to compile the comprehensive biological information (phylogeny, taxonomy, type specimens, geographic distribution, ecology, morphology, karyotype, proteins, DNA, culture strains, culture methods, collecting methods, etc.) of all these Asian drosophilid species, to help taxonomically untrained researchers and/or students in species identification with the aid of matrix-style key system using plentiful image information, and further to facilitate the comprehensive inventory of Asian drosophilids, which are still far from well known especially in tropical countries.

Materials and Methods

The *Adh* sequences were obtained by PCR amplification using genomic DNA as the templates. Nucleotide sequences for the primers are as follows: Adh HEAD+E, 5'-GAATTC AACAAGAAYRTXRTXTTYGY-3'; Adh-D HEAD, 5'–GGGAACAAGAAYATYATY TTYGT - 3'; Adh-S HEAD, 5'-GGGAACAAGAAYATYATYTTYGT-3'; Adh TAIL +E, 5'-GGAATTCTAGATXYSYGARTCCCARTG-3'; Adh-D TAIL, 5'-AATTCTAGATRTGX GARTCCCAGTG-3'; and Adh-HS TAIL, 5'-AATTCTAGATRCCXGARTCCCAGTG-3'. The amplified DNA fragments were cloned into plasmid vector pUC118 by using *E. coli* K12MV1184 as a host. The nucleotide sequences were determined by using ABI 373 or 377 autosequencer according to the protocols supplied by the manufacture. For the phylogenetic analysis, we used only the protein coding regions including 711 nucleotide sites. All sequences were aligned by eye. The minimum-evolution (ME) trees were reconstructed by the method of Rzhetsky and Nei (1992) using MEBOOT program (K. Tamura). The bootstrap test (Felsenstein 1985) was performed with 1000 replicates.

Results and Discussion

Phylogenetic tree of Drosophilidae basd on the *Adh* sequences

The minimum-evolution tree with Jukes and Cantor's (1969) distances is shown in Fig. 1. The percent bootstrap values are shown along with each interior branch. In this tree, *Amiota magna* and *Leucophenga orientalis*, both of which belong to the subfamily Steganinae of the family Drosophilidae, are used as the outgroups. The phylogenetic tree shows the topology in which the subgenus *Scaptodrosophila* (*D. lebanonensis*) diverges prior to the divergence of major drosophilid lineages and that the subgenus *Sophophora* subsequently diverges from the others. The subgenus *Drosophila* does not form a monophyletic clade but to form a large clade together with other genera and subgenera. These results are on the whole compatible with Throckmorton's (1975) hypothesis rather than Grimaldi's (1990) hypothesis. However, additional findings, which are also different from Throckmorton's hypothesis, are shown in the phylogenetic tree.

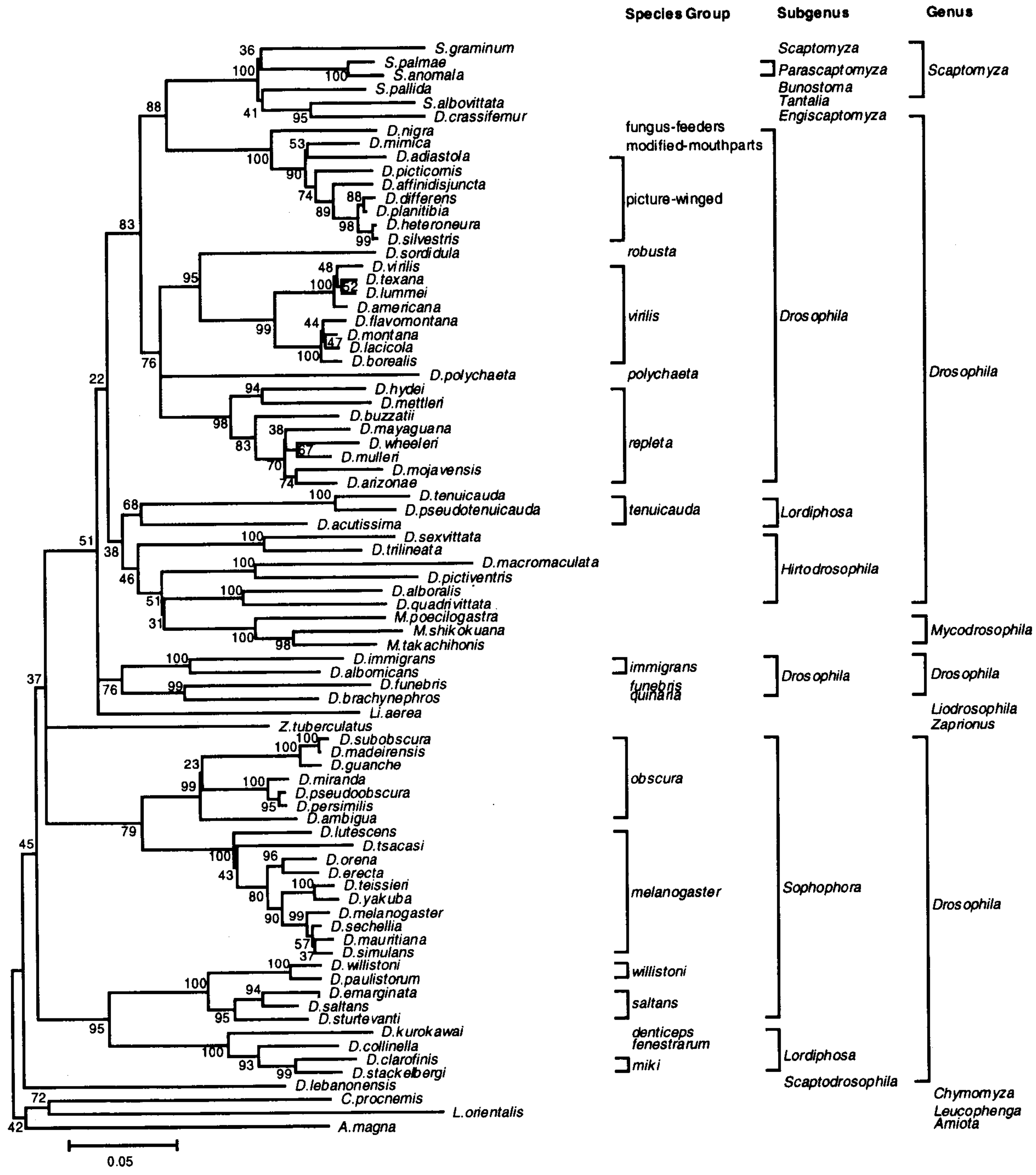

Fig.1. Molecular phylogenetic tree of Drosophilidae based on the *Adh* sequences

1. The genus *Chymomyza* is included in the clade of the subfamily Steganinae. Throckmorton proposed that *Chymomyza* is associated with the *Sophophora* radiation. However, our results suggest that *Chymomyza* is distantly related to the subgenus *Sophophora*.
2. The subgenus *Dorsilopha* and the genus *Zaprionus* are placed outside the clade including the subgenera *Drosophila* and *Hirtodrosophila*. Throckmorton suggested that both *Dorsilopha* and *Zaprionus* are originated in the *immigrans-Hirtodrosophila* radiation. However, in the phylogenetic tree these species are shown to diverge prior to the divergence of *Drosophila* and *Hirtodrosophila*.

3. The subgenus *Lordiphosa* is polyphyletic. The *tenuicauda* group of *Lordiphosa* is placed as a sister group to *Hirtodrosophila* and *Mycodrosophila*. On the other hand, remaining species of *Lordiphosa* makes an another monophyletic clade, and it is placed as a sister group to the *willistoni* and *saltans* groups of *Sophophora*.
4. Hawaiian Drosophilidae forms a monophyletic clade which is placed as a sister group to the *virilis-repleta* lineage. Throckmorton suggested that Hawaiian Drosophilidae is closely related to the *immigrans-Hirtodrosophila* lineage. However, our results suggest that Hawaiian Drosophilidae is more closely related to the *virilis-repleta* lineage than to the *immigrans-Hirtodrosophila* lineage.

Database system being planned for Asian drosophilid species

As we intend to adopt the matrix method in the system, users can begin to search with any feature of the fly. The comprehensive biological information and plentiful images will help taxonomically untrained researchers to identify the species (Fig. 2).

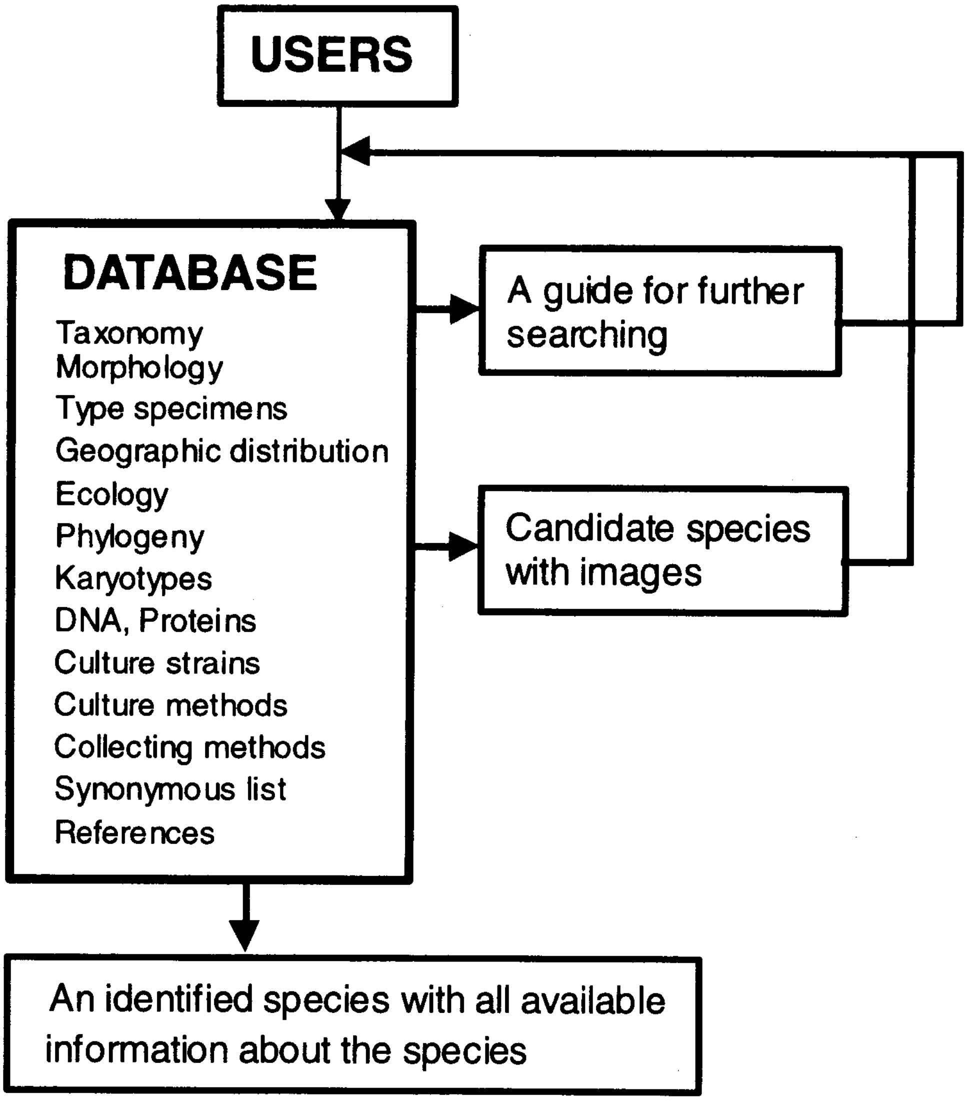

Fig.2. Database system being planned for Asian drosophilid species

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Revisiting an Early Appraiser of Biodiversity in the Japanese Islands: Taxonomic Studies on the 1880-81 Döderlein Collection in European Museums

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Abstract

Ludwig Döderlein's collection of Japanese animals made in 1880-81 has proved to remain in good condition at the Musée Zoologique Strasbourg, the Museum für Naturkunde der Humboldt-Universität zu Berlin, the Zoologische Staatssammlung München, and the Naturhistorisches Museum Wien. The 1997-8 project team's *in situ* examintion revealed that his collection consists of more than 3,078 specimens in total, belonging to the Protozoa and 9 phyla of Animalia, including at least 857 types for about 340 species, and many yet unstudied marine and land animals of diverse groups. Significance of museums and their long-kept specimens was emphasized, with reference to thier possibility for future multi-dimentional studies in terms of biodiversity.

Key words: Taxonomy, Japanese biota, Museum, Specimen, Biodiversity, Döderlein.

Introduction: Historical Background

Initial stages in the modern taxonomic studies of the Japanese biota were performed by Western scientists since Linnaeus, based mainly on many collections of Japanese specimens deposited at the European and American museums. The collections hold numerous name-bearing types. One of the most famous examples seems the huge collection of Philipp Franz von Siebold (1796-1866) housed at the Nationaal Naturhistorish Museum in Leiden, which includes the holotype of an endangered bird "toki", *Nipponia nippon* (Temminck) (Yamaguchi, 1994). Intimate examinations of such collections have given, and will give, significant results to taxonomists and other scientists interested in the biodiversity in Japanese islands and vicinity, and its recent deteriorations due to abruptly increased human impacts on environments.

Such initial stages include activities of the German biologist Prof. Ludwig Heinrich Philipp Döderlein (1855-1936). He stayed in Japan for about 2 years from Nov. 1879 as a "yatoi" (=foreign employee) professor of natural history in the Preparatory Course of the Medical Department, University of Tokyo (Kreiner, 1981; Isono, 1986). During this short period, he made a giant collection of organisms from not only the sea but also freshwater and land, mainly in the southern part of the Japanese islands (Döderlein, 1881a, 1883a).

The details of Döderlein's entire biological collection have so far remained unclear, although some taxonomic papers were published covering certain marine animal groups, both by himself and other zoologists whom he invited to conduct taxonomic studies (see Table 1). Thus, the collection became to include many name-bearing types and other taxonomically important specimens. Fortunately we succeeded in organizing a project team for taxonomic studies of the whole collection to visit some European museums in 1997 and 1998.

Table 1. Previous taxonomic studies and present location of the Japanese protozoan and animal specimens of the Döderlein collection. Types include holotypes, paratypes, syntypes, lectotypes, and paralectotypes, designated originally or subsequently in the previous studies. Blank columns indicate that no information is available. (Revised from Table 1 of Nishikawa, 1999)

Taxon name	Previous studies	Present location* of specimens no. of specimens/no. of types				Number of species-group represented by types
		Strasbourg	Berlin	München	Elsewhere	
FORAMINIFERA	Döderlein (1892)	0	0	11/11(?)		1
PORIFERA						
Calcarea	Döderlein (1892)	21/0	0			1
Hexactinellida	Schulz(1887)	43/6	0			6
Demospongiae						
Lithistidae	Döderlein (1883b)	41/8	2/1			4
Others	Thiele(1898)	146/36	42/22			64
CNIDARIA						
Hydrozoa	No	7/0	0	1/0		0
Anthozoa						
Hexacorallia	Ortmann (1888a)	23/1	0	0		1
Octocorallia	Studer (1888)	12/0	0	0		6
CTENOPHORA				0		
PLATHYHELMINTHES						
Turbellaria			0	0		
Trematoda				0		
Cestoda			0	0		
NEMERTEA			0	0		
"ASCHELMINTHES"			0	0		
MOLLUSCA						
Cephalopoda	Ortmann(1888b) Robson(1929) Adam(1960) Toll & Voss(1998)	157/89		0		9
Others	No	>200/0		0		0
ANNELIDA						
Polychaeta	Marenzeller (1884,1902)	4/0	0	0	Wien	14
Oligochaeta				0	0	
Hirudinea	Blanchard(1896)		1/1	0		1
ARTHROPODA						
Pycnogonida	Ortmann(1891a)	9/6		0		3
Crustacea						
Isopoda	Ortmann(1895)	43/0		0		1
Amphipoda	No	0		0		0
Cirripedia	No	>400/0		0		0
Decapoda	Ortmann (1890b,91b,92a,b,c,93a,b,94)	661/529				55
PRIAPULIDA		0		0		

*)Strasbourg, Berlin, München, and Wien represent the Musée Zoologique Strasbourg, the Museum für Naturkunde der Humboldt-Universität zu Berlin, the Zoologische Staatssammlung München, and the Naturhistorisches Museum Wien, respectively.

Table 1. (continued)

Taxon name	Previous studies	Present location* of specimens (no. of specimens/no. of types)				Number of species-group represented by types
		Strasbourg	Berlin	München	Elsewhere	
ECHIURA	No	0	0	0		0
SIPUNCULA	No	0	0	0		0
BRYOZOA	Ortmann(1890a)	251/?		2/1		99
BRACHIOPODA	Davidson (1886a,b,87,88)	8/0		0		1
ECHINODERMATA**)						
Crinoidea	Loriol(1900)	7/0	0	0		0
Asteroidea	Döderlein (1902b)	23/1	1/0	143/15		11
Ophiuroidea	Döderlein (1902a,1911)	9/0	0	>121/5		20
Echinoidea	Döderlein (1885,1887,1906)	20/0	3/0	325/56		18
Holothuroidea	No	2/0	0	0		0
CHORDATA						
Ascidiacea	Hartmeyer(1906) Nishikawa(1991)	0	36/6	0	0	4
Cephalochordata	No					0
Pisces	Döderlein(1882) Steindachner & Döderlein (1883a,b,84,87)	205/33	54/30		Wien	18
Amphibia	No	12/0				0
Reptilia	No	5/0				0
Aves	No					0
Mammalia	No	27/0				0
Total		>2336/709	139/60	>603/88	?	337

**) Listed by Jangoux (1986) and Jangoux et at al. (1987).

Results

The project team has revealed that the major part of animal specimens in Döderlein collection still remain in good condition at the Musée Zoologique Strasbourg, the Museum für Naturkunde der Humboldt-Universität zu Berlin, the Zoologische Staatssammlung München, and the Naturhistorisches Museum Wien.

Table 1 gives a summation of our present knowledge about the collection. This table shows the following: (1)The collection consists of more than 3,078 specimens in total, belonging to the Protozoa and 9 phyla of Animalia, so far as our results are concerned; (2)The collection includes at least 857 types (=holotypes, paratypes, syntypes, lectotypes, and paralectotypes) for about 340 species or subspecies of Foraminifera, Porifera, Cnidaria, Mollusca (Cephalopoda), Annelida, Arthropoda (Decapoda), Bryozoa, Echinodermata, and Chordata (Ascidiacea and Pisces), and they are undoubtedly important in terms of taxonomy and nomenclature; (3)The collection includes many yet unstudied marine and land animals of diverse groups; possibly, some of these represent undescribed species and now rare or endangered species; and (4)The collection is so large and systematic, containing such a diversity of organisms, that the whole collection may contribute to reconstructing the biota of about 120 years ago when organisms (whether *Homo sapiens* itself be included or not) seem to have lived their lifes in and around the Japanese islands far more safely and comfortably than nowadays in terms of human impacts.

On the other hand, the many blank columns of Table 1 also show that much still remains to be studied. This may become a part of a future target for the next step of the project. Döderlein's concern about plants should also be mentioned here. Döderlein (1881a) mentioned many plant species in Amami Oshima, and he also gave explanatory remarks concerning some Japanese botanical books (Döderlein, 1881b). Unfortunately, we have failed to find plant specimens in the Döderlein collection in Strasbourg.

Lists of various animal groups of specimens in the collection based primarily on label information, were given elsehwere (Nishikawa, 1999). We believe the lists are to be used as a database for future various studies of the collection.

Making use of the collection, some nomenclatural and other detailed taxonomic studies have already been published by our team mates, such as Mawatari & Suwa (1998) on bryozoans, Yabe & Mawatari (1998) and Kato & Mawatari (1999) on polychates, and Komai & Yu (1999) and Komai (1999a, b) on crustaceans.

Discussion: Signigicance of museums and their long-kept specimens

The present project could not have been carried out if the collection had failed to survive World War II and other unfavorable situations for museum materials. Great respect is deserved by those who have kept the specimens in good condition for a long time. This cannot be emphasized too repeatedly. Japanese museums should also keep their progress to deserve such international respect in a distant future.

Needless to mention, name-bearing types are indispensable because they are the objective standard for scientific names. However, museum specimens in general are signigicant because they are all unique as historical entities. Museum materials await our multi-dimentional approaches.

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Plants of Iriomote Island and Their Conservation

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Abstract

Iriomote Island is located near the southern end of the Ryukyu Archipelago. Its most part is covered with subtropical forests and includes diverse plant species: 172 species in 22 families of Pterophyta; 4 species in 3 families of Gymnosperms; 958 species in 142 families of Angiosperms. These figures mean that about one-fifth of Japanese vascular plants occur in the island. There are seven endemic species. Because of the increase of recent human activities, many species are threatened from extinction Floristic analysis in the island is still inadequate, and intensive studies are urgently needed.

Key Words: conservation, flora, Iriomote Island, Ryukyu Archipelago, vascular plants

Introduction

We have two major subtropical forests in Japan: one is called Yambaru located near the northern end of the Okinawa Island, and the other in Iriomote Island located close to Taiwan. These two forests are separated by 500 kilometers and have different geological histories. Yambaru forest is floristically more related to temperate ones, while Iriomote forest is more tropical ones. Iriomote forest comprises mangroves around estuaries in addition to terrestrial forests. The island forest is extremely interesting in view of the biodiversity and biogeography, as well as of its importance as natural resources. The island appears to have sustained rich biodiversity; however, it is obviously under heavy pressure from industrial development. We now have to watch it with deep concern particularly with respect to the status of natural environment of the island.

Lists of plants in Iriomote Island

Floristic studies of Iriomote Island are less advanced compared with other regions of the Ryukyu Archipelago probably because of difficulty in access, especially in southwest areas of the island. However, fragmentary information of the flora is available from comprehensive studies of the flora of the Ryukyu Archipelago by Walker (1976), Hatusima and Amano (1994) and Shimabuku (1997). Despite such information, a list of native plants growing in Iriomote Island is not available as a publication. As mentioned above, a large subtropical forest extends in Iriomote Island, and a handy list of plants is needed for various purposes such as research itself, education, and conservation. Under these circumstances, we have prepared the list of the native plants in Iriomote Island, which were collected from "Flora of the Ryukyus, south of Amami Island" by Hatusima and Amano (1994). The list includes 1134 vascular plants, and the names of families and genera are given in Table 1. According to Shimabuku (1989), seven endemic species and three endemic subspecies occur in Iriomote Island (Table 2).

Table 1. Families and genera of vascular plants in Iriomote Island

Pteridophyta		
	Psilotaceae	Psilotum
	Lycopodiaceae	Lycopodium
		Selaginella
	Ophioglossaceae	Helminthostachys
		Ophioglossum
	Marattiaceae	Angiopteris
	Osmundaceae	Plenasium
	Schizaeaceae	Lygodium
		Lygodium
		Schizaea
	Gleicheniaceae	Dicranopteris
		Gleichenia
	Parkeriaceae	Ceratopteris
	Hymenophyllaceae	Cephalomanes
		Crepidomanes
		Trichomanes
	Dipteridaceae	Dipteris
	Cyatheaceae	Alsophila
		Sphaeropteris
	Plagiogyriaceae	Plagiogyria
	Cheiropleuriaceae	Cheiropleuria
	Pteridaceae	Acrostichum
		Adiantum
		Cibotium
		Histiopteris
		Lindsaea
		Microlepia
		Pityrogramma
		Pteridium
		Pteris
		Sphenomeris
		Tapeinidium
	Blechnaceae	Blechnum
		Woodwardia
	Davalliaceae	Humata repens
		Nephrolepis
	Aspidiaceae	Arachniodes
		Bolbitis
		Ctenitis
		Cyrtomium
		Deparia
		Diplazium
		Dryopteris
		Hemigramma
		Lomariopsis
		Polystichum
		Pronephrium
		Stegnogramma
		Tectaria
		Thelypteris
	Aspleniaceae	Asplenium
	Vittariaceae	Antrophyum
		Vittaria
	Polypodiaceae	Colysis
		Crypsinus
		Lepisorus
		Microsorium
		Neocheiropteris
		Polypodium
		Pseudodrynaria
		Pyrrosia lingua
	Salviniaceae	Azolla
	Marsileaceae	Marsilea
Gymnospermae		
	Cycadaceae	Cycas
	Podocarpaceae	Nageia
		Podpcarpus
	Pinaceae	Pinus
Angiospermae		
	Saururaceae	Saururus
	Piperaceae	Peperomia
		Piper
	Chloranthaceae	Sarcandra glabra
	Myricaceae	Myrica rubra
	Fagaceae	Castanopsis
		Quercus
	Ulmaceae	Celtis
		Trema
	Moraceae	Broussonetia
		Fatoua
		Ficus
		Maclura
		Morus
	Urticaceae	Boehmeria
		Debregeasia
		Elatostema
		Gonostegia
		Nanocnide
		Oreocnide
		Pellionia
		Pilea
		Pipturus
		Pouzolzia
	Proteaceae	Helicia
	Santalaceae	Thesium
	Olaceae	Schoepfia
	Loranthaceae	Korthalsella
		Taxillus
	Balanophoraceae	Balanophora
	Aristolochiaceae	Aristolochia
		Asarum
	Rafflesiaceae	Mitrastemon
	Polygonaceae	Polygonum
		Rumex
	Chenopodiaceae	Atriplex
		Chenopodium
		Suaeda
	Amaranthaceae	Achyranthes
		Alternanthera
		Amaranthus
		Deeringia
		Philoxerus
	Aizoaceae	Mollugo
		Sesuvium
		Tetragonia
	Portulacaceae	Portulaca
		Boerhavia
		Pisonia
	Caryophyllaceae	Arenaria
		Drymaria
		Sagina
		Silene
		Stellaria
	Ceratophyllaceae	Ceratophyllum
	Trochodendraceae	Trochodendron
	Ranunculaceae	Clematis
		Ranunculus
	Lardizabalaceae	Stauntonia
	Menisoermaceae	Cocculus
		Cyclea
		Stephania
	Magnoliaceae	Illicium
		Kadsura
		Michelia
	Annonaceae	Polyalthia
	Lauraceae	Beilschmiedia
		Cassytha
		Cinnamomum
		Litsea
		Neolitsea
		Persea
	Hernandiaceae	Hernandia
	Papaveraceae	Corydalis
	Capparidaceae	Cleome
	Cruciferae	Cardamine
		Coronopus
		Raphanus
		Rorippa
	Droseraceae	Drosera
	Crassulaceae	Kalanchoe
		Sedum
	Saxifragaceae	Cardiandra
		Deutzia
		Hydrangea
		Itea
		Pileostegia
	Pittosporaceae	Pittosporum
	Hamamelidaceae	Distylium
	Rosaceae	Duchesnea
		Osteomeles
		Photinia
		Prunus
		Rhaphiolepis
		Rosa
		Rubus
	Leguminosae	Abrus
		Aeschynomene
		Albizia retusa
		Alysicarpus
		Atylosia
		Bauhinia
		Caesalpinia
		Canavalia
		Cassia
		Christia
		Crotalaria
		Dalbergia
		Derris
		Desmodium
		Entada
		Euchresta
		Flemingia
		Indigofera
		Kummerowia
		Lespedeza
		Lotus
		Maackia
		Mucuna
		Ormocarpum

	Pithecellobium
	Pongamia
	Pueraria
	Pycnospora
	Rhynchosia
	Sophora
	Thermopsis
	Uraria
	Vicia
Oxalidaceae	Oxalis
Rutaceae	Citrus d
	Euodia
	Glycosmis
	Melicope
	Murraya
	Toddalia
	Zanthoxylum
Simaroubaceae	Picrasma
Meliaceae	Melia
Polygalaceae	Polygala
Malpighiaceae	Ryssopterys
	Tristellateia
Daphniphyllaceae	Daphniphyllum
Euphorbiaceae	Acalypha
	Alchornea
	Antidesma
	Bischofia
	Breynia
	Bridelia
	Croton
	Discocleidion
	Drypetes
	Euphorbia
	Excoecaria
	Glochidion
	Macaranga
	Mallotus
	Margaritaria
	Melanolepis
	Phyllanthus
	Sapium
	Securinega
Callitrichaceae	Callitriche
Anacardiaceae	Rhus
Aquifoliaceae	Ilex
Celastraceae	Celastrus
	Euonymus
	Maytenus
	Microtropis
Staphyleaceae	Euscaphis
	Turpinia
Icacinaceae	Nothapodytes
Sapindaceae	Allophylus
	Dodonaea
	Sapindus
Sabiaceae	Meliosma
Rhamnaceae	Berchemia
	Colubrina
	Paliurus
	Rhamnella
	Rhamnus
	Sageretia
Vitaceae	Ampelopsis
	Cayratia japonica
	Vitis
Elaeocarpaceae	Elaeocarpus
Tiliaceae	Corchorus
	Triumfetta
Malvaceae	Abelmoschu
	Abutilon
	Hibiscus
	Malvastrum
	Sida
	Thespesia
	Urena
Sterculiaceae	Firmiana
	Helicteres
	Heritiera
	Kleinhovia
Actinidiaceae	Actinidia rufa
	Saurauria
Theaceae	Adinandra
	Camellia
	Cleyera
	Eurya
	Schima
	Ternstroemia
	Tutcheria
Guttiferae	Calophyllum
	Garcinia
	Hypericum
Elatinaceae	Elatine
Violaceae	Viola
Flacourtiaceae	Idesia
	Scolopia
Begoniaceae	Begonia
Thymelaeaceae	Wikstroemia
Elaeagnaceae	Elaeagnus
Lythracea	Pemphis
	Rotala
Sonneratiaceae	Sonneratia
lecythidaceae	Barringtonia
Rhizophoraceae	Bruguiera
	Kandelia
	Rhizophora
Alanglaceae	Alangium
Combretaceae	Lumnitzera
	Terminalia
Myrtaceae	Syzygium
Melastomataceae	Bredia
	Melastoma
	Osbeckia
Onagraceae	Ludwigia
Haloragidaceae	Haloragis
	Myriophyllum
Araliaceae	Dendropanax
	Kalopanax
	Schefflera
Umbellifera	Angelica
	Apium
	Centella
	Glehnia
	Hydrocotyle
	Oenanthe
	Peucedanum
	Sanicula
	Torilis
Cornaceae	Cornus
Diapensiaceae	Shortia
Pyrolaceae	Monotropastrum
Ericaceae	Rhododendron
	Vaccinium
Myrsinaceae	Ardisia
	Maesa
	Rapanea
Primulaceae	Anagallis
	Androsace
	Lysimachia
Plumbaginaceae	Limonium
Sapotaceae	Planchonella
Ebenaceae	Diospyros
Symplocaceae	Symplocos
Styracaceae	Styrax
Oleaceae	Fraxinus
	Ligustrum
	Osmanthus
Gentianaceae	Centaurium
	Nymphoides
	Swertia
Apocynaceae	Anodendron
	Cerbera
	Ecdysanthera
	Neisosperma
	Parsonsia
	Trachelospermum
Asclepiadaceae	Cynanchum
	Hoya
	Marsdenia
	Stephanotis
	Tylophora
Convolvulaceae	Calystegia
	Dichondra
	Evolvulus
	Ipomoea
	Stictocardia
Boraginaceae	Argusia
	Bothriospermum
	Carmona retusa
	Cordia
	Ehretia
	Heliotropium
Verbenaceae	Avicennia
	Callicarpa
	Clerodendrum
	Phyla
	Premna
	Verbena
	Vitex
Labiatae	Ajuga
	Anisomeles
	Clinopodium
	Hyptis
	Leonurus
	Leucas
	Mosla
	Salvia
	Teucrium
Solanaceae	Lycianthes
	Tubocapsicum
Scrophulariaceae	Centranthera
	Dopatrium
	Limnophila
	Mazus
	Microcarpaea
	Siphonostegia
	Veronica
Orobanchaceae	Aeginetia
Gesneriaceae	Aeschynanthus
	Conandron
	Cyrtandra

	Hemiboea
	Rhynchotechum
	Titanotrichum
Lentibulariaceae	Utricularia
Acanthaceae	Codonacanthus
	Dicliptera
	Hygrophila
	Justicia
	Lepidagathis
	Staurogyne
	Strobilanthes
Myoporaceae	Myoporum
Plantaginaceae	Plantago
Rubiaceae	Argostemma
	Coptosapelta
	Damnacanthus
	Diplospora
	Galium
	Gardenia
	Hedyotis
	Lasianthus
	Morinda
	Mussaenda
	Neanotis
	Ophiorrhiza
	Ophiorrhiza
	Paederia
	Psychotria
	Randia
	Tarenna
	Wendlandia
Caprifoliaceae	Lonicera
	Sambucus
	Viburnum
Cucurbitaceae	Diplocyclos
	Gynostemma
	Mukia
	Trichosanthes
	Zehneria
Campanulaceae	Codonopsis
	Lobelia
	Wahlenbergia
Goodeniaceae	Scaevola taccada
Compositae	Adenostemma
	Ainsliaea
	Artemisia
	Aster
	Blumea
	Carpesium
	Centipeda
	Cirsium
	Conyza
	Crossostephium
	Dichrocephala
	Eclipta
	Eupatorium
	Farfugium
	Gnaphalium
	Hemistepta
	Ixeris
	Kalimeris
	Lactuca
	Lagenophora
	Siegesbeckia
	Solenogyne
	Sonchus
	Vernonia
	Wedelia
	Youngia
Typhaceae	Typha
Pandanaceae	Freycinetia
	Pandanus
Potamogetonaceae	Cymodocea
	Halodule
	Potamogeton
	Ruppia
	Syringdium
	Zannichellia
	Zostera
Najadaceae	Najas
Alismataceae	Alisma
	Sagittaria
Hydrocharitaceae	Blyxa
	Enhalus
	Halophila
	Ottelia
	Thalassia
Triuridaceae	Sciaphila
Gramineae	Apluda
	Arthraxon
	Arundo
	Bothriochloa
	Brachiaria
	Capillipedium
	Chikusichloa
	Chrysopogon
	Cymbopogon
	Cynodon
	Cyrtococcum
	Dactyloctenium
	Dogitaria
	Digitaria
	Eccoilopus
	Echinochloa
	Eleusine
	Eragrostis
	Eriochloa
	Eulalia
	Garnotia
	Hackelochloa
	Hemarthria
	Ichnanthus
	Imperata
	Isachne
	Ischaemum
	Leersia
	Leptochloa
	Lepturus repens
	Lophatherum
	Microstegium
	Miscanthus
	Oplismenus
	Panicum
	Paspalum
	Phacelurus
	Phragmites
	Pleioblastus
	Pogonantherum
	Polypogon
	Saccharum
	Sacciolepis
	Schizachyrium
	Setaria glauca
	Spinifex
	Sporobolus
	Thaumastochloa
	Thuarea
	Zoysia
Cyperaceae	Bulbostylis
	Carex
	Cladium
	Cyperus
	Diplacrum
	Eleocharis
	Fimbristylis
	Fuirena
	Gahnia
	Lepironia
	Lipocarpha
	Machaerina
	Rhynchospora
	Schoenus
	Scirpus
	Scleria
	Arenga
Palmae	Livistona
	Nypa
	Satakentia
Araceae	Alocasia
	Pinellia
	Rhaphidophora
Lemnaceae	Lemna
	Spirodela
Flagellariaceae	Flagellaria
Eriocaulaceae	Eriocaulon
Commelinaceae	Amischotolype
	Commelina
	Murdannia
	Pollia
Pontederiaceae	Monochoria
Philydraceae	Philydrum
Juncaceae	Juncus
Liliaceae	Aletris
	Asparagus
	Dianella
	Heloniopsis
	Hemerocallis
	Heterosmilax
	Lilium
	Liriope
	Ophiopogon
	Scilla
	Smilax
	Tricyrtis
Hypoxidaceae	Curculigo
Amaryllidaceae	Allium
	Crinum
Dioscoreaceae	Dioscorea
Zingiberaceae	Alpinia
Cannaceae	Canna indica
Burmanniaceae	Burmannia
Orchidaceae	Acanthephippium
	Anoectochilus
	Aphyllorchis
	Arundina
	Bletilla
	Bulbophyllum
	Calanthe
	Cephlantheropsis
	Corymborkis

Cymbidium
Didymoplexis
Disperis
Epipogium
Eria
Galeola
Gastrochilus
Gastrodia
Geodorum
Goodyera
Habenaria
Lecanorchis
Liparis
Listera
Macodes
Malaxis
Microtis
Nervilia
Oberonia
Phaius
Platanthera
Spathoglottis
Spiranthes
Stereosandra
Thrixspermum
Trichoglottis
Tropidia
Zeuxine

Table 2. Endemic species and subspecies of Iriomote Island

Nesopteris thysanostoma (Makino) Copeland
Asarum glasinum (F. Kaekawa) Hatusima
Asarum yaeyamaensis Hatusima
Heterotropa monodraeflora F. Maekawa
Deutzia yaeyamensis Ohwi
Chikusichloa brachyanthera Ohwi
Alpinia koidzumiana Kitamura
Ctenitis eatoni (Baker) Ching var. iriomotensis H. Ito
Hedyotis tenelliflora Blume var. longipes Hatsusima
Mussaenda parviflora Miquel var. yaeyamensis (Masamune) Yamazaki

Current Status

Iriomote Island, with a population ca. 1800, covers an area of 284.4 square kilometers, and nearly 80% of the area belongs to a national forest. Within this forest an area of 99.8 square kilometers is environmentally protected.

Major industries in the island are agriculture, cattle breeding and tourism. Broad areas of the forest have been utilized as sugarcane and pineapple fields and as pasture grounds. Recently roads, bridges and harbor facilities are constructed extensively, and this has brought major environmental concerns. Because of the human activities, habitats of many plants, especially orchids, have been lost or threatened, and we have to consider conservation programs seriously. There are 25 endangered species according to Red-data Okinawa (Table 3; Okinawa government, 1996).

Table 3. Endangered species in Iriomote Island

Lycopodium salvinioides (Herter) Tagawa
Lycopoiumu sieboldii Miquel var. christensenianum (Christ et Herter) Tagawa
Helminthostachys zeylanica (L.) Hooker
Sceptridium formosanum (Tagawa) Holub
Cephalomanes apiifolium (Presl) K. Iwatsuki
Antrophyum formosanum Hieromymus
Pteris grevilleana Wallich ex Agardh
Polypodium formosanum Baker

Polyalthia liukiuensis Hatusima
Asarum monodoriflorum Hatusima et Yamahata
Asarum yaeyamaensis Hatusima
Terminalia nitens Presl
Limonium sinense (Girard) O. Kuntze
Limnophila fragrans (G. Foster) Seemann
Solenogyne mikadoi Koidzumi
Burmannia coelestris D. Don
Diplacrum caricinum R. Brown
Anoectochilus formosanus Hayata
Anoectochilus koshunensis Hayata
Calanthe densifloria Lindley
Cryptostylis arachnites (Blume) Hasskarl
Cryptostylis taiwaniana Masamune
Cymbidium sinsnse (Andrews) Willdenow
Phaius mishmensis (Lindley) Reichenbach fil.
Trichoglottis ionosma (Lindley) J. J. Smith

For the conservation of the endangered species, the protected areas should be reconsidered to catch up the recent rapid destroy of environment. Further, transplantation as well as other methods of propagation like tissue culture should be tried for the species conservation. Basic researches are also needed for floristic aspects, pollination mechanisms, and genetic diversity of endangered species. There should be many plant species which can be used as ornamentals, fragrance or sources of medial products. Utilization of these plants can be beneficial for local economy, and the vitalization of the local economy depends on the conservation of the natural diversity.

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Relationship Between Ozone Climate and Ozone Resistance in Populations of *Plantago Major*

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Abstract

The ozone resistance of geographically distinct populations of *Plantago major* L. was calculated from the decrease in seedling relative growth rate induced by exposure to 70 nmol mol^{-1} ozone 7 h d^{-1} over a 2 wk period in controlled environment chambers. Populations exhibited contrasting sensitivities to the pollutant, in the absence of visible symtoms of foliar damage. A positive relationship between ozone resistance and cumulative ozone exposure at the original site of seed collection was found. No significant relationships between ozone resistance and other climatic factors were evident. The findings suggest that ambient levels of ozone may be high enough to drive the evolution of ozone resistance in plant populations.

Key Words: air pollution, evolution, ozone, Plantago major, resistance

Introduction

Ozone (O_3) is widely perceived to be one of the most ubiquitous and damaging air pollutants to which vegetation is exposed. Current levels of the pollutant exceed United Nations Economic Commission for Europe (UN-ECE) guidelines for the protection of crops, forests, natural and semi-natural vegetation in many regions of Europe (UN-ECE, 1996). There is growing evidence that ambient O_3 concentrations in some regions may be high enough to drive the selection of resistant genotypes within populations (Berrang et al., 1988; Heagle et al., 1991; Reiling and Davison, 1992; Davison and Reiling, 1995; Whitfield et al., 1997; Barnes et al., 1999), as has been shown to occur to other novel stresses (Bradshaw and McNeilly, 1991). Previous work on British populations of *Plantago major* L. has demonstrated relationships between O_3 resistance and environmental variables at the site of seed collection, in particular between resistance and O_3 climate (Reiling and Davison, 1992; Davison and Reiling, 1995). The present study was instigated, in co-operation with the UN-ECE/ICP-Crops initiative (International Co-operative Programme to Investigate the Effects of Air Pollutants and Other Stresses on Agricultural and Semi-Natural Vegetation), to examine in greater detail the relationship between ozone exposure at the site of seed collection and the inherent resistance of populations to ozone (see Lyons et al., 1997).

Materials and Methods

Seed of *P. major* was obtained from a number of locations (see Table 1)). Mean seed weight was recorded for each population. Seed was germinated, and (after 6 days) seedlings transferred to controlled environment chambers (see Barnes et al., 1995) where they were exposed to either charcoal/Purafil® filtered air (CFA) or CFA plus O_3 (70 nmol mol^{-1} O_3 for 7 h d^{-1}).

Table 1. Sites of *Plantago major* seed collection and sources of climate data.

Population	Collection	Source of climate data
Benaki, Greece	1990	Dr D Velissariou, Benaki Phytopath Inst, Athens, Greece
BELP, Switzerland	1994	Dr J Fuhrer, IUL, Liebefeld-Bern, Switzerland
Gasterntal, Switzerland	1994	Dr J Fuhrer, IUL, Liebefeld-Bern, Switzerland
Liebefeld, Switzerland	1994	Dr J Fuhrer, IUL, Liebefeld-Bern, Switzerland
Ebro, Spain	1990	Dr B Sanchez-Gimeno, CIEMAT, Madrid, Spain
Giessen, Germany	1994	Dr A Fangmeier, Inst Pflanzenokol, Giessen, Germany
Oberbutschel, Switzerland	1994	Dr J Fuhrer, IUL, Liebefeld-Bern, Switzerland
Lullington, UK	1990	Warren Springs Laboratory, Stevenage, UK
Redecesio, Italy	1994	Dr G Violini, Inst Patologia Vegetale, Milan, Italy
Jokioinen, Finland	1994	Dr T Ylaranta, Fin Agric Res Centre, Jokioinen, Finland
Siebersdorf, Austria	1994	Dr G Soja, Res Centre Siebersdorf, Siebersdorf, Austria
Braunschweig, Germany	1994	Prof H-J Weigel, Inst Okotoxikol, Braunschweig, Germany
Cadenazzo, Switzerland	1994	Dr J Fuhrer, IUL, Liebefeld-Bern, Switzerland
Tervuren, Belgium	1994	Dr L de Temmerman, Inst Chem Res, Tervuren, Belgium
Ithaca, USA	1989	Dr J Laurence, Cornell University, Ithaca, USA
ISP, UK	1991	Warren Springs Laboratory, Stevenage, UK
Valsain, Spain	1993	Dr B Sanchez-Gimeno, CIEMAT, Madrid, Spain

After 14 d plants were harvested. Mean plant relative growth rate of plant (R) was calculated, and the relative O_3 resistance of each population (R%) expressed as R_{O3}/R_{CFA} x 100. Climate data for each site (or the closest available monitoring station) was obtained from the original collectors of the seed (see Table 1). AOT40 and AOT30 values were calculated according to UN-ECE guidelines (accumulated hourly O_3 exposure over a threshold of 40 nmol mol^{-1} [AOT40] or 30 nmol mol^{-1} [AOT30] calculated during daylight hours [defined as the period of the day when irradiance exceeds 50 W m^{-2}] for the consecutive three-month period of the year experiencing the highest O_3 concentrations)(see UN-ECE, 1996). Additional O_3 exposure indices and environmental parameters employed in regressions were calculated over the same three month period used to calculate AOT40s and AOT30s.

Results and Discussion

Populations exhibited contrasting sensitivities to O_3, without the development of typical visible symptoms of injury. A positive relationship was found between relative O_3 resistance and descriptors of the O_3 climate at the site of seed collection. The best predictors of inherent resistance were the calculated AOT40s and AOT30s. Fig. 1 shows the relationship between O_3 resistance and AOT40 at the original sites for the year before seed collection; amalgamating the data from the present study (Lyons et al., 1997) with the findings of a previous invetigation (Reiling & Davison, 1992).

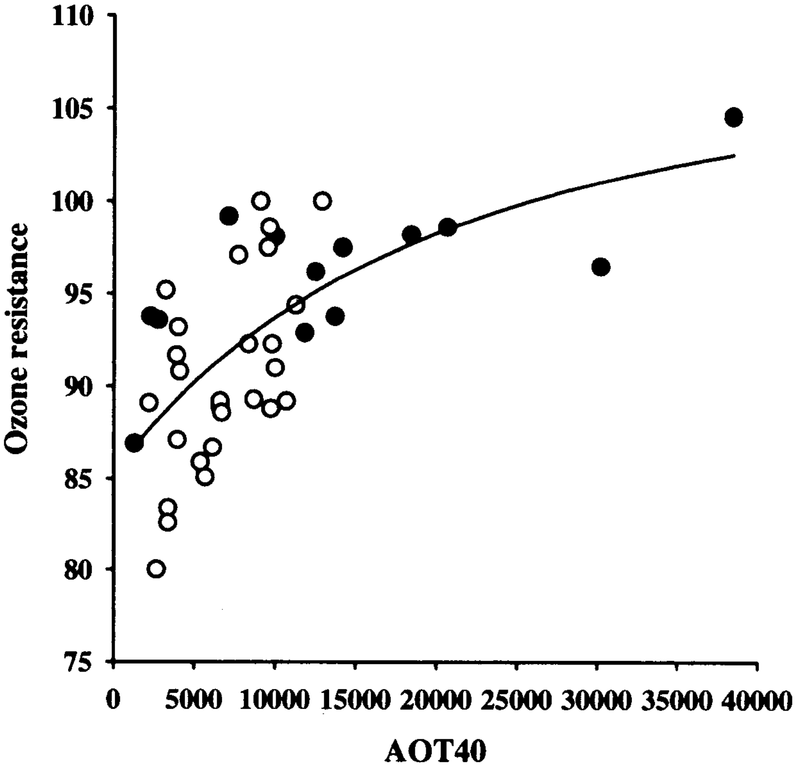

Fig. 1. Relationship between ozone resistance (R_{O3}/R_{CFA} x 100) and AOT40 for populations of *Plantago major*. Filled circles represent data from Lyons et al. (1997), open circles from Reiling and Davison (1992). The equation of the fitted line is y=108.3[23/(1+0.000025x)$^{2.049}$]; r^2=0.426, P=0.0002 (redrawn from Barnes et al., 1999).

Based on the limited site data available, AOT30 was found to provide a better predictor of O_3 resistance than the AOT40 - suggesting that that current UN-ECE guidelines (based on AOT40) may be set too high to protect sensitive components of natural ecosystems (Ashmore and Davison, 1996). No significant relationships were observed between O_3 resistance and intrinsic growth rate or seed weight, nor were there any significant relationships with available data relating to climate and other air pollutants. This finding is consistent with the view that O_3 was the major factor responsible for the difference in the O_3 resistance of the populations investigated. However, the possibility that other factors (e.g. soil quality, nutritional status) may contributeto selection for O_3 resistance cannot be discounted.

Acknowledgements

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Workshop on Biodiversity Research and Information in Asia Oceania

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Joint Forum: Taxonomy Initiatives for Biodiversity Conservation in an IT Era

January 13-14, 2001

Dipterocarpaceae in Gunung Berui, West Kalimantan, Indonesia: Rates of Recruitment, Mortality and Growth

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Abstract

Data on the trees of Dipterocarpaceae have been extracted from a 1-ha permanent plot of mixed dipterocarps forest in Gunung Berui, Serimbu, West-Kalimantan for their growth and mortality analysis. The Dipterocarpaceae trees with the girth at breast height of more than 15 cm within the study plot consisted of 19 species (193 individuals), including: *Anisoptera grossivenia*, *Dipterocarpus* (2 spp.), *Dryobalanops beccarii*, *Hopea dryobalonoides*, *Shorea* (12 spp.), and *Vatica* (2 spp.). The dominant species was *D. beccarii*, sharing 24.6% of total basal area of all species, while the most abundant species in density was *H. dryobalonoides*. The individual life history strategy, mortality and growth rate of those Dipterocarpaceae species during the study periods (1992-1998) were discussed.

Key Words: Dipterocarpaceae, tree dimensions, annual increment, temporal allocation and strategy

Introduction

Recruitment, mortality and growth imply the dynamics of a population, and are important aspects on understanding forest ecology. These aspects in tropical rain forest are not well known and not much studied (Primack *et al.*, 1985). Recruitment and mortality were analyzed based on the numbers of dead and newly recruited trees in a population, while the growth rate was calculated from the diameter increment during a defined census interval. It was well known that tree height is related to ability to intercept light and diameter is related to the supporting and absorbing capacity (Kohyama *et al.*, 1990), whereas crown area is related to the leaf areas for biomass production. Further, the relationship between the parameters of tree form is directly determined by the physiology of tree growth, which is in turn influenced by natural selection (King, 1981). In this respect, growth strategy of individual tree might be approached through the examination of relationships among tree dimensions, such as diameter, height and crown area of individuals.

The present paper intends to discuss the recruitment, mortality, growth rate, and growth strategy of Dipterocarpaceae, the most dominant family in mixed dipterocarp forests (MDF) of West Kalimantan.

Methods

Data on trees of Dipterocarpaceae were extracted from a 1-ha permanent plot (100 m by 100 m) established on lowland mixed dipterocarp forest in Gn. Berui, near Serimbu village (Air Besar district), West Kalimantan-Indonesia. The plot, S_2 of Kohyama *et al.* (1992) was established in November 1992 to monitor population and community dynamics of the forest. The plot was laid on gentle plateau of a hilltop, with extremely humid condition characterized by high annual precipitation of 4,265 mm at Serimbu Village (Yamada and Suzuki 1996, Suzuki *et al.* 1992).

The 1-ha plot was divided into 100 sub-plots of 10 x 10 m^2. All trees with stem girth more than 15 cm at 130 cm above the ground (*gbh*) were individually numbered with aluminum tag, mapped the position in the plot, identified to species, and measured *gbh*, tree height, and two horizontal diameters of crown at right angles including the maximum. Initial census was completed in November 1992, and then the *gbh* was re-measured in August 1994, November 1995 and September 1998 (see also Kohyama *et al.*, 1992; Suzuki *et al.*, 1992). Based on these measurements, total basal areas, number of species, number of individuals and total crown area in each sub-plot were determined.

The crown area was assumed to be an ellipse and the area was calculated based on the crown diameter as projected onto the ground. In this respect, the total areas of tree crowns in a plot can be larger than the total area of the plot, since the tree crowns in the field may be overlapped. The Malthusian parameter (*m*) of population increment was analyzed using the equation(see Sheil *et al.*, 1995):

$$m = (1 - \{1 - (N_0 - N_1)/N_0\}^{\wedge(1/t)}) \qquad (1)$$

where N_0 and N_1 are respectively number of individuals at the beginning t_1 and the end t_2 of the measurement interval $t = t_2 - t_1$ (year). When m is 0, >0 and <0, the number of recruit in comparison to died trees were equal, smaller and bigger, respectively. The growth rate of species was analyzed based on the trunk diameter change in the periods of 1992-1998. Mean relative growth rate (*RGR*) was calculated based on the following equation:

$$RGR = (\ln H_2 - \ln H_1)/(t_2 - t_1); \qquad (2)$$

where H_2 and H_1 are respectively height (*m*) or diameter at breast height (cm) of trees at time t_1 and t_2 (year), see Kohyama and Hotta (1986). The growth strategy was examined through the pattern of relationships among measurable characteristic dimensions of tree individuals of diameter (*D*, in cm), height (*H*, in m) and crown area (*C* in m^2).

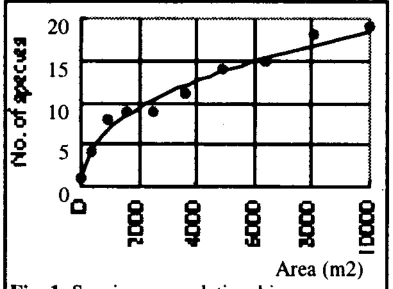


Fig. 1. Species-area relationship

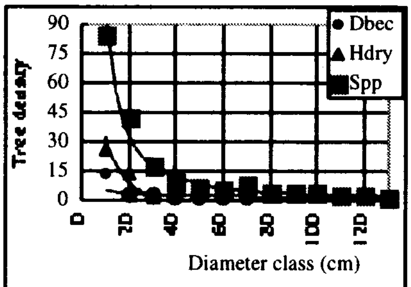


Fig. 2. Diameter class distribution

Results

Species diversity

The plot consisted of 326 species, 1430 trees and total basal areas was 44.7 m^2; among them number of species and individuals of Dipterocarpaceae were 19 and 193, respectively. The plot was considered to be very high in species number, and so far, is the highest in the areas of Kalimantan. Among Dipterocarpaceae were included: *Anisoptera grossivenia*, *Dipterocarpus* (2 spp.), *Dryobalanops beccarii*, *Hopea dryobalanoides*, *Shorea* (12 spp.), and *Vatica* (2 spp.). The dominant species was *D. beccarii*, sharing 24.6% of total basal area of all species (or 47.9% of Dipterocarpaceae). The most frequent species was *H. dryobalanoides*, (43 trees) followed by *D. beccarii* (38 trees). The most infrequent species was *A. grossivenia*

(1 tree), while emergent tree species were mainly *D. beccarii, Shorea dasyphylla, S. parvifolia, S. parvistipulata, S. pinanga, and S. virescens*. The high species diversity of Dipterocarpaceae was also indicated by the relationship between species number and area, where species number still increases up to the total area of study site (Fig. 1).

The trunk diameter class distribution of Dipterocarpaceae trees in the study site performed an inverse *J*-shaped curve. The shape was mainly performed by species with relatively abundant individuals, such as *H. dryobalanoides, D. beccarii, S. multiflora* and *Dipterocarpus* sp. (Fig. 2). The species *H. dryobalanoides* is the most abundant among Dipterocarpaceae in the plot, but the biggest individual was only 21.2 cm in diameter while the species might grow up to more than 100 cm. The inverse *J*-shaped curve implicates that the family was well regenerated and has a stable population in the study site. In this respect, the persistent domination of *D. beccarii* in the plot will be reasonable since the species was the second abundant, showing a wide range of diameter classes distribution and emergent tree species.

Relationships among measured tree dimension parameters

The biggest tree in the study plot was *S. pinanga* (123.3 cm in *D*; 52.4 m in *H*, and 389 m^2 in *C*) and the highest was *D. beccarii* (83.9 cm in *D*; 64.8 m in *H*, and 226 m^2 in *C*). Meanwhile, the tree with widest crown area was another individual of *D. beccarii* (80.6 cm in *D*; 42.5 m in *H*, and 517 m^2 in *C*). Among tree dimension parameters (diameter, height and crown area) of individual Dipterocarpaceae was closely related one to each other (coefficients "*r*" was nearly 1), indicating the similarity in growth performance among them (Figs. 3a-c).

The relationship between diameter and height of 3 most abundant species of the family and of Dipterocarpaceae as a group performed a curve-shaped line. Inversely, relationship between height and crown area of the similar group performed a *J*-shaped curve, while between height and crown area drew a weakly *J*-shaped, nearly linear. The relationships among parameters were expressed by the following equations:

$$H = 14.06 \ln D - 15.58 \qquad r = 0.97 \qquad (3)$$

$$C = 0.0245\, H^{\wedge 2.2104} \qquad r = 0.89 \qquad (4)$$

$$C = 0.392\, D^{\wedge 1.4351} \qquad r = 0.93 \qquad (5)$$

Figs. 3a-c show some changes on the slope of relationships among *D-H-C*, from relatively faster height growth, into faster diameter growth. However, since the relationships among *D-H* and *H-C* dimensions were in smooth curve lines (Fig. 3a-b), the critical points of changes were very difficult to be determined. While Fig. 3c showed a relatively constant and proportional on the increment rate of both *D* and *C*.

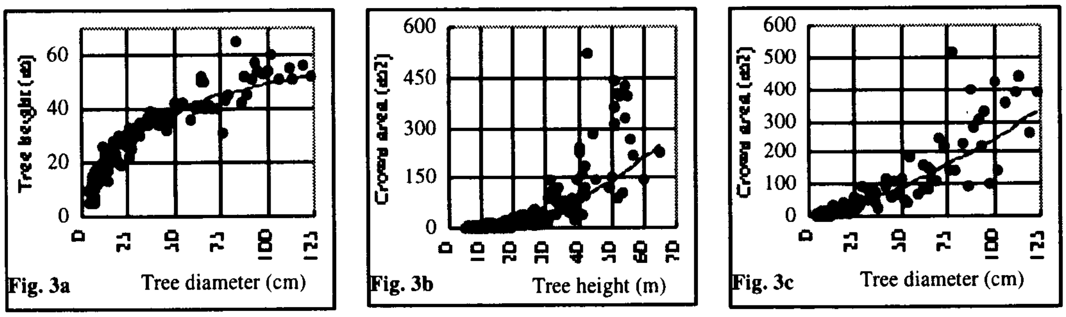
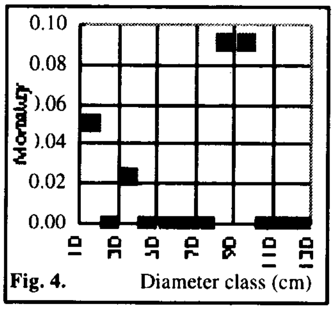


Fig. 3. Relationships among tree dimensions (**a.** diameter and height, **b.** height and crown area, and **c.** diameter and crown area) of Dipterocarpaceae

Population increment

During 1992-1998 study periods, it was found that *m* values of 11 species were 0; 1 species was <0 (found on *S. quadrinervis, m* = – 0.043) and 7 species were >0. The highest population decline was occurred on *S. parvistipulata* (*m* = 0.047). As a whole, the number of died trees was larger than recruited (193 trees in 1992 and 182 trees in 1998). Some big trees were found dead in 1998: 2 individuals *D. beccarii* (58.6 and 85.8 cm in *D*); an individual *S. quadrinervis* (75.5 cm), and an individual *S. dasyphylla* (25.5 cm) were found dead in the 1998 census, created some gaps in the study plot.

A statistical analysis showed insignificant relationship between the diameter classes of trees and population increment rate *m* (Fig. 4). The result was not parallel with the inverse *J*-shaped curve of trunk diameter class distribution that indicates the high rate mortality in lower diameter classes. The recruitment and mortality rates of individual tree in each sub-plot during 1992-1998 period were also not related to the parameters representing stand structure such as basal areas, species number, tree density and crown area. The figure may be resulted from the insufficient amount of data, where the number of dead individuals, especially on species with small sample size need to be further analyzed.



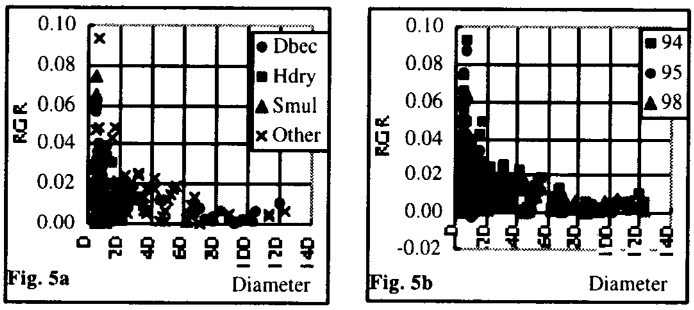


Fig. 4. Mortality rate of class diameter.

Fig. 5. *RGR* of Dipterocarpaceae trees (**a.** by species, **b.** by year).

Growth rate

The relationship between diameter and *RGR* shows a tendency of decreasing *RGR* in hyperbolic manner with diameter (Fig. 5a-b). Based on the 1992-1998 girth measurement, tree diameter (*D*) was not related to the annual diameter increment (*ΔD*), but positively related to the tree volume increment (Fig. 6a-b). The variation of annual increment among individuals even in the same species of the same year were relatively high (Table 1). The high variability was also indicated by high values of standard deviation that were almost similar to the mean of annual increment rate in these study periods. The biggest mean annual increment of diameter was found on *Shorea parvifolia,* while the smallest was on *Dipterocarpus* sp., and the pattern was performed in the whole 3 successive times of studies.

Table 1. Mean annual diameter increment (*ΔD*) of Dipterocarpaceae species between 1992-1998

Species	Year	***ΔD* in mm**			**Species**	Year	***ΔD* in mm**		
		94	**95**	**98**			**94**	**95**	**98**
Dryobalanops beccarii	mean	2.60	1.90	2.80	*Dipterocarpus* sp.	mean	0.58	0.35	0.41
	s. d.	2.45	1.76	2.37	(K4490)	s. d.	0.56	0.40	0.61
Hopea dryobalanoides	mean	1.48	1.09	1.00	*Shorea parvifolia*	mean	5.32	3.87	3.99
	s. d.	1.17	1.00	1.14		s. d.	2.40	1.87	0.19
Shorea multiflora	mean	1.27	1.32	1.20	Other *Shorea* spp.	mean	3.38	2.48	5.66
	s. d.	1.24	1.20	0.98		s. d.	3.09	2.24	2.41
Dipterocarpus crinitus	mean	1.52	1.06	1.45	Other s (*A. grossivenia,*	mean	2.80	1.77	1.71
	s. d.	1.50	0.86	1.43	*Vatica* spp.)	s. d.	1.45	1.13	1.05

Discussion

Species diversity

Mixed dipterocarp forests in the lowland areas of Kalimantan have been considered to be one of the highest in its tree species diversity. Our study confirmed this were 326 species of trees were found in a 1-ha plot. Number of Dipterocarpaceae species in the plot is also relatively high (19 species in 1-ha). Among 163 species of *Shorea* found in Malesia, 62 species are distributed widely in Borneo and 12 species of them were found in the study site. Only 2 out of 35 Borneo species of *Vatica* and 1 out 5 Borneo species of *Dryobalanops* were found in the study site. There are about 70 species of *Dipterocarpus* and 11 species *Anisoptera* but only 2 and 1 species were respectively found in the study site. Some other genera distributed in Borneo were not found in the study site, however, these absent genera were usually minor in the lowland mixed dipterocarp forest in Borneo.

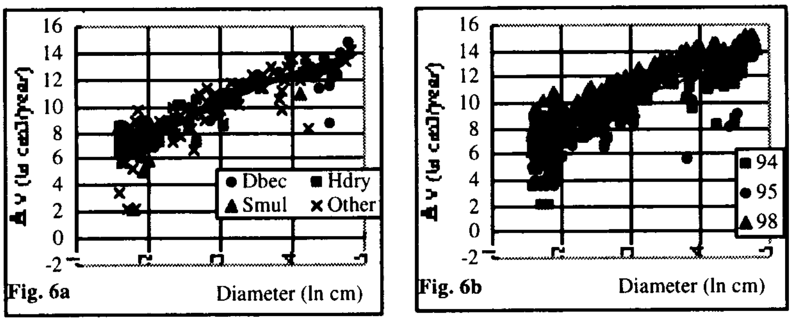


Fig. 6. Tree volume increment per year of Dipterocarpaceae trees (**a.** by species, **b.** by year).

Growth strategy and rate

The significant and the consistent pattern of the relationships among parameters of diameter, height and crown area might explain the common growth pattern during the individual life history of Dipterocarpaceae species. The three different rates of growth performed in *D-H-C* relationships (Figs. 3a-c) also reflect the growth stages of dipterocarp trees. As has been explained, each stage of growth was characterized by the exclusively higher rate of increment in diameter, height or crown area (reflected by the slope changes of the curve among them). These growth stages also implicate the main allocation of assimilated resources during the life history of individual plant.

In the early stage of growth after seedling establishment, individuals of Dipterocarpaceae increased their height very fast while the diameter and canopy cover increment rates were low, thus the period can be called *height growth stage*. The height growth stage is continued until a tree grows up to the height of the lower layer of forest canopy stratum. This pattern was considered to be a strategy of tree to "put on" its main photosynthesis apparatus in the position for effective to forage enough sunlight at the forest canopy stratum, in order to increase the rate of organic matter production in the next stage, namely *building stage*.

When a tree reaches up the lower layer of forest canopy stratum the *height growth stage* is switched into height-diameter-crown area growth, and may be called *building stage*. In the building stage, the height growth is slowing down while diameter growth and crown area developments are increased up. The tree concentrates their growth to produce leaves for photosynthetic activities and by the similar rate on the trunk diameter increment for supporting the canopy biomass and nutrient absorbing capacity (Kohyama *et al.*, 1990).

Increasing up the crown area is a strategy for tree to increase its leaf areas for inducing photosynthetic activity.

Most species in the forest community reach their maximum height during the building stage in canopy stratum. However, some species such as *D. beccarii, Shorea dasyphylla, S. parvifolia, S. parvistipulata, S. pinanga,* and *S. virescens* still continue to grow over the height of upper canopy stratum to become emergent trees. These species may grow up to about 50-70 m height and to about 120 cm in diameter, and the period may be called the *emergent tree establishment stage.*

The results suggested that the Dipterocarpaceae species have a temporal main allocation of assimilated resources to the growth of specific organs during the life history of an individual tree. In the early stage, assimilated resources are mainly allocated to height growth, and when the tree height reaches the forest canopy stratum, the main allocation of assimilated resources is changed to induce the growth of diameter and then crown area. The temporal main allocation of assimilated resources is considered to be a strategy of the species for adapting to respective environmental condition during the life history. Seedlings of Dipterocarpaceae are relatively shade tolerant; while the young plant in the early growth stage would suffer due to dense and closed canopy of forest community. To adjust the stress, the plant allocates assimilated resources to induce mainly height growth.

This pattern is parallel with common known character of Dipterocarpaceae species and other emergent tree species that are shade tolerant in the early stage and switches into light demanding in the late stage of growth. Beside the temporal shift of the allocation of assimilated resources, it is clear that the production of organic matter is increased as tree diameter increases as indicated by the relationship between diameter and annual tree volume increment (Fig. 6). However, it is difficult to determine the critical points of growth changes, since the relationships among dimensions *D*, *H* and *C* changed smoothly with size (Figs. 3).

The relative growth rate of Dipterocarpaceae species tended to decline hyperbolically with increase of *dbh*. The pattern have been reported for other species (Kohyama and Hotta, 1986, Yoneda *et al.*, 1994). Mean annual increment of either height or diameter shows a great variability and standard deviations of most categories are large, even larger than mean increment. These data suggest that even in the same diameter class, some trees have low growth rate and some others high growth rates. The high variability reveals that the growth of individual tree may be related to the great variability of individual environment. The mean *D* increment of some Dipterocarpaceae are comparable to the growth rate of Moraceae tree species in Sarawak (Primack *et al.*, 1985), but *S. parvifolia* and other *Shorea* spp. were higher than growth of *Artocarpus* spp. (2.1-2.7 mm/year) from East Kalimantan (Dilmy, 1980).

The recruitment and mortality rates of individual tree during 1992-1998 period were not clearly related to the parameters representing stand structure, such as basal areas, species number, tree density or crown area. It may be due to insufficient number of observed individuals and relatively short period of study for perennial tree species. But it was clear that number of died individuals were larger than of recruited individuals. Analysis on the died trees during 1992-1998 periods did not clearly show the size-specific relationship. However, the inverse *J*-shaped curve of diameter distribution of Dipterocarpaceae may suggest the high mortality rate of trees in the lower classes. As for the mortality of some large trees during the study period, it might be related to the maximum size, height or age of tree species.

Acknowledgements

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Microbial Information Network of China

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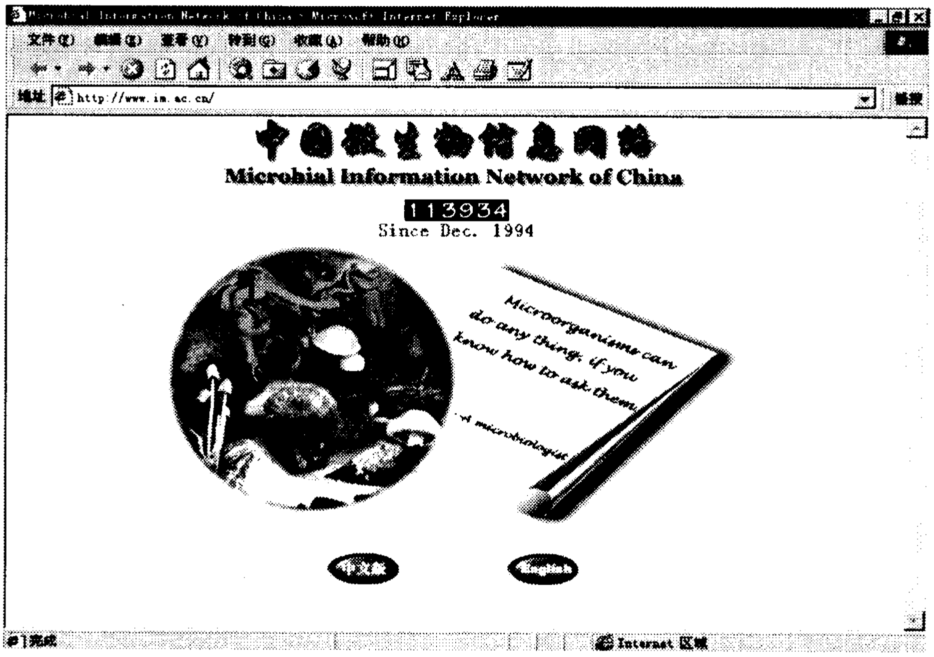
Introduction

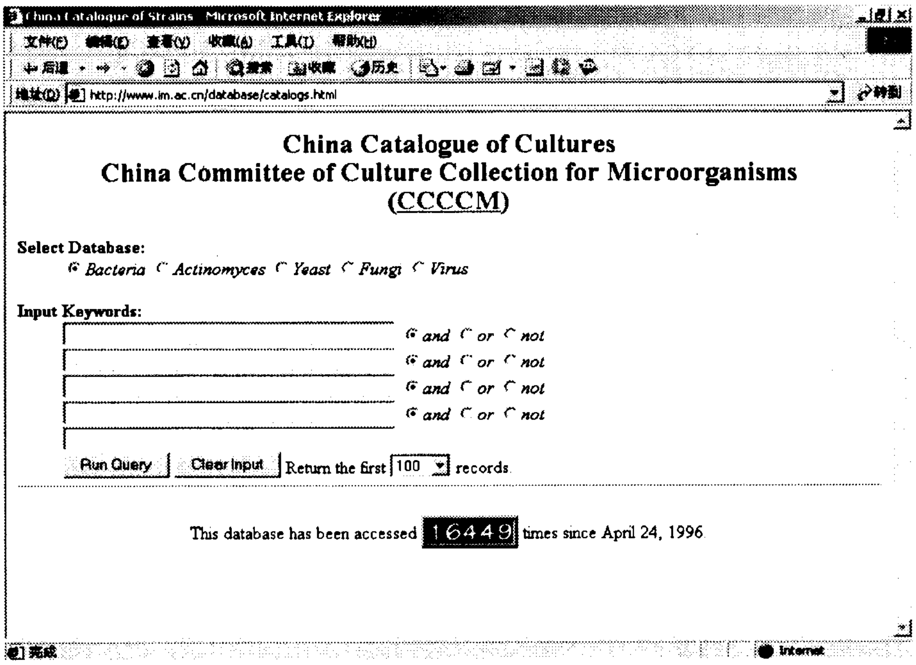
Microbial Information Network of China (MICRO-NET) was founded in 1994. Its purposes are to collect and share the Chinese microbial information resources to abroad, and introduce the popular foreign information resources to Chinese scientists. Now MICRO-NET and its information resources are supported Scientific Database Project, State Key Laboratory of Microbial Resources, Biodiversity Project, National Natural Science Foundation of China (NFSC), and Ministry of Science and Technology. The URL of MICRO-NET is http://www.im.ac.cn.



Information Resources

1. Database of China Catalogue of Cultures

The data in this database is from China Committee of Culture Collections of Microorganisms (CCCCM). In CCCCM, there are 12 national culture collections divided into general microbiological, agricultural, industrial, medical, antibiotic, veterinary and forestry center. China Catalogue of Cultures (English version) includes 10,716 strains of bacteria, actinomyces, yeast, fungi and virus.



China Catalogue of Cultures
China Committee of Culture Collection for Microorganisms
(CCCCM)

Select Database:
● *Bacteria* ○ *Actinomyces* ○ *Yeast* ○ *Fungi* ○ *Virus*

Input Keywords:
● *and* ○ *or* ○ *not*
● *and* ○ *or* ○ *not*
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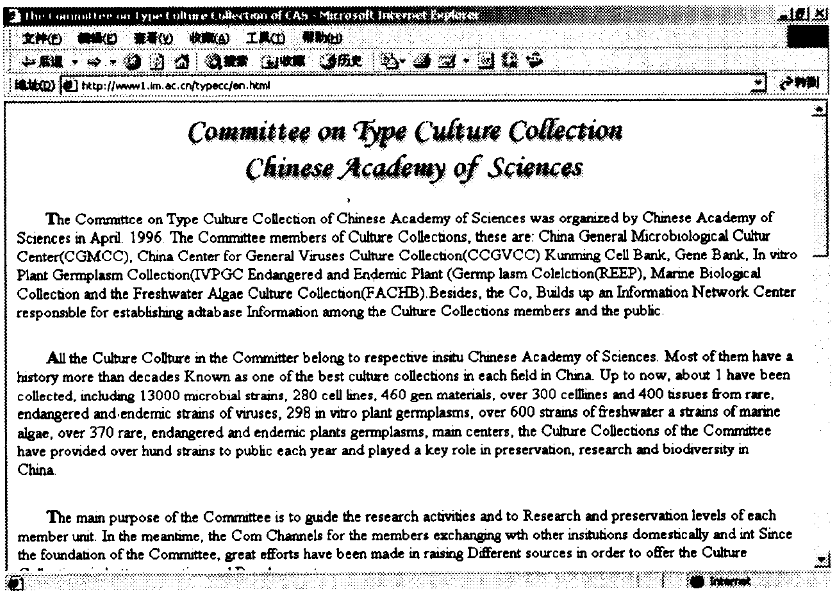
Run Query | Clear Input | Return the first 100 records.

This database has been accessed 16449 times since April 24, 1996

2. Database of Type Cultures of Chinese Academy of Sciences

The Committee on Type Culture Collection of CAS (CTCCCAS) was organized in April, 1996. There are seven Culture banks under CTCCCAS, namely, Microbial Culture Bank, Cell Bank, Gene Bank, Virus Bank, Kunming Cell Bank and Freshwater Algae Bank,the Rare, Endangered and Endemic Plant Germplasm Bank, Marine Biological Germplasm Storehouse and In Vitro Plant Germplsm Collection. Up to the present, 15,418 cultures have been collected.



Committee on Type Culture Collection
Chinese Academy of Sciences

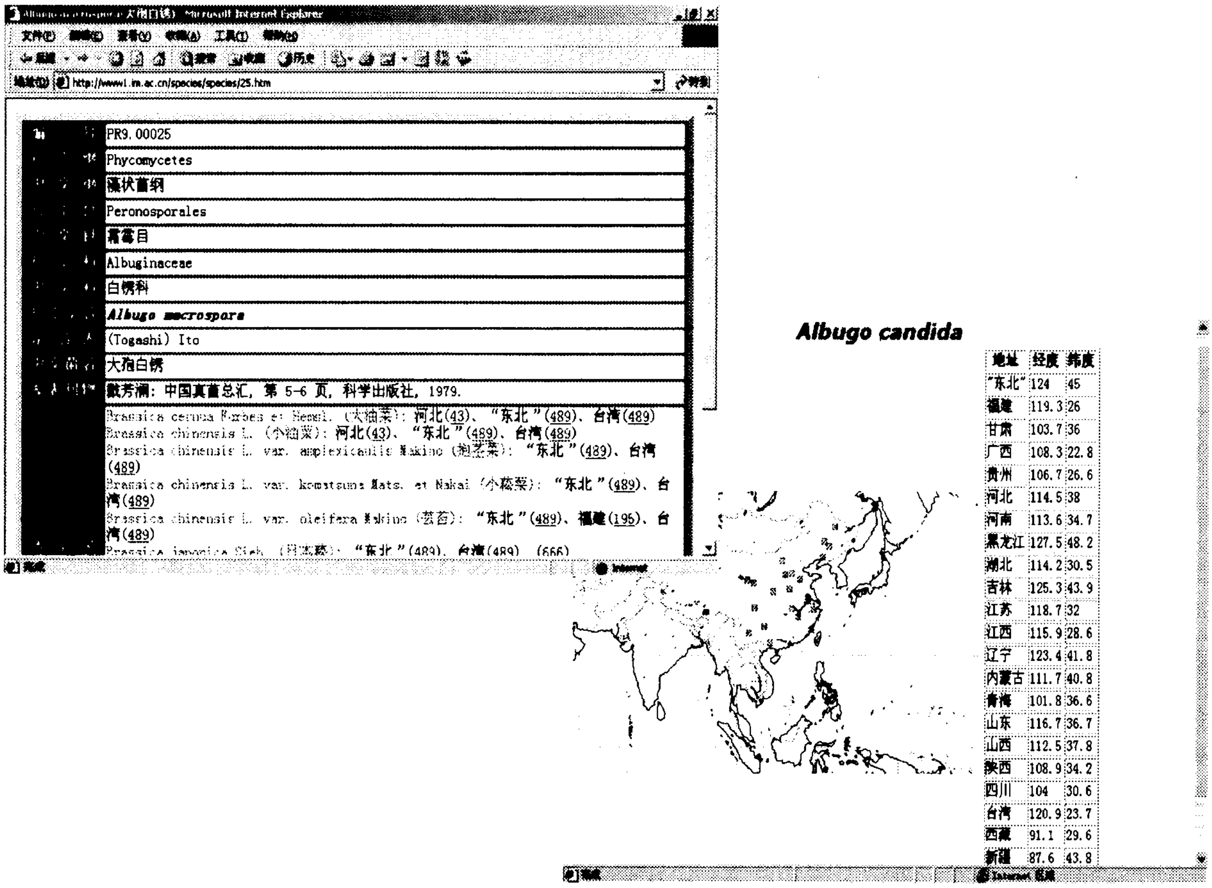
The Committtce on Type Culture Collection of Chinese Academy of Sciences was organized by Chinese Academy of Sciences in April. 1996. The Committee members of Culture Collections, these are: China General Microbiological Cultur Center(CGMCC), China Center for General Viruses Culture Collection(CCGVCC) Kunming Cell Bank, Gene Bank, In vitro Plant Germplasm Collection(IVPGC Endangered and Endemic Plant (Germp lasm Colelction(REEP), Marine Biological Collection and the Freshwater Algae Culture Collection(FACHB).Besides, the Co, Builds up an Information Network Center responsible for establishing adtabase Information among the Culture Collections members and the public.

All the Culture Collture in the Committer belong to respective insitu Chinese Academy of Sciences. Most of them have a history more than decades Known as one of the best culture collections in each field in China. Up to now, about 1 have been collected, including 13000 microbial strains, 280 cell lines, 460 gen materials, over 300 celllines and 400 tissues from rare, endangered and endemic strains of viruses, 298 in vitro plant germplasms, over 600 strains of freshwater a strains of marine algae, over 370 rare, endangered and endemic plants germplasms, main centers, the Culture Collections of the Committee have provided over hund strains to public each year and played a key role in preservation, research and biodiversity in China.

The main purpose of the Committee is to guide the research activities and to Research and preservation levels of each member unit. In the meantime, the Com Channels for the members exchanging wth other insitutions domestically and int Since the foundation of the Committee, great efforts have been made in raising Different sources in order to offer the Culture

3. Database of Inventory of Fungi Species

In this database, there are the information on more than 6,500 fungi, including Latin name, Chinese name, host, isolated place and references. A distribution map of each species can be made automatically.



http://www1.im.ac.cn/species/species/25.htm

PR9.00025
Phycomycetes
藻状菌纲
Peronosporales
霜霉目
Albuginaceae
白锈科
Albugo macrospora
(Togashi) Ito
大孢白锈
戴芳澜：中国真菌总汇，第 5-6 页，科学出版社，1979.
Brassica cernua Forbes et Hemsl. (大油菜)：河北(43)、"东北"(489)、台湾(489)
Brassica chinensis L. (小油菜)：河北(43)、"东北"(489)、台湾(489)
Brassica chinensis L. var. amplexicaulis Makino (抱茎菜)："东北"(489)、台湾(489)
Brassica chinensis L. var. komatsuna Mats. et Nakai (小松菜)："东北"(489)、台湾(489)
Brassica chinensis L. var. oleifera Makino (芸苔)："东北"(489)、福建(195)、台湾(489)
Brassica japonica Sieb. (日本芜)："东北"(489)、台湾(489) (666)

Albugo candida

地址	经度	纬度
"东北"	124	45
福建	119.3	26
甘肃	103.7	36
广西	108.3	22.8
贵州	106.7	26.6
河北	114.5	38
河南	113.6	34.7
黑龙江	127.5	48.2
湖北	114.2	30.5
吉林	125.3	43.9
江苏	118.7	32
江西	115.9	28.6
辽宁	123.4	41.8
内蒙古	111.7	40.8
青海	101.8	36.6
山东	116.7	36.7
山西	112.5	37.8
陕西	108.9	34.2
四川	104	30.6
台湾	120.9	23.7
西藏	91.1	29.6
新疆	87.6	43.8

4. Database of Economic Fungi

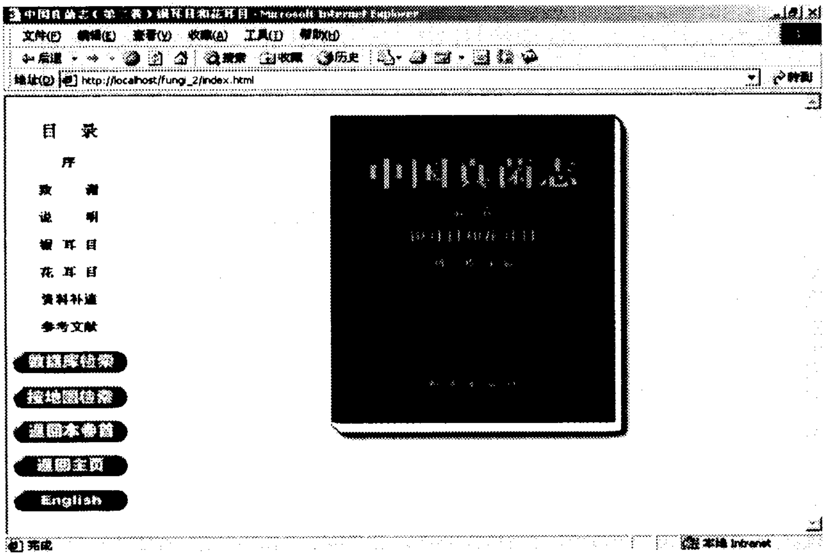
We have collected 1,000 fungi with the information on Latin name, Chinese name, taxonomy position, description of behavior and shape, usage and contents of tranditional Chinese medicine. All the records have a black/white picture, and some records have color pictures.

http://www.im.ac.cn/ecofungi/fungimenu.html

蘑菇 Agaricus campestris	木耳 Auricularia auricula	梭柄松苞菇 Catathelasma ventricosum	冬虫夏草 Cordyceps sinensis	灵芝 Ganoderma lucidum	白蜡伞 Hygrophorus eburneus
金盖鳞伞 Phaeolepiota aurea Pholiota aurea	尖鳞环锈伞 Pholiota spuarrosoides	红毛盘菌 Scutellinia scutellata	松乳菇 Lactarius deliciosus	焰耳 Phlogiotis helvelloides	金耳 Tremella aurantialba

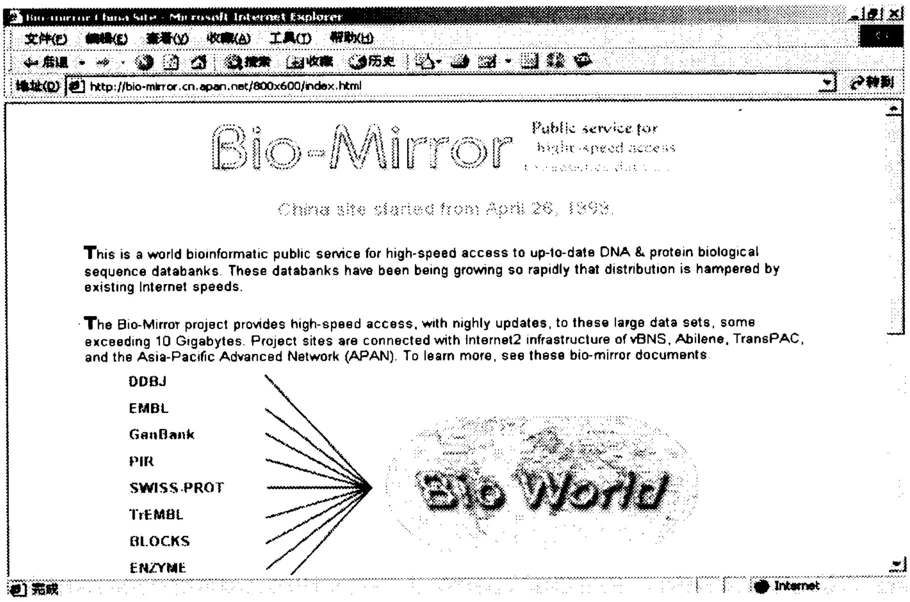
5. Full Text Database of Flora Fungorum Sinicorum (FFS)

The project named Electronic Version of Flora Fungorum Sinicorum is supported by NSFC (National Natural Science Foundation of China). In the coming five years, about one hundred books of FFS will be published. Up to now, full text of four booked has been inputted into database.



6. Bio-mirror China Node

As China Node of Bio-mirror Project, now we are mirroring DDBJ/EMBL/GENBANK and some other biological databases. DDBJ/EMBL/GENBANK in our web site is daily updated. The data in ftp site of Bio-mirror China node is updated termly.



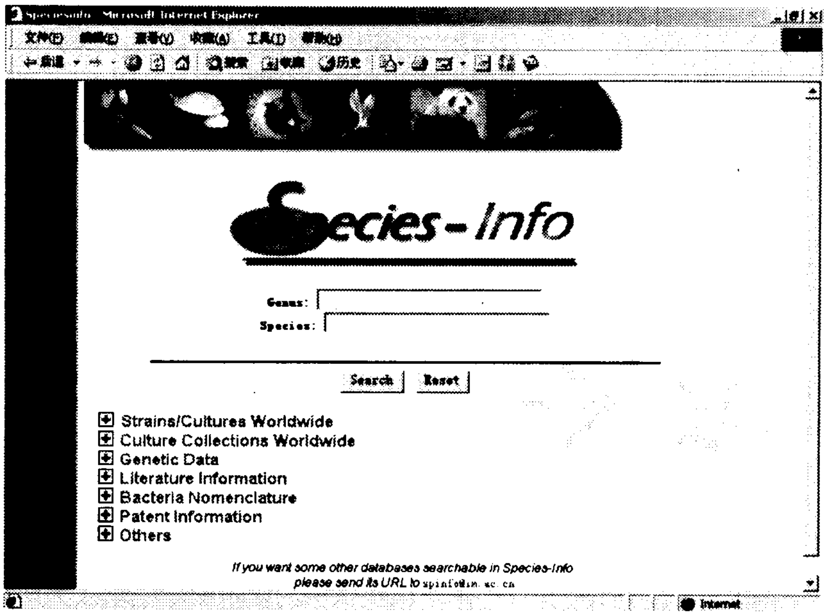
China site started from April 26, 1999.

This is a world bioinformatic public service for high-speed access to up-to-date DNA & protein biological sequence databanks. These databanks have been being growing so rapidly that distribution is hampered by existing Internet speeds.

The Bio-Mirror project provides high-speed access, with nighly updates, to these large data sets, some exceeding 10 Gigabytes. Project sites are connected with Internet2 infrastructure of vBNS, Abilene, TransPAC, and the Asia-Pacific Advanced Network (APAN). To learn more, see these bio-mirror documents

7. Species-Info

SPECIES-INFO is a powerful search engine to help biologists find species information in Internet more easily and more efficiently. User just input a species name, then ***SPECIES-INFO*** can seek the information on this species automatically, and bring back all the search results together in one html page. All the information that ***SPECIES-INFO*** can search at this moment is divided into 7 groups. They are *Strain/Cultures Worldwide, Culture Collections Worldwide, Genetic Data, Literature Information, Bacteria Nomenclature, Patent Information* and *Others.*



If you want some other databases searchable in Species-Info please send its URL to spinfo@im.ac.cn

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Biological Diversity Research and Information in Malaysia

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Abstract

Malaysia ratified the Convention on Biological Diversity (CBD) in 1994 and has since doubled its efforts to fulfill its obligations. A National Biological Diversity policy was developed and adopted in 1998 which underlines fifteen strategies for effective management of biological diversity in the country. In addition, a country report evaluating the status of biological diversity and gaps in knowledge were completed.

Efforts into improving the scientific knowledge base on biological resources; conservation and sustainable utilisation of resources have been strengthen. Along these lines, research programmes to address the criteria and indicators for sustainable forest management; reduced impact on forest harvesting systems; conservation and management of forest biodiverdity and environmental aspects of forestry have also been prioritised.

The acquired information has been systematically compiled by the relevant agencies undertaking the research activities. In addition, the power of information technology (IT) , has been harnessed to help transform basic information into ordered knowledge and hence providing an improved platform for decision making. Various databases addressing different groups of plants have been developed both on international and national collaborative programmes. This paper highlights the various databases available in the country.

***Key Words:* biological diversity, research, information, Malaysia**

Introduction

Malaysia ratified the Convention of Biological Diversity in 1994 and is working towards incorporating it into its national policies and planning a set of commitments under the treaty. A national policy on biological diversity addressing the policy, 15 strategies for effective management of biological diversity in the country and action plans. In addition a report, Assessment of biological diversity in Malaysia highlights the available information and knowledge on biological diversity and identifies gaps and needs for effective conservation and rational use of these resources; the necessary supportive measures to meet these needs ad the benefits associated with the implementation of these measures. The policy and Assessment of biological diversity in Malaysia are available through FRIM's homepage; http://www.frim.gov.my, under the icon CHM.

The natural ecosystems of Malaysia harbour a very rich and diverse flora, fauna and habitats. There are over 15,000 known species of flowering plants, 286 species of mammals, over 150,000 species of invertebrates, over 1,000 species of butterflies, and over 4,000 species of marine fishes in Malaysia's varied ecosystems (WCMC, 1994). Hence, to be able to manage our biological resources sustainably, accurate baseline information would be crucial to provide management decisions for best forestry practices and conservation.

One of the major threats to the survival of species and habitats is the lost of the forest areas over the years. The hunger for land also saw most of the lowland forest areas converted to agriculture, particularly to rubber and later to oil palm plantations. In 1960, Peninsular Malaysia was still over 70% forested but with land conversion, by 1997, only 44.5% of the land area in Peninsular Malaysia remained under natural forest cover, as most of the land more suitable for agriculture has been taken up leaving only the hills and the mountains.

Priority Research Programmes on Biological Diversity

1. Sustainable Management of Natural Forests

There are several definitions of sustainable forest management by the forestry experts. Some emphasize continous yield of timber (Schmidt, 1987; Poore *et al.* 1989, Hartshorn, 1990) while others stress on the maintenance of biological diversity and ecological functions (Wyatt-Smith, 1987; Perl *et al.* 1991). Generally the extent of damage on water quality, soil physical properties, forest regeneration and wildlife is closely related to logging practices. Thus, forest management must follow strict specifications and regulations to sustain key ecological functions. Sustainable forest management, which should largely mimic natural regeneration processe (Whitmore 1990) would be compatible with the maintenance of biological diversity.

Priority Areas:

- Criteria and indicators for sustainable forest management
- Reduced impact forest harvesting systems
- Growth and yield assessments
- Pre- and post-harvest silvicultural treatments Rehabilitation of logged forests
- Quantification of forest and non-timber resources Remote sensing and GIS
- Silviculture and management of rattan, bamboo and other commercial plants

2. Conservation and Management of Forest Biodiversity

Forestry practices and other uses on the forest resources are also impacting the ability of the natural system to recover as a result of man's intensive use. The ability of the native species of plants and animals to withstand such intrusion of man is often not well understood. In a recent exercise to list threatened tree species of Malaysia using the new IUCN threat categories and criteria, Malaysia has 737 species listed in some threat categories. This programme will make assessment and study in the development of conservation strategies in dealing with threats to species and natural habitats in both managed areas and protected areas.

Priority Areas:

- Documentation of flora, fauna and habitat diversity
- Ecology and conservation of forest biodiversity
- Genetic diversity of flora and fauna
- Protection and management of forest conservation areas

3. Policy and Socio-Economic Aspects of Forestry

With the implementation of sustainable forest management practices, harvesting costs would increase and timber output would shrink. This would affect the whole wood-based industries, and rationalization of both economics and policies would be needed to sustain the industry.

The value of natural forests would shift away from timber as the principal crop to other environmental services. Provision of water, ecological services, biodiversity prospecting, minor forest produce, ecotourism, etc. would appreciate in value. Management would accordingly shift away from that of pure timber harvesting.

New issues that researchers have to contend with include impact of forest management on local climatic patterns, impacts of changing global climate on forests, the ameliorating role of forests as carbon sinks, protection of coastal zones and coastal forests facing potential sea level rise and other threats of land development.

Priority Areas:

- Eco-labelling and certification Impacts of SFM on the wood-based industries
- Sustainability of timber resources for the wooden furniture industry
- Economic valuation of environmental services of the forest
- International issues relating to the forestry sector.

Information Available Related to Biological Diversity

The changing scene in biological sciences, including rapid developments in biotechnology and information technology (IT) presents new challenges in decision making. In the biological sciences, we can expect a continuing flow of new devices that improves our capabilities in decision making in three areas: gathering information, managing and transforming information and dissemination of results.

Examples of Information Available Electronically

a. Pasoh 50 ha. Plot – documents ecological information on all plants occurring within a the 50ha plot in a lowland forest in Pasoh
b. PROSEA – consists of information related to plant resources of South East Asia
c. BRAHAMS – systematic documentation of herbarium specimen

Examples of Information Available via the INTERNET

a. INFOPLANT – database on plants suitable for urban planting
b. MEDICPLANT – medicinal properties and their uses
c. Malayan Vascular Plants – plants found in Peninsular Malaysia, their distribution and synonyms

Conclusion

Despite the rapid phase of development in the country, the government has emphasized on the need for sustainable development. Efforts have been geared towards conservation and wise utilisation of natural resources. The current gaps in knowledge on biological diversity are addressed by top down priority research programmes to be conducted in the next five years. In addition, the power of IT is harnessed to help transform basic information into ordered knowledge and hence providing a platform for improved decision making. CD-ROM, the INTERNET provided new opportunities for efficient dissemination of information.

Acknowledgement

The author would like to thank the organisers for the support and opportunity to present this paper.

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Status of Australian Fish Taxonomy and Fish Collections, Databases and Networks

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Abstract

Australia's marine habitat exclusive of territorial islands (Norfolk, Macquarie, etc.) extends from 10° to 47° S and exceeds nine million km^2. The first significant work describing fish species from Australia was in 1790, with 11 species described. The current estimate of described Australian fish species (excluding those of territorial islands) is 4100+, with a further 200+ species recognised but undescribed, up from 2450 in 1964. Increases in Australian fish collections have preceded the increases in fish species. The Australian Museum fish collection has increased from 70,000 non-larval specimens in 1968 to 457,000 in 1993 to 583,000 in 2001. There are 11 major fish collections in Australia, the most important being those of the seven state museums and CSIRO Marine Laboratories. The total number of registered specimens in Australian fish collections is currently some 1.6 million non-larval fishes. All of the Australian fish collections have started a database and nine have 100% of their identified specimens computerised. In 1985 a workshop was held to standardise data entry for Australian fish collections, with agreement on format of fields such as locality, date, time, etc. Collection management workshops are now held with the annual conference of the Australian Society for Fish Biology. The 1996 workshop agreed to start a proposed Australian Fish Databases Network. Problems with database security, lack of funds and administrative enthusiasm were insurmountable. The 1997 Workshop agreed that new fields to indicate quality of identifications and locality data should be added to each database, but dealing with the backlogs is slow. A national fish database network is now tied to a proposed network linking all museum databases in Australia. Some Australian fish databases will be associated with the international fish networks FISHNET and FISHBASE. Databases and networks with mapping facilities are especially valuable for conservation studies to show both areas requiring sampling and species with restricted distributions.

Key Words: Australian fishes, Fish collections, Collection databases, Database networks, Mapping facilities, Conservation

Introduction

The aim of this paper is to show how taxonomy, collections, databases and networks can be utilised in conservation, using the experience with Australian fishes as an example. Conservation, that is conserving biodiversity, means saving species from extinction.

Australia's marine habitat exclusive of territorial islands extends from 10° to 47° S. The Exclusive Economic Zone (EEZ) is more than nine million km^2, greater than the continental area, with some 36,000km of coastline. While the EEZ is the 3rd largest in the world, fisheries production ranks only 55th, due in large part to relatively narrow continental shelves and low nutrients because of low rainfall and runoff. More than 50% of our EEZ has depths exceeding 2000m, some with more than 4000m bottoms that are clearly unavailable for commercial fishing (Kailola *et al.*, 1994).

Australian Fish Biodiversity

While Australia's fishery production is low, fish biodiversity is high, due in part to the wide latitudinal range and variety of habitats. In 1790, White described 11 new species of fishes from the Sydney region, the first description of more than one new species from Australia. From this inauspicious beginning, the known Australian fish fauna has grown to an estimated 4300+ species today (Hoese *et al.*, unpublished)(Fig. 1). This total includes more than 200 species recognised as distinct but not yet formally described, and excludes species found only around territorial islands such as Lord Howe, Christmas, and Macquarie Islands.

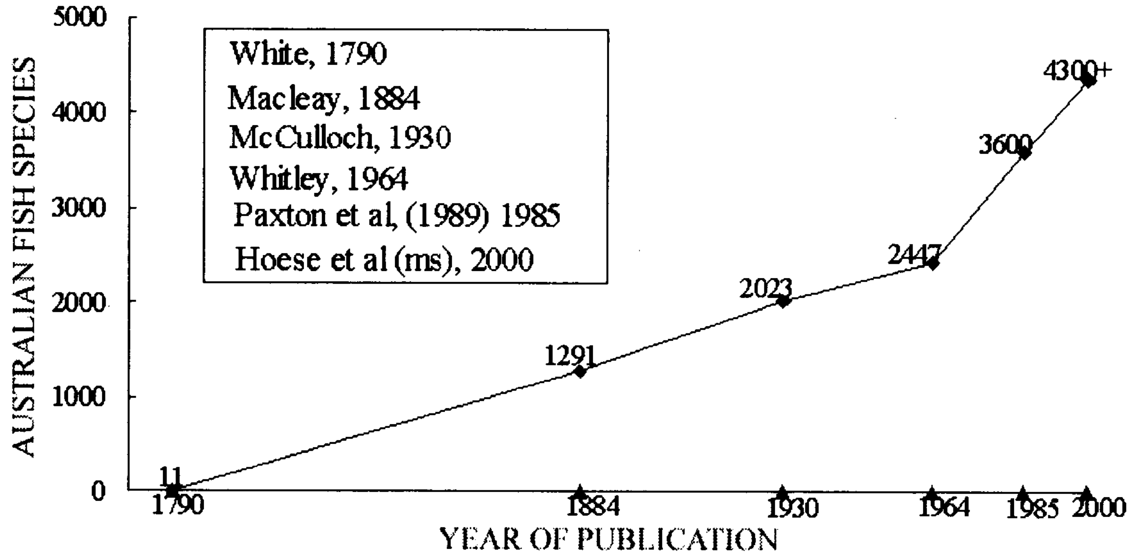

Fig. 1. Total fish species recorded from Australian waters excluding territorial islands (Lord Howe, etc.)

In the last 35 years the species total increased by more than 1800 species, or some 75%. The major increases have come from exploratory commercial fishing and research vessels in deepsea waters below 200 m, and scuba collections with the ichthyocide rotenone, that has only been used in Australia in the last 35 years.

Australian fish biodiversity is very similar to that of Japan, with waters extending over many degrees latitude from cold temperate to the tropics. The total fish faunas exceed 4000 species dominated by marine fishes, with only about 200 freshwater species. Only the Southeast Asian countries of Indonesia and the Philippines have more fish species.

Rather than detail the development of Australian fish taxonomy as evidenced by the known fish biodiversity, it can be summarised as follows: 1) Current valid 'continental' Australian fish species = 4300+; 2) Freshwater species insignificant portion of fauna, some 200 species; 3) Marine shore fish species perhaps 90% known, but individual distribution limits poorly known, especially in tropics); 4) Predicted 'continental' Australian fish species >5000; 5) Increases to come from deep sea (> 200m): a) slope WA; b) slope tropics > 400m; c) all slope > 1200m; d) midwater tropics; e) all midwaters > 1000m.

It is relevant to briefly examine the current number of fish taxonomists in Australia. In 1970 there were five full time fish Australian fish taxonomists (although a number of others worked part time in taxonomy). By 1987 there were 14 full time taxonomists, but the number had fallen to six by 1997 with retirements and movements to administration. No retiring fish taxonomist has been replaced by another in Australia in more than 10 years, during which time five have retired and two have moved into administration. As a result, the following conclusions can be made: 6) Australian fish taxonomists are an endangered species; 7) Completion of Australian fish biodiversity survey and continued production of identification handbooks, etc. require: a) Reversal of trend of decreasing museum taxonomists; b) Recognition of taxonomy as legitimate science by more universities: i) Increase in number of taxonomists on university staffs; ii) Increase in number of graduate students in taxonomy; c) Support for taxonomy by state fisheries departments; d) Reversal of trend to decrease number of deepsea research vessels.

Australian Fish Collections

The increase in the number of known Australian species has been preceded by increases in the fish collections, necessary prerequisites before the faunal increases could be documented. The Australian Museum Fish Collection, largest in the country, has increased by more than 100,000 specimens, or more than 20%, in the eight years since the last summary survey was done (Fig. 2).

A 1992/3 survey of the 12 major fish collections in Australia, including the seven in state museums, indicated a total of about 1.1 million fish specimens of adults and juveniles, excluding larvae (Paxton and McGrouther, 1997:Table 1). The unidentified backlog totalled almost 100,000 specimens over all the collections. One of the problems of a significant unidentified backlog is that when a specialist visits the collections, those specimens are unavailable. For many years the Australian Museum carried from 20,000 to 40,000 unidentified fish specimens. The problem was solved by identifying only to genus, or even family, those difficult specimens so they would be on the shelves and in the database, available for visiting taxonomists and loans. Often visitors examine specimens identified only to family first in the hopes of finding rarities. This method of clearing the unidentified backlog results in a hidden database backlog that will be referred to below.

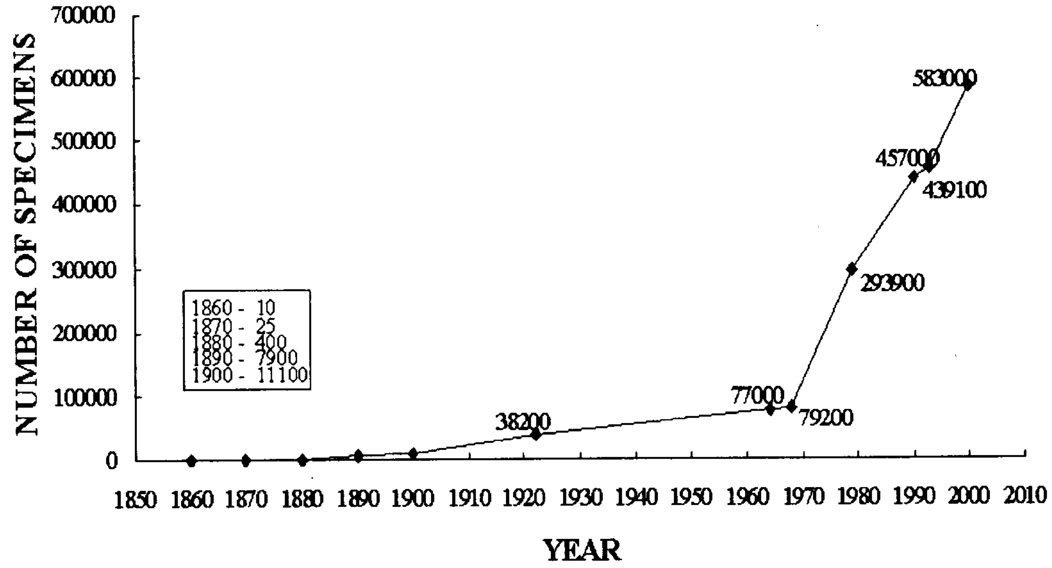

Fig. 2. Numbers of adult and juvenile fish specimens in the Australian Museum Fish Collection

Most of the major Australian fish collections have had significant increases in their collections since the last survey eight years ago (Table 1). The figures are approximate in many instances, because for some only lots have been entered in the databases until recently, and all of the backlogs, and therefore totals, are approximations. All of these figures exclude larvae. The grand total for all 11 collections (one of the Tasmanian collections has since gone to the state museum) is an increase of some half million specimens for a total of 1.6 million fishes. A part of this increase is a more accurate estimate of the number of specimens due to computerisation. The large current backlog at the Australian Museum includes an estimated 5000 specimens from a Philippines expedition last year that have not yet arrived.

Australian Fish Collections Databases

In 1992/3 seven of the 12 collections had 100% of their identified specimens in a computer database and two of the other five collections had begun computerisation. Today all of the 11 collections have a database and all but two have 100% of their identified specimens in their database (Table 1).

Table 1. Numbers of specimens and database details of Australian fish collections; Acronyms follow Leviton *et al.* (1985).

Australian Fish Collection	Survey Year	Adults Registered	Adults Backlog	Adults Total	% Identified in Database	Quality Qualifiers		Database Software	Operating System
						Identification	Locality		
ADH	1992-3	7000	0	7000	100			Access	Windows
	2000	8500	500	9000	100	--	--		
AMS	1992-3	457000	20000	477000	100			Texpress	Unix
	2000	575000	8000	583000	100	+	+		
CSIRO	1992-3	72000	20000	92000	100			Texpress	SunOS
	2000	80000	15000	95000	100	+	--		
MAMU	1992-3	3000	0	3000	0				
	2000	3000	0	3000	10	--	--	Access	Windows
NMV	1992-3	67000	30000	97000	100			Texpress ⇒ KE Emu	Unix
	2000	180000	100000	280000	100	+	--		
NTM	1992-3	89000	10000	99000	100			Texpress	Unix
	2000	150000	9000	159000	100	--	--		
QM	1992-3	140000	4000	144000	100			Rbase	Windows
	2000	163000	3000	166000	100	--	--		
QVMT	1992-3	10000	500	10500	20			Texpress	Unix
	2000	5725	0	5725	100	+	+		
SAMA	1992-3	62000	5000	67000	30			Texpress	Unix
	2000	72000	5000	77000	100	+	+		
TIFC	1992-3	50000	5000	55000	0				
	2000	⇒ TMH	⇒ TMH	⇒ TMH					
TMH	1992-3	2500	0	2500	0				
	2000	52500	5000	57500	50	--	+	Filemakerpro	Macintosh
WAM	1992-3	120000	0	120000	100			Biolink	Windows
	2000	164000	0	164000	100	--	--		

With Australia lacking a national natural history museum, the fish research scientists, curators, and collections managers from the various state museums and other collections have worked closely together to identify common problems and discuss future developments. In the period of greatest collection growth since 1970, almost all of the fish collections moved quarters to accommodate that growth. Thus it was relatively easy for all to adopt a common family system of 470 families that is now utilised in almost all Australian fish collections, as well as those in New Zealand and Papua New Guinea.

In 1985 the Australian Biological Resources Survey sponsored a workshop on Australian fish collection databases, as the various museums moved towards computerisation of collections. The workshop was held in conjunction with the annual meeting of the Australian Society for Fish Biology (ASFB). It was the fish community that requested the funding, to try to agree on common parameters for the databases. It was recognised that all museums would never have the same kind of programs, and indeed had problems even having similar fields in the database, as some museums were adamant that one common database would be the same for all their animal collections. It was argued that it was more important for all fish collection databases in the country to be similar rather than fish and birds, for instance.

That workshop concentrated on such issues as having the same definition of data in the fields, such as degrees, minutes and tenths of minutes (rather than seconds), day, month, year (rather than some other order), and locality information from largest to smallest, ocean to point on beach (rather than vice versa). The problems of data security were raised, but at that time few solutions were found.

In the last decade a collection management workshop has been held almost annually with each ASFB meeting. While no workshop ever attracts representatives from all collections, significant advances have been made. One of the most important decisions has been that any change in the basic field data will have to be agreed to by all or almost all, and the same is true for proposed changes in the family classification system. Most now recognise that it is impossible to keep up with the continuing changes in fish family classification and the effort needed to relabel bottles would not be cost effective. While the collection classification is out of date, it works quite well as a retrieval system, much like a library Dewey Decimal System.

At a 1994 collection management workshop, the problem of data quality was raised, particularly as collection data goes up on the web or is utilised in some kind of network. The problems involve the quality of specimen identification and the quality of the locality data for the specimens. While fish taxonomists are able to judge data quality by, for instance, the name and date of the identifier, zoogeographers, ecologists and conservationists may not have that expertise. Species identifications have a quality code of 1-5, or N if no code has been applied (Table 2).

Table 2. Quality codes for specimen identification, locality origin and locality precision

Code	Identification Accuracy	Code	Locality Origin	Code	Locality precision
N	no code applied			0	accurate to 0-1 m (not currently used)
1	highly reliable, identified by specialist	GPS	original GPS	1	accurate to 1-10 m (not usually used)
2	high degree of confidence, identified by trained indiv.	OCM	original chart or map	2	accurate to 10-100 m, with seconds to first decimal
3	identification probably correct	OES	original estimation/ approximation	3	accurate to 100 m-1 km, original from chart or map with whole seconds
4	identified with limited confidence	CMG	subsequent chart, map,or gazeteer	4	accurate to 1-10 km, subsequent atlas, gazetteer, or short GPS, trawls to minutes
5	identification superficial	UNK	unknown	5	accurate to 10-100 km, place name only and trawls
--		--		6	accurate to > 100 km, very poor data eg coast of NSW

Fish Database Networks

The Australian fish collection management workshop in 1996 agreed to take the first steps towards an Australian fish database network. As a start the fish collections at the Australian Museum, Sydney and the Museum of Victoria, Melbourne tried to make their collection databases available to each other on line via modem. Overwhelming problems were encountered, including the old problem of security, the ever-present problem of lack of funds, and a lack of enthusiasm by the administrations of both museums. As a result, the computer specialists in each institution essentially dictated museum policy, and the attempt at networking failed. The lack of enthusiasm has continued until recently and consequently the project was never given the priority required to make it successful.

In March 1997 a workshop was held at Scripps Institution of Oceanography funded by the Sloan Foundation to examine the feasibility of a 'Census of Marine Fishes'. This first of a series of workshops over two years included 20 ichthyologists from around the world to address the Census, defined as knowing how many fishes there have been, how many there are now, and how many there will be in the future. The completed Censes would be of obvious benefit to both species conservation and commercial fisheries. The Census has expanded from fishes to a Census of Marine Life with the same goals on numbers past, present, and future (Ausubel, 1999). The relevancy of the Census to this paper is that two grants, of one half million dollars each, have been awarded to two different fish database networks.

The first is FISHBASE, run by ICLARM and now also with the California Academy of Sciences, which is described in an abstract by Reyes and Froese at http://www-sp2000ao.nies.go.jp/whatsnew/2001/january/jointforum/abstract.html.

The second network is FISHNET, run from the University of Kansas. This network is joining together the fish databases of 20 of the largest fish collections in the world, including that at the Australian Museum. That old problem of individual institutional security has been solved by providing each participant institution with a separate server joined to FISHNET, onto which is downloaded the relevant fish collection database, or whatever part thereof the participant chooses. These will be periodically updated to remain current, but the network is not directly linked to the institutional database, thus avoiding security problems. Details of FISHNET are available at the web site http://habanero.nhm.ukans.edu/fishnet. While the Australian fish workers would still like to see an Australian network of fish collections, this is now tied to a national network of all zoological collections that has yet to be finalised.

Databases and Conservation

The ability to map both collecting stations and species distributions based on locality data in the collection database is immensely valuable for conservation purposes. The total marine collecting stations in the state of NSW for the Australian Museum Fish Collection suggests the state is well covered, with 1907 collections from 1880 to 1997 (Fig 3). However, a breakdown by the type of collecting shows the 97 collections with the ichthyocide rotenone, which is one of the few methods of comprehensive collecting, are restricted to limited areas of the coast, with most undersampled (Fig. 3 inset). The vast majority of collections are from other inshore methods and trawls.

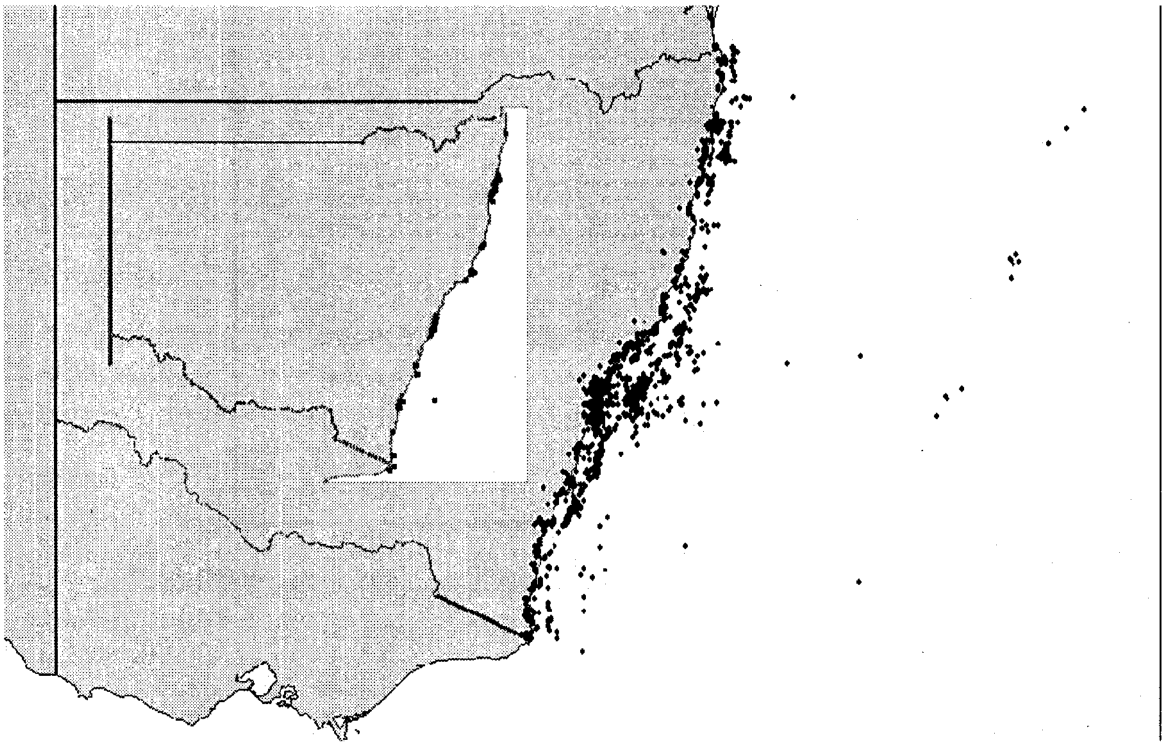

Fig. 3. New South Wales marine collecting stations in AMS Fish Collection, 1880-1997; inset rotenone stations, 1965-1997

Another mapping program, which is now available to the general public on the Australian Museum Fish Section website www.austmus.gov.au/fishes/about/maps/index.htm, is that of individual species distributions. The weedy seadragon, *Phyllopteryx taeniolatus*, of the seahorse and pipefish family Syngnathidae is found around the southern half of Australia (Fig. 4). Clicking on any locality will provide additional information, such as specimen habitat, capture depth, date of collection, and size range of specimen(s). Provision of the exact latitude and longitude is restricted to scientists or others who register with the Fish Section. The size of the dots on the map limits the precision of the locality, thus making the information on endangered or valuable species secure. While these distribution maps are limited to the data in the Australian Museum fish collection, the value of utilising national or international networks to provide similar maps, particularly for conservation, is unquestioned. They are also an exceptional collection-management tool for the correction of erroneous latitudes and longitudes, as marine fishes with terrestrial localities are obvious.

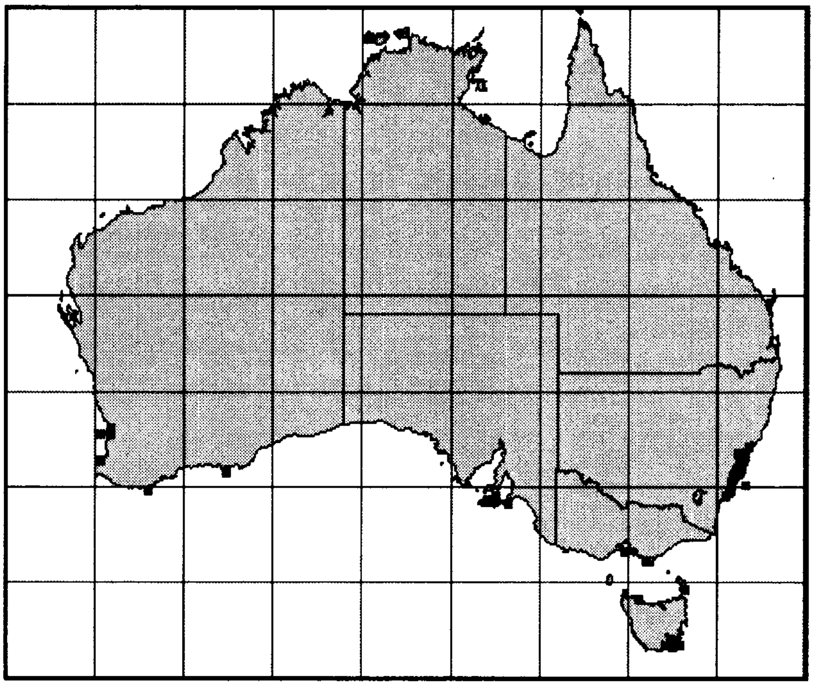

Fig. 4. Weedy seadragon specimen localities in the AMS Fish Collection

The correct identification of species is essential for the conservation of biodiversity. The hidden backlog of specimens identified only to family or genus, or indeed incorrectly identified, can only be cleared by the identifications of specialist taxonomists. The worldwide decrease in taxonomists should be a concern for all involved in conservation. If we are to be successful in minimising species extinctions until the human population size ultimately stabilises and decreases, the continued expertise of taxonomists will be required and more permanent positions for them will be necessary.

Acknowledgements

The collection managers and research scientists of the Australian fish collections have again been generous in the provision of data summarised in Tables 1 and 2. We are grateful for the help of Richard Williams (ADH), Alastair Graham (CSIRO), Stuart Norrington (MAMU), Dianne Bray (MV = NMV), Helen Larson (NTM), Jeff Johnson (QM), Craig Reid (QVMT), Debbie Churches (SAMA), Kathryn Medlock (TMH), and Sue Morrison and Barry Hutchins (WAM). The idea of a hidden database backlog is that of Jeff Leis.

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Fish Databases in Japan with Special Reference to Fish-image Database and Its Role in Biodiversity Study

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Abstract

A brief review on fish collections in Japanese institutions is shown with an emphasis on computerization processes. A new fish database based on digitized underwater photographs has recently been established through a joint project of the Kanagawa Natural History Museum and the National Science Museum. This fish-image database including 30,000 photographs was put on a home page of the National Science Museum. It greatly contributes to understanding of fish diversity. Many new species and new records have been found through this image-database, and new information on ecology of deep-water fishes has become available.

Key Words: Fish databases, Japan, fish-images, biodiversity, museums

Introduction

Although Japan is a small country, the Japanese Archipelago is extended for 3000 km from north to south, being almost equal in length to the east coast of Australia. The Pacific coasts of the main islands of Japan are washed by the warm Kuroshio Current transporting tropical fishes to the central part of Honshu Island in summer, and the cold current Oyashio, on the other hand, comes down from the northern part of Pacific. This situation makes Japanese sea environments greatly diversified, ranging from developed coral reefs in the Ryukyu Islands to a very cold realm (even the surface of the sea frozen in winter) along the eastern north coast of Hokkaido Island. This is the reason why Japanese fish fauna is rich, making the number of fish species around 4000.

The rich fish fauna has attracted many ichthyologists, and they made large fish collections in museums and universities. These collections are crucially important for systematic and ecological studies on fishes (Matsuura, 1997) and some of them have recently been computerized to build databases for ichthyology. In addition to these collection databases, we have succeeded to establish a new database based primarily on underwater photographs taken by SCUBA divers. The main purpose of this paper is to show that the fish-image database can contribute to understanding of fish diversity.

Fish Collections in Japan

There are five large fish collections in the following Japanese institutions: the National Science Museum (NSMT), Hokkaido University (HUMZ), Kyoto University (FAKU), Kochi University (BSKU) and University of Tokyo (ZUMT). Computerization of fish collections in Japan started in the mid-1980s at the Hokkaido University followed by the National Science Museum. These two collections make important databases for systematic and ecological studies on Japanese fishes. The fish collection of the Hokkaido University including 160,000 specimens has fully been computerized in the late 1990s. The National Science Museum is still going on computerization process of its collection; sixty percent of the collection has already been computerized. This museum will soon provide a URL for searching its huge freshwater fish collection including 1.2 million specimens. The other three collections have not yet been computerized, although the Kochi University has recently begun computerization of their collection. Because university collections have not been given adequate budget and manpower, they have still struggled to make progresses in collection managements.

Fish-image Database

In 1995 we started building another large fish database, which should be called a fish-image database. We established close relationships with amateur SCUBA divers. They have continuously brought us surprising amount of underwater photographs including great shots of new species, new records, and color variations. Over the past five years, they provided us with about 30,000 photographs of fishes; most of them are underwater photographs. Digitized fish-images were put into a computer to make fish-images available for scientists and the public through the internet. A huge number of underwater photographs of fishes have enabled us to make faunal researches, to record seasonal occurrences of fishes along the Pacific coast of Japan, to find new species, and to observe interesting fish behavior.

New species and new records. Because there are so many fishes in Japanese waters, there still remain many unknown fishes. Our literature survey on issues of *Ichthyological Research* and *IOP Diving News* revealed that more than four new species have annually been found from Japan over the past decade, and about 15 new records of fishes have annually been published. Although there are larger possibilities for SCUBA divers to encounter new fishes in coral reefs than in warm waters (Fig. 1), careful and experienced SCUBA divers have found and photographed interesting fishes including deep-water fishes in the central part of Honshu Island (Fig. 2).

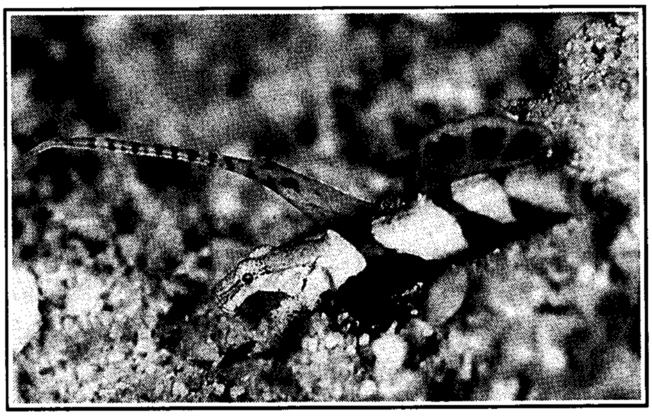

Fig. 1. An undescribed species of the gobiid genus *Discordipinna*, NE Borneo, 30 m depth, photo by F. Kaneno (registered number: KPM-NR 0022220FA).

Fig. 2. *Ateleopus tanabensis*, Izu Peninsula, Japan, 30 m depth, photo by Y. Fukazawa (registered number KPM-NR0003525).

Faunal and zoogeographical studies. There are many diving spots along Sagami Bay and Suruga Bay being reached within the distance of several hours by car from Tokyo (Fig. 3). Many SCUBA divers enjoy diving in weekends and holidays, and most of them are interested in watching and photographing fishes. Because many of them dive on the same periods (usually weekends) along the coasts of these two bays, their observations are great in total and can contribute to recording fishes including cryptic fishes such as solenostomids and triplefins.

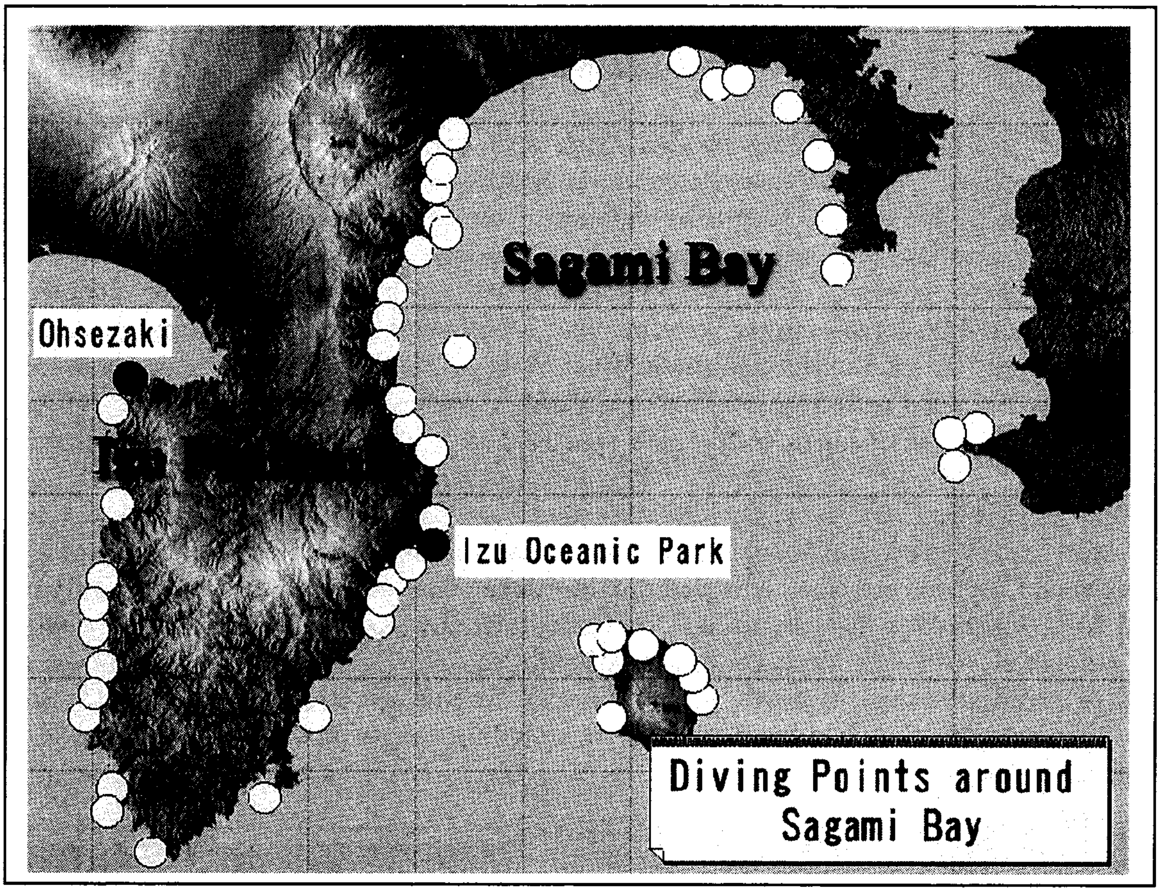

Fig. 3. Diving points along Sagami Bay and adjacent region in Japan.

It is not easy to keep continuous observations in particular places in the sea, because it needs lengthy efforts by using SCUBA gear. However, huge number of SCUBA divers have brought us adequate records of solenostomids in Sagami Bay, showing clearly seasonal changes (Fig. 4). Their observations and photographs indicated that solenostomids appeared in summer through early winter but never survived to reproduce descendants in the bay.

Making lists of fishes usually need great efforts to collect many fishes of particular areas. However, fish-image database has provided adequate photographs to make lists of fishes in the Izu Islands and Sagami and Suruga Bays within relatively short periods. Because superb underwater photographs allowed us to identify fishes to species level, we could make lists of fishes occurring in the Izu Islands (Furuse et al., 1996) and Sagami and Suruga Bays (Senou et al.1997, 1998)). The number of photographs sent to us has continuously been large ranging from 5000 to 6400; this suggests that the fish-image database will provide high possibilities to understand the entire Japanese fish fauna.

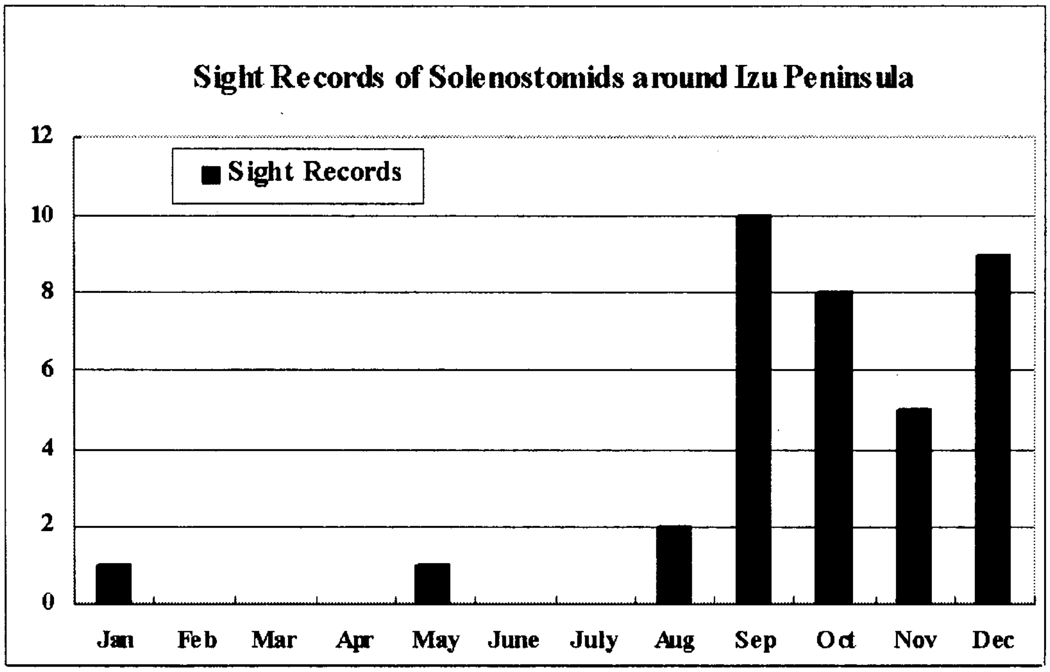

Fig. 4. Sight records of solenostomid fishes around the Izu Peninsula, Japan.

Studies on fish behavior. Most SCUBA divers are interested in watching beautiful and interesting fishes such as gobiids, chaetodontids, labrids, pomacentrids, etc. However, well-trained underwater photographers became interested in watching and photographing fish behavior. We found surprising shots among their photographs. Snapping shrimps are well known to show symbiosis with gobiid fishes; snapping shrimps make tunnels where gobies can live, and gobies sit on the entrance of the tunnel to watch enemies. However, the fish-image database shows that another symbiotic relationships between snapping shrimps and gobies. Cleaning behavior has been reported between some groups of shrimps and fishes, but that of snapping shrimps has never been reported in the sea. Snapping shrimps clean out the mouth and gill chamber of gobies (Figs. 5 & 6). In addition to this, exciting photographs have recently revealed that surprisingly snapping shrimps eat gobies' dropping (Fig. 7).

Fig. 5. Snapping shrimp cleaning the mouth of an undescribed species of the gobiid genus *Stonogobiops*, Ryukyu Islands, Japan, photo by J. Nakamoto (registered number KPM-NR 0036488A).

Fig. 6. Snapping shrimp cleaning the gill chamber of an undescribed species of the gobiid genus *Stonogobiops*, Ryukyu Islands, Japan, photo by J. Nakamoto (registered number KPM-NR 0036344A).

Fig.7. Snapping shrimp just picking the dropping (indicated by arrow) of a goby, *Stonogobiops nematodus* (unregistered photo).

Underwater photographs of fish larvae and juveniles. It is very difficult to see fish larvae in the sea because they are very small and usually transparent. However, exciting underwater photographs of fish larvae and juveniles were brought to us by SCUBA divers. Several photographs shown here were taken by our collaborators in the Ryukyu Islands (Figs. 8 & 9). They are trachipterid fishes, and their juveniles and larvae have rarely been observed alive. The fish-image database clearly shows swimming forms of trachipterid juveniles, which have never been reported.

Fig. 8. Trachipterid juvenile, 4 cm in total length, Ryukyu Islands, Japan, 0.1 m depth, photo by M. Takada (registered number KPM-NR 0028243FA).

Fig. 9. Trachipterid juvenile, 10 cm in total length, just below surface, Ryukyu Islands, Japan, photo by Y. Adachi (registered number KPM-NR 0028250FA).

Future of the Fish-image Database

As shown above the fish-image database provides tremendous information on fishes including new species, new records, faunal and zoogeographical records, new behavioral observations, rare fish larvae and juveniles, etc. It is surprising that photographs more than 5000 have constantly been sent to us annually (Fig. 10); we expect that the total number of fish-images will soon reach to 50,000. This large image-database on fishes will contribute to know the entire aspect of Japanese fish diversity. Some serious SCUBA divers have sent us underwater photographs taken in depths below 70 m, and another group of divers provided us with deep-water fishes photographed at night. This suggests us that the fish-image database may be able to expand to cover fishes not usually found in shallow waters.

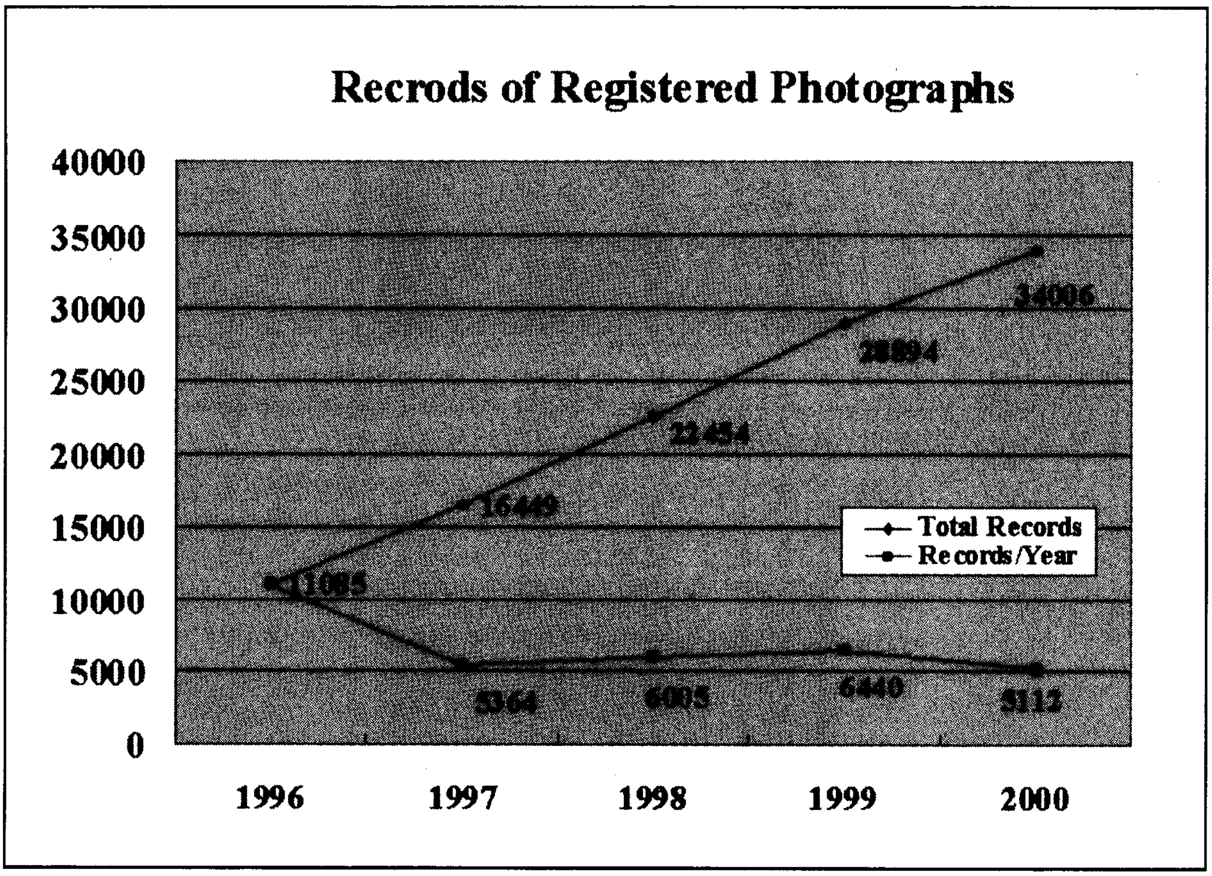

Fig. 10. Record of registered photographs from 1996 to 2000

Although the Japanese version of fish-image database is available through the internet, the English version has not yet been prepared. We will soon start translating the Japanese version into English. It is a great task when considering the huge number of registered photographs, but we expect that we can finish the translation within one year. The English version will surely be useful for ichthyologists being interested in the Indo-Pacific fishes and the public for understanding natural history of fishes.

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Bacteriology Insight Orienting System (*BIOS*)

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Abstracts

Bacteria and Archaea are two major domains of recognized domains of the known species. Their size in microscopic order made difficulty to be recognized by humans unless their data is accessible. To provide access and analysis on microbial diversity information, Bacteriology Insight Orienting System (*BIOS*) has been developed. *BIOS* contains 6943 described species and subspecies names of bacteria and archaea, 2606 names of cyanobacteria by November 2000. *BIOS* of which web based analytical tool provides windows to compare the results of phylogenetic analysis based on 16S rDNA sequence and the results of cluster analysis on proteome profiling. The sequence data and 2 dimensional gel electrophoresis analysis data were accumulated in *BIOS* database content for cyanobacteria reclassification and taxonomy.
***BIOS* URL: http://www-sp2000ao.nies.go.jp/*BIOS*/index.html**

Key Words : Bacteria, Archaea, Biodiverisity, Database, Proteome, Taxonomy

Introduction

There are growing numbers of information resources for researchers to use. To access the reliable data and knowledge for studying biodiversity is however, becoming more and more difficult due to uncontrolled and distributed nature of the information sources. The system to navigate users to the appropriate information of 1.75 million of known species in the world is desired by researchers and decision makers. To cover the relevant biodiversity information and to allow users searching those distributed data and knowledge as if it was a single integrated system, large scale thesauri and harmonizing gateway interface for different existing databases are necessary. Taking these necessities into account, Species 2000 programme called for participation of existing databases to create Catalog of Life (http://www.sp2000.org, Bisby, F.A. 2000). While, Global Biodiversity Information Facility (GBIF)is established (http://www.gbif.org, Edwards J.L.et al. 2000) as a new international organization.

We have developed a prototype information facility with interests in bacteriology. *BIOS* is a challenging system to create an open ended virtual facility to see insight of bacteriology by submitting and using distributed data resources on internet.

Materials and Methods

Two relational databases (Oracle 8 running on Sun Ultra Sparc II Deskside Workgroup Server, GP7000) were set up by compiling existing and newly developed species information files. We compiled data from "List of Bacterial Names with Standing in Nomenclature" (Euzeby, J.P. 1997, http://www-sv.cict.fr/bacterio/) supplemented with "Bacterial Nomenclature up-to-date" (http://www.dsmz.de/bactnom/bactname.htm) to build this database with an agreement. Cyanobacteria names controlled by botanical code (International Code of Botanical Nomenclature, 1972) were newly made in digital form and stored in a database. Common gateway interface (CGI) program to send query to the two separate databases was developed in Perl language (ver. 5). We developed software to calculate the similarity value of 2-DE profile among tested species by simple matching of spots to an out-group species.

This standardized similarity matrix was subjected to cluster analysis to deduce tree view of the relationship of the species. The cluster analysis for 2-DE spots was performed by unweighted pair-group method using arithmetic averages (UPGMA). The module to analyze sequences was used a public domain software, CLUSTAL W Multiple Sequence Alignment Program(ver.1.7,1997) (http://bioinformer.ebi.ac.uk/newsletter/archives/2/clustalw17.html).

Gel images were made into digital form by using FLA-2000 (Fuji Photofilm Co., ltd., Japan). Detection of spots from gel images was performed by the Phoretix Gel Analysis Software 2D Professional Ver. 5 (Phoretix International, UK) in manually set sensitivity.

Results and Discussion

BIOS was built by assembling three databases, two of species names and one database for Proteome image analysis. First database is for referring bacteria and archaea names that are solely controlled by International Code of Nomenclature of Bacteria (ICNB) 1992, and another one as separate database for cyanobacteria, which previously controlled by International Code of Botanical Nomenclature (ICBN). Third database is described below. The *BIOS* interface was designed to allow accessibility to relevant taxonomic data and to use taxonomic tools through WWW browser from remote clients. The system components in *BIOS* were shown in Fig. 1.

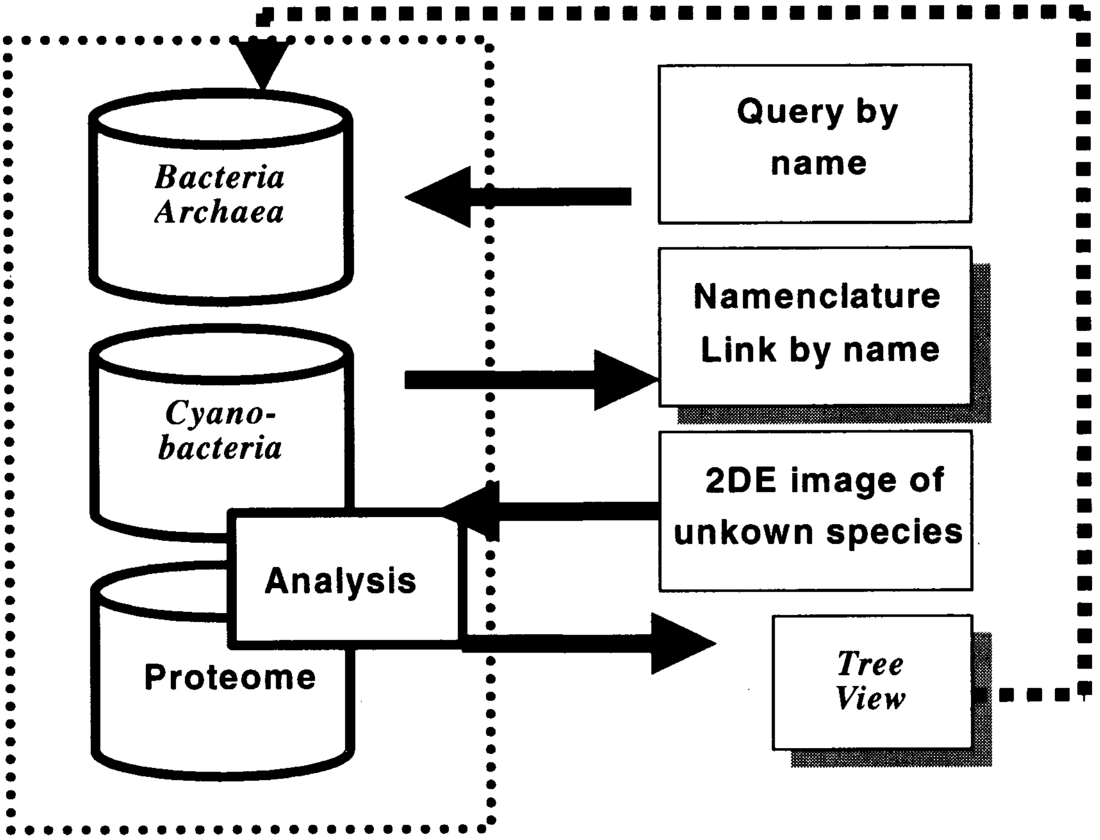


Fig. 1. System Components of BIOS

Bacteria and archaea database and its CGI software to send query by names provides the screen views shown in Fig. 2. The window on top of Fig. 2 is a search screen by species names or by names above genus. *BIOS* provides alphabetical index of all name records with status of nomenclature to support users who are not familiar with scientific names of bacteria. When search button is pressed by a user, data is retrieved and query result comes on the screen in alphabetical order. Each line of retrieved record is linked to onward sites including NCBI/PubMed, CDC newsletter, and catalogs of culture collection that are publicly available on the internet. Query result screen also provides clickable position indicated "See the hierarchy?". When a user click the position the names are listed from family down to subspecies level of which data corresponded.

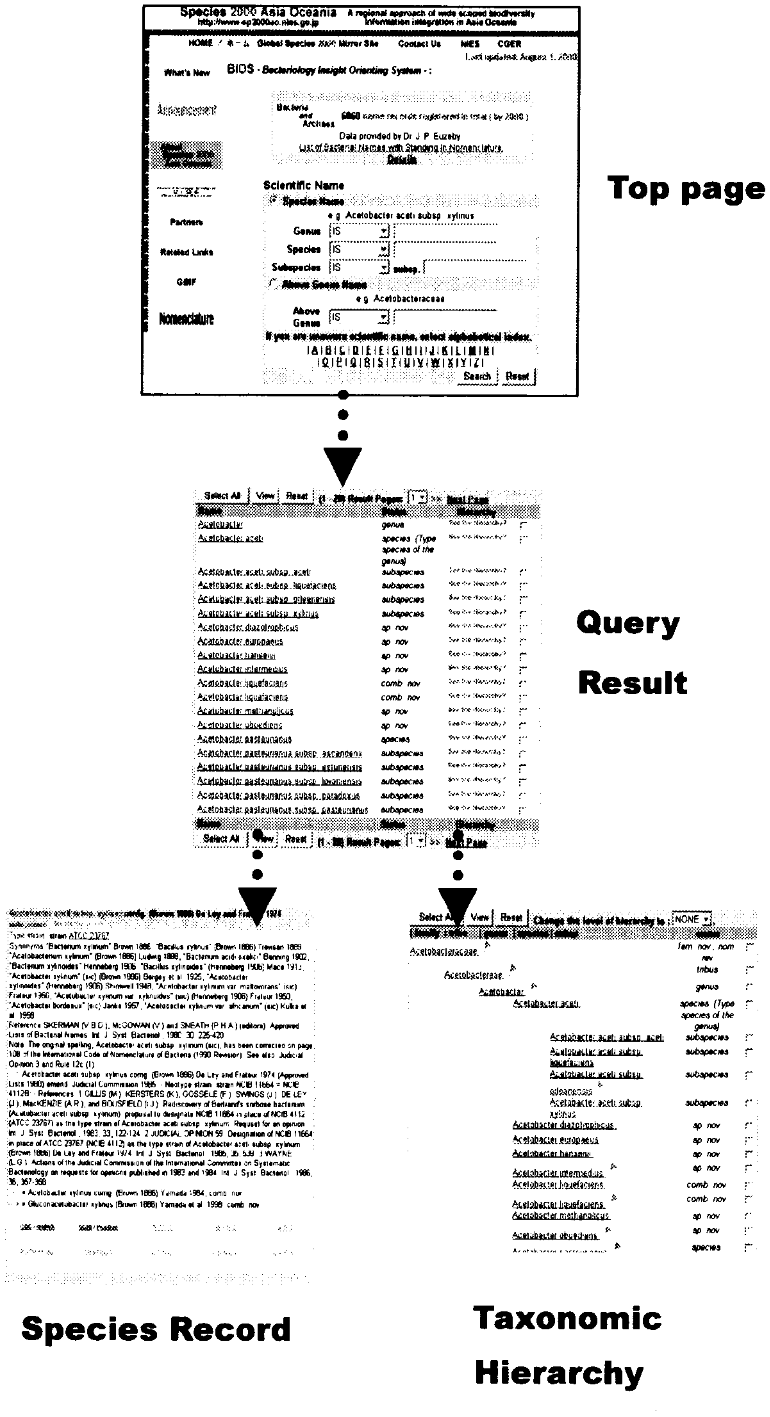
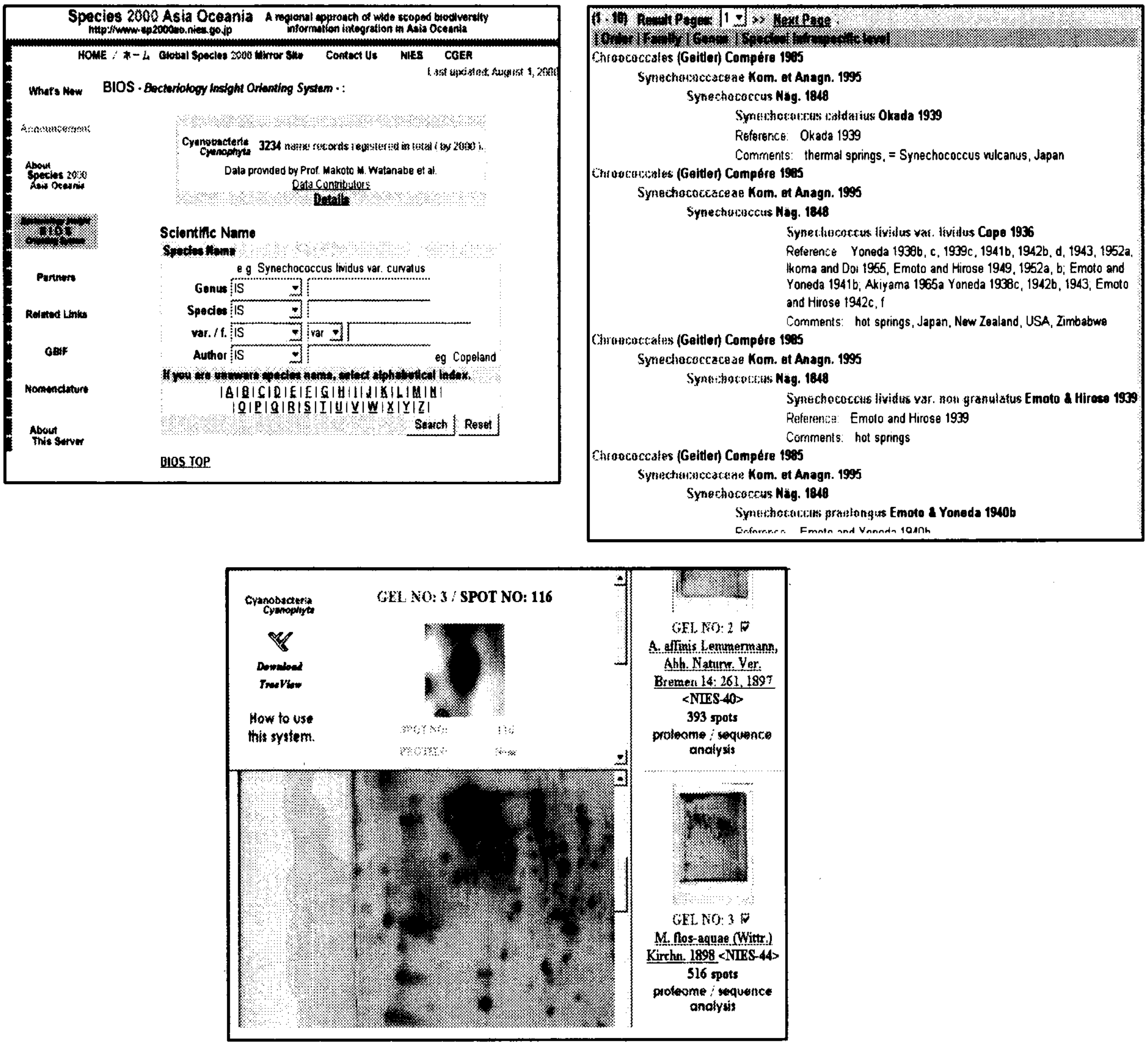


Fig. 2. Screens of *BIOS* User Interface

The data shown with flag is indicating the name is currently accepted. The flag indicator in the alphabetical index of species is useful to apply this database to further integrate into global biodiversity information systems with other existing databases for plants, animals etc. in future. Users can also send type strain number to retrieve the valid species name and through the interface of *BIOS* currently accepted name for the strain can be reached. History of changing species name due to new combination can also be found in the contents of the database and it is indicated with arrow on the screen of WWW browser. Other synonyms than new combination including illegitimate names and very old names such as publication before 1980 are also listed in "synonym".

User interface screens to use cyanobacteria database on WWW are shown in Fig. 3. To search species names for cyanobacteria a matched screen with bacteria and archaea was developed. In cyanobacteria infraspecific epithet carries other than subspecies and this reflected to the screen to assist users. Query result is shown in the middle of Fig. 3. Taxonomic hierarchy and detailed information of the species are in one screen. Currently no link to culture collection was made. User interface for proteome analysis is shown in the bottom.



Last updated: August 1, 200

BIOS - *Bacteriology Insight Orienting System* - :

Cyanobacteria *Cyanophyta* 3234 name records registered in total (by 2000).

Data provided by Prof. Makoto M. Watanabe et al.

Data Contributors

Scientific Name

Species Name

e g Synechococcus lividus var. curvatus

Genus: IS

Species: IS

var. / f.: IS var

Author: IS eg Copeland

If you are unaware species name, select alphabetical index.

| A | B | C | D | E | F | G | H | I | J | K | L | M | N |
| O | P | Q | R | S | T | U | V | W | X | Y | Z |

Chroococcales **(Geitler) Compére 1985**
Synechococcaceae **Kom. et Anagn. 1995**
Synechococcus **Näg. 1848**
Synechococcus caldarius **Okada 1939**
Reference: Okada 1939
Comments: thermal springs, = Synechococcus vulcanus, Japan

Chroococcales **(Geitler) Compére 1985**
Synechococcaceae **Kom. et Anagn. 1995**
Synechococcus **Näg. 1848**
Synechococcus lividus var. lividus **Cope 1936**
Reference Yoneda 1938b, c, 1939c, 1941b, 1942b, d, 1943, 1952a, Ikoma and Doi 1955, Emoto and Hirose 1949, 1952a, b; Emoto and Yoneda 1941b; Akiyama 1965a Yoneda 1938c, 1942b, 1943; Emoto and Hirose 1942c, f
Comments: hot springs, Japan, New Zealand, USA, Zimbabwe

Chroococcales **(Geitler) Compére 1985**
Synechococcaceae **Kom. et Anagn. 1995**
Synechococcus **Näg. 1848**
Synechococcus lividus var. non granulatus **Emoto & Hirose 1939**
Reference: Emoto and Hirose 1939
Comments: hot springs

Chroococcales **(Geitler) Compére 1985**
Synechococcaceae **Kom. et Anagn. 1995**
Synechococcus **Näg. 1848**
Synechococcus praelongus **Emoto & Yoneda 1940b**

Cyanobacteria *Cyanophyta*

GEL NO: 3 / SPOT NO: 116

GEL NO: 2 ☑
A. affinis Lemmermann, Abh. Naturw. Ver. Bremen 14: 261, 1897
<NIES-40>
393 spots
proteome / sequence analysis

GEL NO: 3 ☑
M. flos-aquae (Wittr.) Kirchn. 1898 <NIES-44>
516 spots
proteome / sequence analysis

Fig. 3. Screens of user interface of *BIOS* for cyanobacteria

In fig. 4, Proteome image analysis that is accessible through WWW browser screen is shown. Three frames provides operability for users to select data to subject them to cluster analysis, and to retrieve species information from cyanobacteria species name database. 16S rDNA sequences are also be retrieval by clicking corresponding words on the screen. Each spot on the image of gels carries link to single spot image and relevant information including coordinates and protein identification. Information pops up on the third screen (top left) by clicking at the spot on gel image.

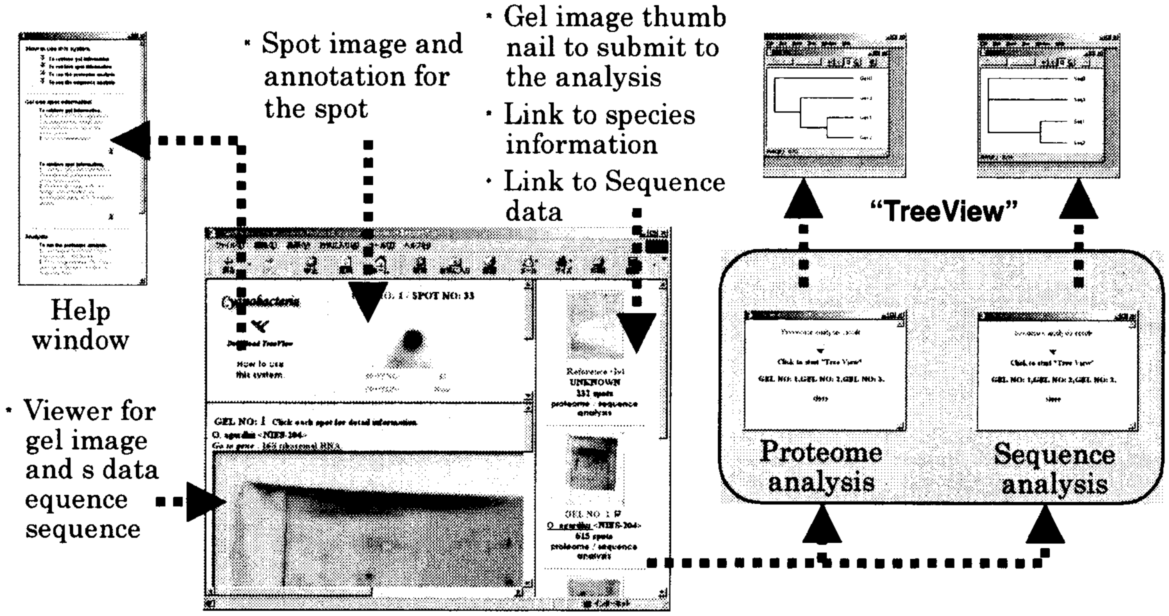


Fig. 4. Screens of Proteome Analysis for Cyanobacteria

To facilitate to subject cyanobacteria into systematic taxonomy of bacteriological view, we developed tools to analyze phylogeny based on sequence information and proteome data. In the evolution of life, genetic mutations are successively transferred from an ancestor to descendants. Substitution, insertion, inversion, deletion, duplication and crossing over of genes are concerned to contribute to the divergence of species. Comparing mutations in a common gene sequence has been thought that it can trace the evolutionary path of the organisms as deductive geneological tree. However, studies have shown that sequences of a single gene from different species would sometimes not result in a consistent phylogenetic tree when different genes or different algorithm were applied to the analysis (Russo, C.A., et al. 1996, Takezaki N. and Nei, M. 1996). These phylogenetically deduced group could reveal that the grouping is discrepant from the morphological, physiological or biochemical grouping of the subjected species (Neilan, B.A. et al. 1997, Rudy, K.et al.1998, Stackebrandt E. et al. 1996). This evidence implies that comparing only one gene does not fulfill the required information to analyze the evolution of the species in general.

Cyanobacteria has recently been studied in 16S rRNA/DNA or 16S to 23S internal transcribed spacer sequences. Again, evidences showed that monophyletic group could include independent taxonomic lineages which were based on their phenotypic characters (Otsuka et al. 1999).

New approach to deduce the evolutionary effected gene product to find reasonably explaining the divergence of species among cyanobacteria is therefore strongly desired. Two dimensional gel electrophoresis (2-DE) is an approach to visualize the most of gene product of the cell. Proteome analysis on Synechocystis sp. strain PCC6803 has successfully made a linkage between genome information and 2-DE spots (Sazuka et al. 1999). This suggests that 2-DE patterns may represent the whole genome that produce functioning proteins. Comparing the profiles on 2-DE between species and detecting the particular spot that is found in only particular group of the species can be count as an evolution marker. This marker may be thought as a taxonomic marker to lead to new insights into relationship of species. We developed software to calculate the similarity value of 2-DE profile among tested species by simple matching of spots to an out-group species. This standardized similarity matrix was subjected to cluster analysis to deduce tree view of the relationship of the species.

By using this system, we have analyzed proteome in Oscillatoria agardhii, Microcystis aeruginosa, and Anabaena affinis. The results of cluster analysis based on the spot matching among the three known cyanobacteria species and one unknown species (used as an out group) appeared to be acceptable in the similar topology to the result of 16SrDNA sequence based cluster (Fig. 4).

Over three hundred spots were detected from each silver-stained 2-DE gel in the pilot experiments. A single reference gel prepared from an out-group unknown species was repeatedly used to compare the spots from each sample gel. Spot identification based on the relative coordinates to the result of reference gel was also carried out by Phoretix 2D. To perform similarity analysis, data matrix was created between the detected spots in the reference gel and sample gel. The matrix of matched and unmatched spots were taken as Jaccard's asymmetric coefficient and subjected to analysis of similarity coefficients among the samples. The process of identification of spots described above might have neglected the possibility of the irregular location of spots due to post-transcriptional modification of the proteins and it is possible that such spots were counted as newly identified spot. To analyze further on the discrepancy among the monophyletic or polyphyletic groups using this proteome profiling tool, coordinates of spots from different gels are better to be confirmed either by the peptide mass fingerprinting, N-terminal micro-sequencing or immuno-blotting. The potential for gene product modification above is, however, concerned as a part of phenotypic character of organisms and appearance of irregularly located product from the same gene is relevant to subject into the computation of similarity coefficient.

Peptide mass fingerprinting, sequencing and immuno-blotting are important to apply the 2-DE data to further analysis of the expression of protein. Because the expression of the protein responsible for species divergence can be confirmed by analyzing homology to the known genome sequence data that are already available for cyanobacteria and other eubacteria and archaea.The performance of the system was reasonably fast to develop this database as open-ended sharing system on high-speed information network. Further submission of proteome data in different cyanobacteria species and the species clustered in monophyletic or polyphyletic group that are discrepant from phenotypic lineage is expected to evaluate the proteome profiling system.

Acknowledgements

I gratefully thank to Prof. Jean P. Euzeby, Prof. Erko Stackebrandt, Dr. Norbert Weiss, Dr. Manfred Kracht and Dr. Shoichiro Suda for their kind data submission and suggestions for development of BIOS.

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Plastid Phylogeny Inferred from Gene Order Comparison

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Abstract

Gene arrangement is one of the key characters that can discriminate evolutionary relationships among genomes. Completely sequenced genomes provide us with an opportunity to study the evolution of genome organization at a comprehensive level. Phylogenetic determinants were searched for through comparison of gene arrangements on completely sequenced plastid genomes. Gene orders that are shared among red algal plastids but are absent among green plant plastids, or vice versa, were identified. Such gene orders serve as phylogenetic markers. Although an amino acid sequence analysis has suggested that apicomplexan plastids from protists, such as *Plasmodium* and *Toxoplasma*, have arisen from a green alga, our comparisons clearly suggest their red algal origin rather than green algal origin. Specific gene arrangements, from which gene transpositions can be inferred, have been demonstrated to be useful in reconstructing phylogenetic trees. Using this approach, relative branch orders among green algae and land plants were determined, which indicate an earlier emergence of *Mesostigma* than the split of chlorophyta (*Chlorella* and *Nephroselmis*) and streptophyta (land plants).

Key Words: Phylogeny, Plastid, Gene order, Apicomplexa, Red algae, Green algae

Introduction

An understanding of evolutionary relationships among living organisms is one of the most interesting and challenging problems in biological sciences. The evolutionary history is inferred from phylogenetic trees constructed usually on the basis of sequence alignment of homologous genes or proteins from different species. It is known that reconstructed trees are susceptible to various artifacts (Felsenstein, 1978; Philippe and Germot, 2000) due to incorrect sequence alignment, biased base (or amino acid) compositions among species (Lake, 1994; Galtier and Gouy, 1995), evolutionary rate variation among species and/or across sequence sites (Yang, 1996; Philippe and Forterre, 1999), and so on. An alternative approach is gene order comparison (Sankoff et al., 1992; Kunisawa et al., 1997), from which evolutionary relationships can be inferred in the following way. If two genome show an identical gene order, for instance ...*abc*... for the three genes *a, b,* and *c*, then the two extant genomes must have evolved from a common ancestor. This is because the probability of forming the identical gene order, ...*abc*..., independently in two different lineages is very low. So an identical gene order reflects common ancestry. At the same time, their ancestral genome is inferred to have the same gene order, ...*abc*.... If genes *a, c, b* are dispersed on the ancestral genome, the three genes should come together in both of the two extant genomes in the same order ...*abc*.... Such probability is also very low. Based on this idea, a first example is argued on the evolutionary origin of apicomplexan plastids from *Plasmodium* and *Toxoplasma*, for which a green algal orign has been pointed out from an phylogenetic analysis based on protein sequences. However, the gene order comparisons suggest another origin. A simple method of tree-reconstruction based on gene transposition is then illustrated, and relative branch orders among green plant plastids are discussed.

Evolutionary Origin of Apicomplexan Plastids

Figure 1 compares orders of genes coding mainly for ribosomal proteins in various eubacterial and plastid genomes. Ribosomal protein genes tend to form clusters. A contiguous segment is indicated by an arrow, showing the direction of transcription. Eubacterial and plastid gene orders in each segment are identical, except several genes are missing from the plastid genomes. The same gene orders suggest that plastids and eubacteria share common ancestry, being consistent with the endosymbiosis theory. Segmental patterns, however, are different within eubacteria and within plastids. While in *Bacillus subtilis* ribosomal protein genes exist in a single large cluster, in cyanobacterium *Synechocistis*, a split occurs between S10 and L3. The same split can be seen in cyanelle, a plastid from *Cyanophora*. In green plant plastids from green algae, *Mesostigma*, *Nephroselmis*, *Chlorella* and from land plants *Marchantia*, *Nicotiana* and *Pinus*, a similar split occurs around S10. In contrast, in the red algal plastids from red algae *Porphyra* and *Cyanidium*, from diatom *Odontella* and from cryptomonad alga *Guillardia*, the smaller segment encoding S12 to S10 is linked the larger segment encoding from L3 to L31 at its 3' region (Kunisawa, 1997). An amino acid sequence analysis suggested that apicomplexan plastids have originated from a green alga (Kohler et al., 1997). However, the segmental patterns shown in Fig. 1 suggest their red algal origin. The arrangement that S10 is linked to the larger segment, is identical to that found in red algal plastids, suggesting the red algal origin rather than the green algal origin. Thus, analysis of organization of ribosomal protein genes disagrees with the amino acid sequence analysis on the evolutionary origin.

Figure 2 shows tRNA gene clusters that are shared by red algal plastid genomes and by green plant plastids. The gene cluster, serine tRNA with anticodon GCU and aspartic acid tRNA with anticodon GUC, can be found in the red algal plastids. Another gene cluster, cysteine tRNA with anticodon GCA and leucine tRNA with anticodon UAA, is also shared among the red algal plastids. These tRNA clusters cannot be found in the green plant plastid genomes. Conversely, a cluster comprising proline tRNA with anticodon UGG and tryptophan tRNA with anticodon CCA is shared by the green plant plastids, but this cluster are absent from the red algal plastids. The apicomplexan plastids in question have both of the two red algal type tRNA clusters, supporting their red algal origin (Kunisawa, 1997).

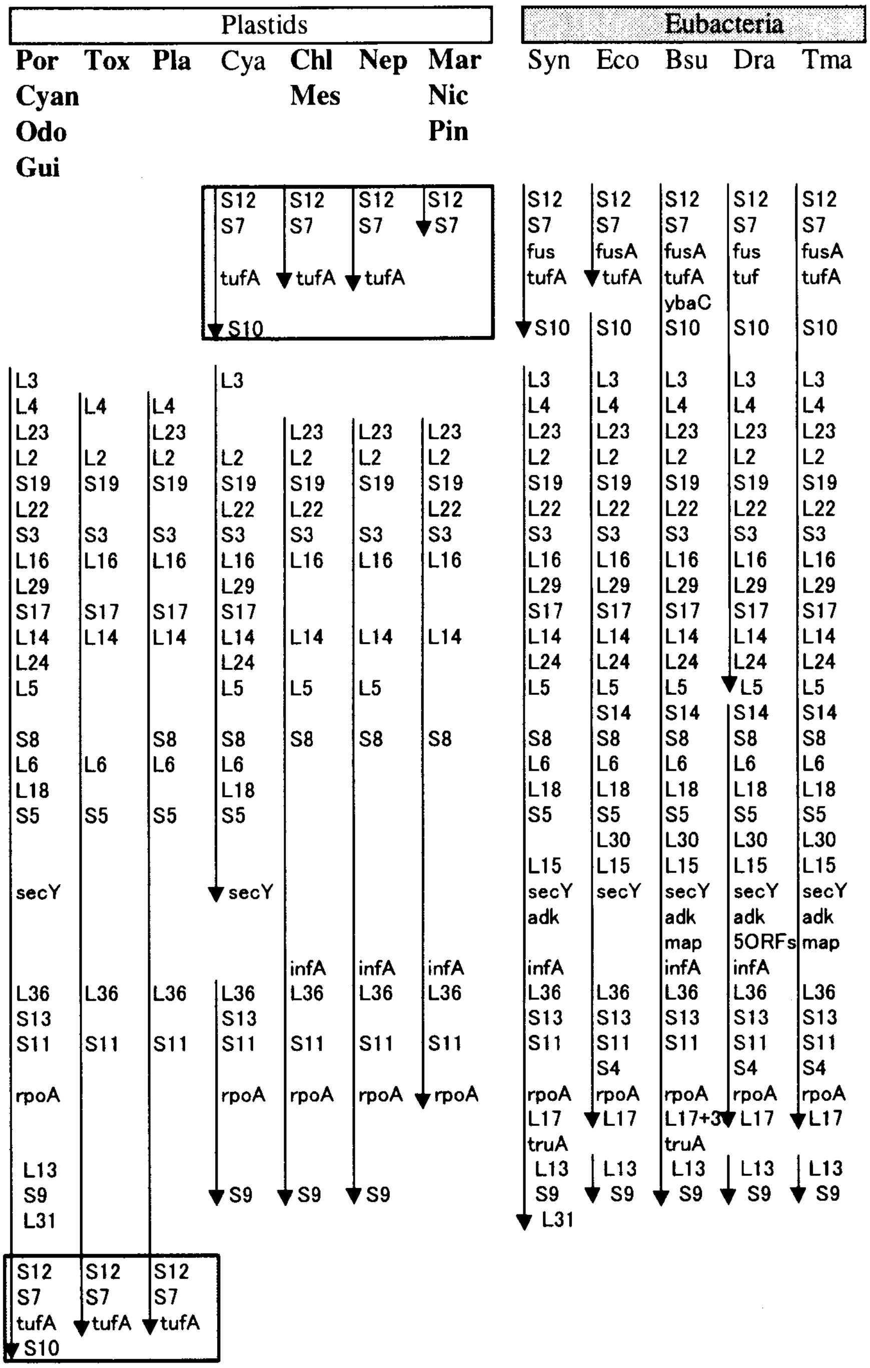

Fig. 1. Organizations of genes coding mainly for ribosomal proteins in eubacterial and plastid genomes. A contiguous DNA segment is shown by an arrow with the transcriptional direction. Arrangements of the boxed segment differ between red algal plastids and green land plant plastids. Abbreviations of species: red algae, Por *Porphyra* and Cyan *Cyanidum*; diatom, Odo *Odontella*; cryptomonad alga, Gui *Guillardia*; apicomplexa, Tox *Toxoplasma* and Pla *Plasmodium*; cyanelle, Cya *Cyanophora*; green algae, Chl *Chlorella*, Mes *Mesostigma* and Nep *Nephroselmis*; land plants, Mar *Marchantia*, Nic *Nicotiana* and Pin *Pinus*. Eubacteria, Syn *Synechocystis*; Eco *Escherichia*; Bsu *Bacillus*; Dra *Deinococcus*; Tma T*hermotoga*. All the genomic data were taken from the GenBank/EMBL/DDBJ databases.

Porphyra	**Ser[GCU]-Aps[GUC]-ftsH**	**cfxQ-Cys[GCA]-Leu[UAA]-ycf4-**
Cyanidium	**Ser[GCU]-Aps[GUC]-ftsH**	**cfxQ-Cys[GCA]-Leu[UAA]-------**
Cyanidioschyzon (partial)		**cfxQ-Cys[GCA]-Leu[UAA]-ycf4-**
Galdieria (partial)		**cfxQ-Cys[GCA]**
Odontella	**Ser[GCU]-Aps[GUC]**	**------Cys[GCA]-Leu[UAA]**
Guillardia	**Ser[GCU]-Aps[GUC]-ftsH**	**cfxQ-Cys[GCA]-Leu[UAA]-------**
Toxoplasma	**Ser[GCU]-Aps[GUC]**	**------Cys[GCA]-Leu[UAA]**
Plasmodium	**Ser[GCU]-Aps[GUC]**	**------Cys[GCA]-Leu[UAA]**

Mesostigma	**Pro[UGG]-Trp[CCA]-psaJ***
Nephroselmis	**Pro[UGG]-Trp[CCA]-psaJ***
Chlorella	**Pro[UGG]-Trp[CCA]-psaJ***
Marchantia	**Pro[UGG]-Trp[CCA]-psaJ***
Nicotiana	**Pro[UGG]-Trp[CCA]-psaJ***
Pinus	**Pro[UGG]-Trp[CCA]-psaJ***

Fig. 2. Transfer RNA gene clusters that are found uniquely in red algal plastids and in green algal plastids.

Evolutionary Relationships among Green Algae and Land Plants Plastids

Gene order similarity and dissimilarity in the comparison among green algae and land plants are shown in Fig. 3. The boxed gene order at the 3' region is shared by all these plastids, suggesting their common ancestry. However, the gene orders at the 5' region divide these plastids into two groups. Actually, the top three are green algae, and the bottom three are and plants. Identical gene orders among the green algae and among the land plants suggest they are derived from different ancestors. It is impossible to reconstruct a phylogenetic tree based on these considerations alone. As shown below, a specific gene arrangement can be a phylogenetic determinant and based on gene transposition phylogenetic trees can be reconstructed.

Mesostigma	`S12-S7-tufA-L19-`	`ycf4-cemA-petA-ORF-petLG`
Nephroselmis	`S12-S7-tufA-L19-`	`ycf4-cemA-petA-ORF-petLG`
Chlorella	`S12-S7-tufA-L19-`	`ycf4-cemA-petA-ORF-petLG`
Marchantia	`rbcL-Arg[ACC]-accD-psaI-`	`ycf4-cemA-petA-ORF-petLG`
Nicotiana	`rbcL----------accD-psaI-`	`ycf4-cemA-petA-ORF-petLG`
Pinus	`rbcL-Arg[ACC]-accD-psaI-`	`ycf4-cemA-petA-ORF-petLG`

Fig. 3. Gene order similarity and dissimilarity among green algae and land plant plastids.

In cyanelle from *Cyanophora*, a gene order, threonine tRNA with anticodon UGU and ribosomal S4 protein genes, is found. A similar order, threonie tRNA and S4 can be found in *Mesostigma*. In this case, S4 gene is located on the complementary strand to threonine tRNA, suggesting an inversion. So their ancestral genome also has the gene cluster comprising threonine tRNA and S4 genes. On the other hand, in *Nephroselmis* and *Chlorella* threonine tRNA gene is found in the neighborhood of psbI and serine tRNA genes, as shown in Fig. 4. So, their ancestor must have the cluster of threonine tRNA, psbI and serine tRNA genes. By connecting these two ancestral genomes (nodes), we have uniquely determined the topology for the four genomes. In the left node, Thr tRNA gene is located in the vicinity of S4, while at the right node Thr tRNA gene is located in the neighborhood of psbI and Ser tRNA genes. What happened between the two nodes? Another gene arrangement found in *Mesostigma* is helpful to resolve this. A gene cluster, psbI and Ser tRNA, can also be found in *Mesostigma*, which is located away from the Thr-S4 cluster. Thus, it seems most likely that Thr tRNA gene was transposed to the neighborhood of psbI and Ser tRNA genes, or vice versa. By this single transposition, Thr tRNA-S4 cluster is broken and a new cluster Thr tRNA-psbI is generated. The direction of transposition can be determined by rooting the tree. In this case, *Cyanophora* can be regarded as an outgroup for these three green algae. Using this knowledge, we can root this tree at the branch leading to *Cyanophora*. So, the left node is more ancient than the right node. Here we have made two assumptions on the outgroup and on the parsimonious solution for gene rearrangements.

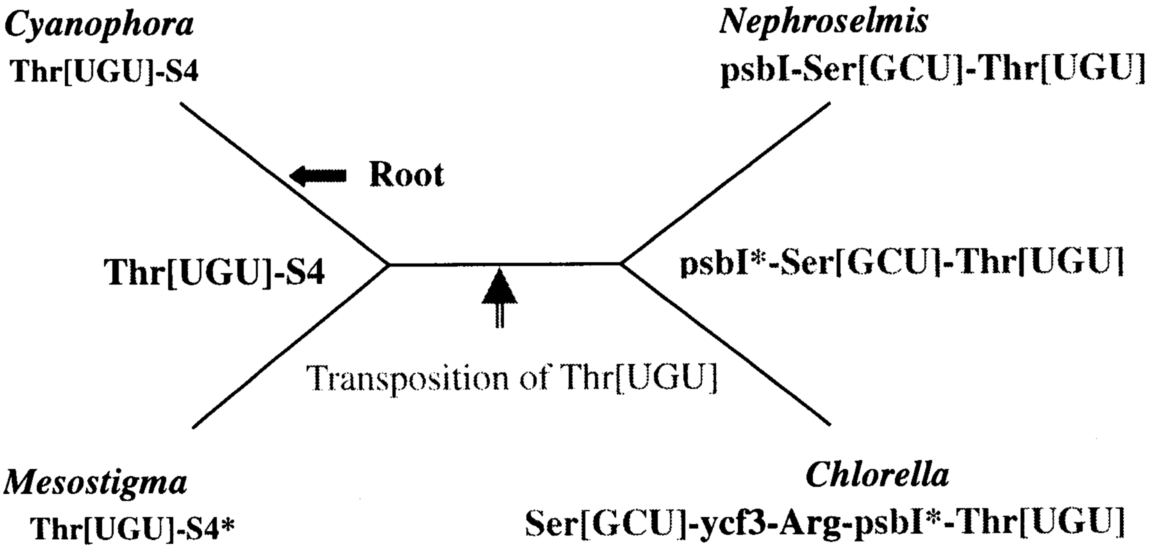

Fig. 4. An unrooted tree for gene rearrangements

It is easier to understand the order of evolutionary events in Fig. 5. *Cyanophore* and *Mesostigma* share the thr tRNA-S4 gene cluster, and their ancestor has the same gene cluster at node beta. At somewhere between the nodes β and γ, thr tRNA gene was transposed to the neighborhood of psbI and ser tRNA genes. So, the ancestral genome at the node γ has a gene cluster comprising psaB, ser tRNA, and thr tRNA genes. Then *Nephroselmis* and *Chlorella* diverged, keeping the psbI-Thr tRNA gene cluster. Here, we have neglected small (local) inversions and translocations, which are prevalent in closely related plastids. Anyway, these non-local gene arrangements are useful as phylogenetic determinant.

What about land plants? Land plants exhibit the order thr tRNA-S4, which is identical to *Cyanophora* and *Mesostigma*. Therefore, these land plants must have diverged prior to the gene transposition. There are three possible phylogenetic positionsfor land plants, as shown arrows in Fig. 5. The following gene arrangement can uniquely determine the phylogenetic position.

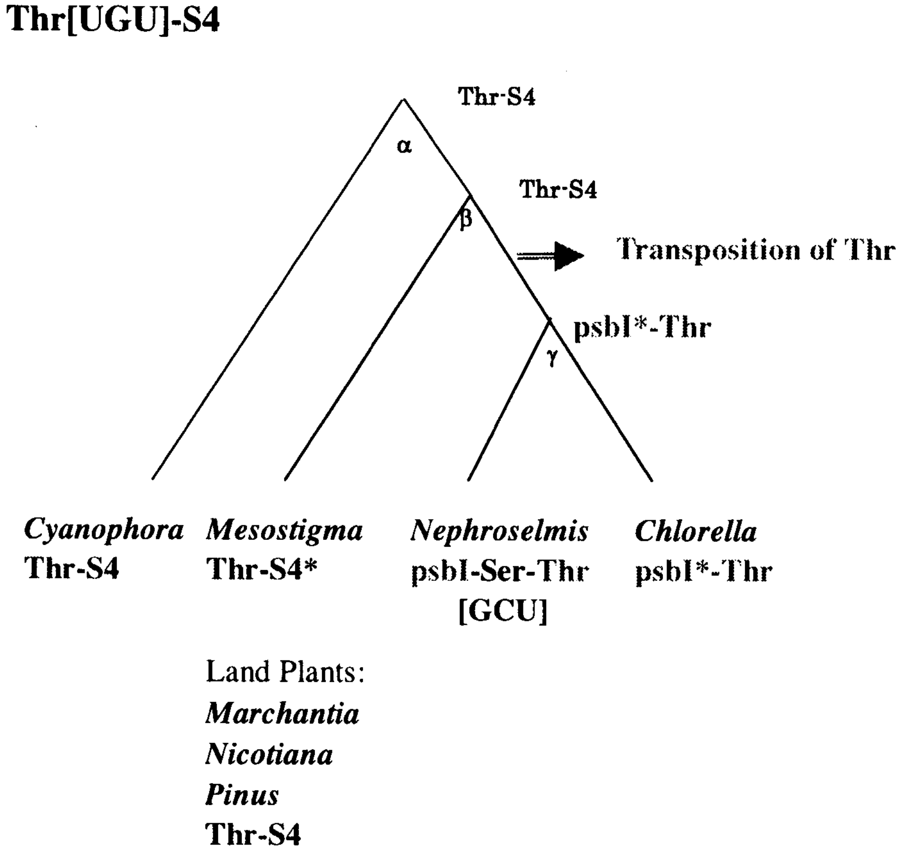

Fig. 5. A most likely rooted tree

In *Cyanophora* and *Mesostigma* psaI gene is adjacent to psbJ gene, while the psaI is linked to another gene accD in *Nephroselmis* and *Chlorella*. Following a similar argument developed in Fig. 4, we can construct a phylogenetic tree (Fig. 6). At somewhere between the two nodes β and γ, psaI must have been transposed to the vicinity of accD. Land plants have accD-psaI cluster. Therefore, the divergence of land plants must have occurred after the transposition of psaI in this case. Combining the preceding and present analyses, the evolutionary emergence of land plants is inferred to have occurred between the two gene transpositions. Thus, *Mesostigma* is likely to have diverged before the split between the chlophyta (*Nephroselmis* and *Chlorella*) and streptophyta (land plants).

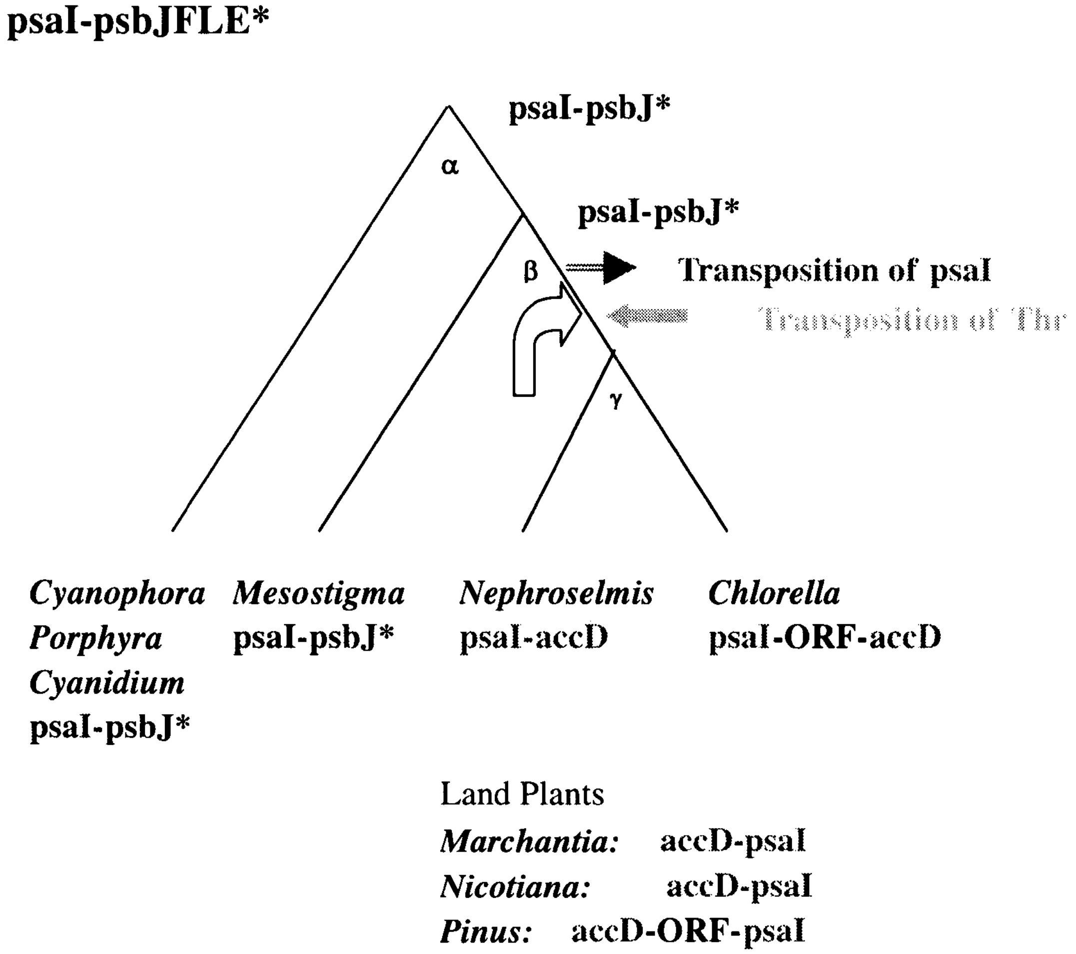

Fig. 6. Relative branch orders among green algae and land plants. The divergence of land plants is determined to have occurred between the two transpositional events (a large open arrow).

Lemieux et al. (2000) concatenated amino acid sequences of 53 plastid proteins. They carried out Maximum Likelihood analysis, and proposed a preferred tree. Their topology is identical to ours. In this case, sequence analysis and gene order comparison agree on the phylogeny of green plant plastids. So the present tree is highly reliable.

Discussion

Reconstructed trees are sometimes misleading for the tree-reconstruction artifacts. In particular, the long branch attraction artifact, which erroneously combines fast evolving species, is a troublesome problem. In the present analysis, trees are constructed on the basis of parsimonious considerations, and there is no room for the long branch attraction artifact. In clarifying gene rearrangements, we assumed that there are no parallel nor back-and-forth gene transpositions. The validity of this assumption can be assessed by comparing gene orders of closely related genomes. Such parallel and revert transpositions will perturb conservation of gene order among closely related genomes. We may anticipate that further study of the relative arrangements of the plastid genes will help to clarify ancient evolutionary relationships among plastid genomes.

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Genetic Diversity, Geographic Differentiation and Artificial Disturbance of the Japanese Firefly, *Luciola Cruciata* (Coleoptera, Lampyridae)

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Abstracts

Firefly is occasionally used as a symbolic animal for natural conservation and reconstruction in Japan. However, the Japanese aquatic firefly, *Luciola cruciata*, is easily introduced to other places for tourist attraction, firefly festival, and environmental education. Therefore, there is a possibility to disturb natural distribution of this species. On the other hand, geographic differentiation has been revealed by mitochondrial cytochrome oxidase II (CO II) gene analysis, and further six haplotype-groups indigenous to local areas have been recognized. According to the distribution map of the haplotype-groups, haplotypes of CO II gene were surveyed to assess artificial disturbance in 20 populations of Tokyo Prefecture. As a result, heterogeneous haplotypes in the different haplotype-groups were found in some populations, and permeation of artificial disturbance was confirmed in mitochondrial DNA level. Based on the result, we propose some policies for natural reconstruction program in firefly. 1) To forbid transplantation of fireflies from other places on the biogeographical basis, 2) to protect original colony before transplantation, even if transplantation is required, and 3) if transplantation is required in the case of extinction of the original colony, fireflies from the nearest river system must be transplanted.

Key Words:* *firefly, Lampyridae, mitochondrial CO II, genetic diversity, artificial disturbance

Introduction

Firefly is occasionally used as a symbolic animal for natural conservation and reconstruction in Japan, because of the beautiful light view displayed by the insect. However, fireflies are easily introduced to other places for tourist attraction, firefly festival, environmental education, and /or personal enjoyment (Watase, 1902; Kanda, 1935; Minami, 1961). In particular, introduction is conspicuous in the Japanese aquatic firefly, *Luciola cruciata*, even though ecological two types have been recognized in their flashing behavior. Namely, *L. cruciata* is distributed in major three islands of Japan, Honshu, Shikoku, and Kyushu, and it has been known that interflash interval of mate-seeking males in the east area is about 4 sec, while that of the west area is about 2 sec (Kanda, 1935; Ohba, 1984). The boundary between the two ecological types nearly corresponds to a great rupture zone called the Fossa Magna which lies from north to south and divides the Honshu into its east and west areas (Ohba, 1984; 1988). Furthermore, genetic differentiation between the two types was also reconfirmed by allozyme analysis (Suzuki *et al.*, 1996; Suzuki, 1997). As we can recognize such ecological types differentiated genetically, there is a possibility that genetic disturbance occurs in this species.

Quite recently, Suzuki *et al.* (2001) analyzed restriction fragment length polymorphism (RFLP) of mitochondrial cytochrome oxidase II (CO II) gene in this species and detected 19 haplotypes (A to S). Based on the nucleotide sequences comparison of the haplotypes, six haplotype-groups (I to VI) were recognized, and their distribution was indigenous to local areas (Fig. 1). Namely, Group I (containing A and D haplotypes) locates in North Honshu area, Group II (B and C) in Kanto to North Chûbu area, Group III (F and G) in Chûbu to Tôkai area, Group IV (E, H, I, and J) in West Japan area, Group V (K, L, M, N, O, and S) in North Kyushu area, and Group VI (P, Q, and R) in South Kyushu area. But the boundary between Groups III and IV is overlapping around Tôkai area. According to the distribution map of the haplotype-groups, haplotypes of CO II gene were surveyed to assess artificial disturbance in 20 populations of Tokyo Prefecture in the Kanto district.

Materials and Methods

Materials

Luciola cruciata fireflies from 20 populations in Tokyo Prefecture were surveyed. Localities of the materials are listed in Table 1, and their locations are also shown in Fig. 1.

Table 1. Haplotypes and their frequencies in the 20 populations in Tokyo prefecture

Population (No. of individuals)	Haplotype (frequency)
1. Sunniwa, Okutama (10)	E(0.90), F(0.10)
2. Kanoto, Hinohara (7)	C(0.72), E(0.14), F(0.14)
3. Senzoku, Hinohara (10)	E(0.90), F(0.10)
4. Nariki, Oume (8)	C(0.75), E(0.25)
5. Irino, Akiruno (8)	C(1.00)
6. Yokosawa, Akiruno (11)	C(0.50), E(0.50)
7. Sugao, Akiruno (7)	C(0.57), E(0.43)
8. Takatsuki, Hachioji (10)	C(1.00)
9. Moto-hachioji, Hachioji (10)	E(1.00)
10. Tangi, Hachioji (4)	F(1.00)
11. Yarimizu, Hachioji (10)	C(0.10), E(0.90)
12. Shimoyugi, Hachioji (2)	C(1.00)
13. Minami-ohsawa, Hachioji (1)	E(1.00)
14. Mogusa, Hino (4)	C(0.50), E(0.50)
15. Onoji, Machida (3)	C(1.00)
16. Sakahama, Inagi (6)	C(1.00)
17. Tamagawa-jyôsui, Kodaira (3)	C(1.00)
18. Ogawa, Kodaira (10)	E(1.00)
19. Kojima, Chofu (9)	E(0.44), F(0.56)
20. Kugayama, Suginami (10)	E(1.00)

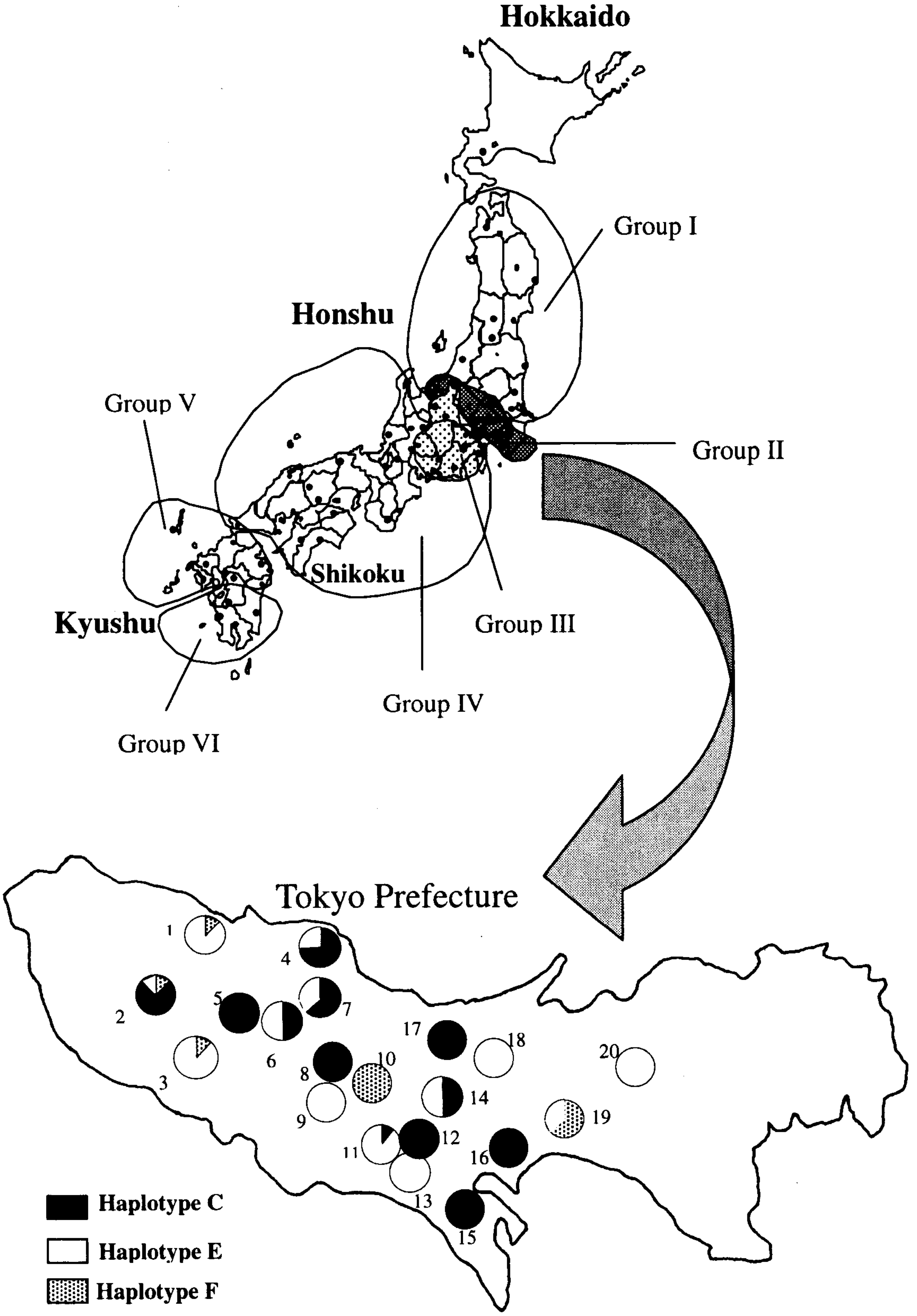

Fig. 1. Distribution map of the CO II gene haplotype-groups of *Luciola cruciata* in Japan (above), and haplotype distribution pattern in Tokyo (below). Circle graphs indicate the percentages of the haplotypes, C, E, and F, at the localities.

Polymerase chain reaction (PCR)

Mitochondrial CO II gene was amplified by means of PCR using a primer set designed in tRNA coding regions of leucine and lysine. Nucleotide sequences of the primers cited from Simon *et al.* (1994) are 5'-ATGGCAGATTAGTGCAATGG (TL2-J-3037) and 5'-GTTTAAGAGACCAGTACTTG (TK-N-3785). PCR amplification was carried out in 50□l reaction volumes containing 10 mM Tris-HCl (pH 8.3), 50 mM KCl, 2 mM $MgCl_2$, 0.1 % Triton X-100, 80 □M of each deoxynucleoside triphosphate, 80 nM of each primer, about 10 ng total DNA, and 2 U of rTaq DNA polymerase (Toyobo). Thirty cycles were performed by the following thermal-cycling parameters: DNA denaturation for 1 min at 94°C, primer annealing for 1 min at 50°C and DNA extension for 1 min at 72°C. Single-banded specificity of the PCR product was assessed by 1% agarose gel electrophoresis.

Restriction fragment length polymorphism (RFLP) analysis

Five microliters of the PCR product were digested with 2U of each restriction endonuclease (*Ase* I, *Hae* III, *Hinf* I, *Hpa* II, *Mva* I, and *Rsa* I) at 37°C for overnight incubation. The digestion fragments were separated in 4% polyacrylamide gel electrophoresis using 0.5X TBE buffer (45 mM Tris-borate, 1mM EDTA, pH 8.0). After electrophoresis, the gel was stained with ethidium bromide (0.1 □g/ml) and the DNA bands were visualized under UV light. Haplotypes (A to S) were determined by the electrophoretic patterns of the digestion products according to the nomenclature of Suzuki *et al.* (2001).

Results and Discussion

Haplotypes and their frequencies in the 20 populations are summarized in Table 1. Totally, 3 haplotypes, C, E, and F belonging to the different haplotype-groups, II, IV, and III, respectively, were observed, even though Tokyo is located in Group II area. However, there are no geographical associations of the haplotype distribution pattern (Fig. 1).

It has been known that fireflies in the six populations, Sunniwa (site No. 1), Moto-hachioji (9), Tangi (10), Ogawa (18), Kojima (19), and Kugayama (20), were transplanted artificially, and haplotypes of them were E and F. The origins of Ogawa, Kojima, and Kugayama populations are in the distribution area of Group IV, but those of other populations are unknown.

In the Sugao (7) population, two haplotypes, C and E were observed. It is known that fireflies of this population were transplanted artificially from group IV area. Therefore, coexistence of the heterogeneous haplotypes found in the different haplotype-groups is considered a consequence of the artificial transplantation.

In other 13 populations, three haplotypes, C, E, and F were found. E was in Minami-ohsawa (13), E and F in Senzoku (3), C, E, and F in Kanoto (2), and C and E in Nariki (4), Yokosawa (6), Yarimizu (11), and Mogusa (4) populations. But it is unknown whether artificial transplantation has been done or not in these populations. On the other hand, haplotype C was fixed in the Irino (5), Takatsuki (8), Shimoyugi (12), Onoji (15), Sakahama (16), and Tamagawa-jyôsui (17) populations, although sample sizes are not so enough.

According to the distribution map of the haplotype-groups, heterogeneous haplotypes from the different haplotype-groups are observed in Tokyo Prefecture and permeation of artificial disturbance in this area is confirmed in mitochondrial DNA level (Fig. 1). The artificial transplantation disturbs ecosystem formed by the evolutionary history such as distribution pattern of the haplotype-group in the species. However, it has been done involuntarily by peoples for natural reconstruction. Therefore, natural reconstruction program based on biogeographic and genetic background is urgently needed, and we consider that the genetic diversity studies within and among populations and data library of the haplotype-groups would contribute to drafting the program.

Recently, many problems of biological invasion, e.g. extinction of native species by ecological competitor and genetic disturbance among closely related species, arise in Japan (Nakamura, 1990). Also in firefly fauna, *L. cruciata* is found in Hokkaido, although Hokkaido is not a native distribution area (Environmental Agency (ed.), 1992). Further, in the Ryukyu Islands, *L. owadai*, the most closely related species to *L. cruciata*, is distributed only in Kume-jima Island. However, *L. cruciata* was also found in Kume-jima Island in 1999. These are marked cases in artificial introduction. In order to promote natural reconstruction programs, we will propose some policies based on the genetic diversity study, especially for firefly that: 1) To forbid transplantation of fireflies from other places on the biogeographical basis, 2) to protect original colony before transplantation, even if transplantation is required, and 3) if transplantation is required in the case of extinction of the original colony, fireflies from the nearest river system must be transplanted.

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Systematic Botanists and International Collaborative Projects

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Abstract

Systematic biologists have a laudable tradition of working over the full geographic range of their study group, no matter whether that coincides with political boundaries or not. They also have a history of collaborating with other biologists, and it is those networks that the Global Taxonomy Initiative needs to understand and use. This collaborative spirit is nowhere more evident than in the many recent Floras and plant-species database projects involving a wide range of botanists. Examples include *Flora Malesiana*, *Flora of China*, *Flora Mesoamericana*, *Flora of Australia*, and databases for particular plant groups (e.g. legumes, cycads and grasses). Access to the products of such projects is helped by initiatives such as the *Global Plant Checklist* database and the *Species Plantarum Project*, both projects of the International Organization for Plant Information (IOPI), that aim to bring all these sources of information together, with a broad global network of collaborators to coordinate the editing of each plant family for the database and World Flora respectively. Electronic access to data assembled in these and other projects will be facilitated by the *Species 2000* initiative, which will also tap into the worldwide systematic resources to validate and maintain the data. Production of Floras and species databases, and collaboration generally amongst systematic botanists has been aided greatly by useful compilations relating to resources and sources of information, e.g. *Taxonomic Literature Edition 2*, *Index Kewensis*, the *Index Nominum Genericorum* and *Index Herbariorum*. Many of these tools are also being made available in electronic form. New electronic tools have sprung up as well, particularly dynamic, self-subscribing Internet lists of workers and institutions. This broad acceptance of the benefits of collaborating internationally and of using electronic resources for Flora and database projects puts plant systematists in a good position to tackle the botanical problems outlined in the Global Taxonomy Initiative, provided adequate funding and resources are available.

Key Words: Systematic botany, Floras, Global Taxonomy Initiative, Species databases

Introduction

Biologists have a laudable tradition of working over the full geographic range of their study group, no matter whether that coincides with political boundaries or not. They also have a history of collaborating with other biologists, and it is those networks that the Global Taxonomy Initiative needs to understand and use.

This collaborative spirit is nowhere more evident than in the many recent Floras and plant-species database projects involving many botanists, examples of which are listed in Tables 1 and 2. It is, of course, not just a desire to collaborate that makes this arrangement popular. This is the only practical way to cover thoroughly the wide range of taxa found around the world because there are so few systematists, either professional or amateur. No organisation employs enough systematists to have a thorough cover of all species in their particular region. What I have to say applies particularly to botanists working on green plants, but I touch on algae and fungi (particularly lichens) because these groups have been traditionally treated as plants, and are still covered by the International Code of Botanical Nomenclature.

Recent estimates (DIVERSITAS 2000) are that there are about 300,000 species of vascular plants (flowering plants, cycads, conifers, ferns and allies) in the world and 20,000 bryophyte species (mosses, liverworts and hornworts), of which 10–15% remain undescribed. Algae number at least 235,000 species, of which at least 80% are still undescribed, while fungi include at least 1.4 million species, of which a frightening 95% are undescribed. Even more frightening is that there are only about 300 systematic phycologists and 500 systematic mycologists working on these groups! And these figures do not take into account that many of these workers are middle-aged or working in their retirement! Even for the much-better known green plants, where there are an estimated 3,000 systematists, there are similar problems with an aging population of workers. These figures highlight one of the problems in coming to grips with the world's biodiversity – the so-called Taxonomic Impediment – which is a stimulus behind the surge in international cooperative projects in the last few decades.

Table 1. Examples of recent and continuing international collaborative Flora projects (most Floras are hard-copy only, but checklists are increasingly available on websites)

Project	Region covered (or to be covered when completed)	Coordinators and Collaborators (by country)
Euro+Med Checklist	European and Mediterranean regions, previously covered by *Flora Europaea, MedChecklist* and more than 100 Floras covering different parts of these regions	European countries
Flora Iberica http://www.rjb.csic.es/floraiberica/principa.htm	Iberian Peninsula	Spain, plus specialists elsewhere
Flora of North America http://www.fna.org	Canada and USA	Canada and USA, plus specialists elsewhere
Flora Mesoamericana http://www.mobot.org/MOBOT/fm/intro.html	Southern Mexico and the countries of Central America	Mexico, UK and USA, plus specialists elsewhere
Flora Neotropica http://www.nybg.org/bsci/ofn/	Monographic; tropical Central and South America	Coordinators in Argentina, Brazil, Denmark, Germany, Switzerland, UK and USA, plus specialists elsewhere
Biodiversity of the Guianas http://www.mnh.si.edu/biodiversity/bdg/ (has been expanded to cover all biota)	Guyana, Surinam and French Guiana	Coordinators in USA and Guyana, plus specialists elsewhere
Checklist of the Guianas http://www.mnh.si.edu/biodiversity/bdg/checklst.html	Guyana, Surinam and French Guiana	French Guiana and USA
Flora of Ecuador http://www.systbot.gu.se/research/floec/floec.html	Ecuador	Ecuador, Denmark and Sweden, plus specialists elsewhere
Catalogue of Vascular Plants of Ecuador http://www.mobot.org/MOBOT/research/ecuador/welcome.htm	Ecuador	Ecuador, Denmark and USA
Flora of Chile http://www.mobot.org/MOBOT/Research/chile/chile.html	Chile	Chile, Germany and USA, plus specialists elsewhere
Flore de la Nouvelle-Calédonie	New Caledonia	France and New Caledonia, plus specialists elsewhere

Flora of Australia http://www.anbg.gov.au/abrs/flora/index.htm	Australia + its island territories	Australia, plus specialists elsewhere
Algae of Australia http://155.187.10.12/abrs/flora/algaust/index.htm	Australia	Australia, plus specialists elsewhere
Australian Plant Name Index (hard-copy and database) http://www.anbg.gov.au/cpbr/databases/apni-introduction.html	Australia	Australia, plus specialists elsewhere
Flora Malesiana and associated database http://nhncml.leidenuniv.nl/rhb/malesia.htm#flora malesiana	Malesia (Malaysia, Brunei, Singapore, Indonesia, Philippines, Papua New Guinea)	Indonesia, Netherlands, Malaysia, Philippines, plus specialists elsewhere
Flora of the Philippines http://www.pnh.com.ph/	Philippines	Philippines, Indonesia, Malaysia, Netherlands, UK and USA, plus specialists elsewhere
Flora of China and associated database http://flora.huh.harvard.edu/china/	China	China, USA and UK, plus specialists elsewhere
Moss Flora of China http://www.mobot.org./MOBOT/moss/China/chprojec.html	China	China and USA, plus specialists elsewhere
Flora of Thailand http://herb132.bio.au.dk/SysBot/home/index.htm	Thailand	Thailand and Denmark, plus specialists elsewhere
Plant information and technology transfer for Nepal http://www.nhm.ac.uk/botany/nepal/index.html	Nepal	Nepal and UK
Flora of Ceylon http://infolanka.com/flora/	Sri Lanka	Sri Lanka, USA, UK, plus specialists elsewhere
Flore des Mascareignes	Mascarenes	Mauritius, France, and UK
Conspectus of the Vascular Plants of Madagascar database http://www.mnhn.fr/mnhn/pha/Recherch.htm; http://www.mobot.org./MOBOT/Madagasc/welcome.html	Madagascar	Madagascar, France and USA
Flora of Tropical East Africa http://www.rbgkew.org.uk/herbarium/ftea/fteaindx.html	Tropical East Africa	UK, Kenya, and Tanzania, plus specialists elsewhere
IOPI Species Plantarum Project http://www.anbg.gov.au/abrs/flora/spplant/spplant.htm	Global coverage	Coordinators in UK, Australia, Spain, USA, South Africa, with a worldwide network of specialists

Table 2. Major examples of international collaborative plant-species database projects

Project	Region covered (or to be covered when completed)	Coordinators and Collaborators (by country)
International Legume Database and Information Service (ILDIS) http://www.ildis.org/	Global coverage	Editors in UK, USA and Russia, with a worldwide network of collaborators
Cycad List http://plantnet.rbgsyd.gov.au/PlantNet/cycad/index.html	Global coverage	Editors in Australia and USA, plus collaborators elsewhere
Catalog of New World Grasses http://nmnhwww.si.edu:80/botany/projects/grass/nwgrass.html	North, Central and South America	Argentina, Brazil, USA, plus specialists elsewhere
IOPI Global Plant Checklist http://bgbm3.bgbm.fu-berlin.de/iopi/gpc/	Global coverage	Coordinators in Australia, Germany, USA, France, UK, Mexico, with a worldwide network of specialists

Flora Projects

Floras were firstly written as individual projects in the 19th century (e.g. Bentham 1863–1878 and Franchet and Savatier1873–1879), when so little was known about a region's plants that this approach was feasible. However, Floras have for many years now usually involved the staff of one main botanical institution (in the region covered by the Flora) with additional contributions from other systematists (or taxonomists – I use the term interchangeably here) specialising in particular families who may belong to many organisations both within that region and elsewhere. This collaborative approach has increased markedly (Table 1) in the last few decades as systematists have come to realise the advantages of collaborating.

Australia provides good examples of the changing approach: from a one- or two-author Flora for a particular region (e.g. Bentham (1863–1878) for Australia, Willis (1962, 1972) for Victoria, Burbidge and Gray (1970) for the Australian Capital Territory), to regional Floras initiated by a single regional organisation but with input by specialists for some families (e.g. Jessop and Toelken (1986) for South Australia, Harden (1990–1993) for New South Wales), and finally to the national *Flora of Australia* project, coordinated by the Australian Biological Resources Study (ABRS) in Canberra but with treatments contributed by specialists throughout Australia and overseas, as described by George et al. (1999). The *Algae of Australia* and the *Fungi of Australia* (http://155.187.10.12/abrs/flora/fungaust/index.htm) are major new initiatives for ABRS, as sister series to the *Flora of Australia*. Together, these three series will describe all the indigenous and naturalised organisms treated as plants by the International Code of Botanical Nomenclature. For historical reasons, lichens will continue to be described in the Flora of Australia. This is a broader scope than for most other Flora projects, which commonly only include flowering plants or vascular plants, sometimes extending to pteridophytes, bryophytes and even charophytes (e.g. the Flora of Southern Africa – see appendix in Leistner (1999)).

Examples of Floras from other parts of the world include the pioneering *Flora Malesiana*, coordinated in Indonesia and the Netherlands but with contributions from specialists in many parts of the world, and the more recent English-language *Flora of China* (coordinated in China, the USA and the UK). Other examples are listed in Table 1. Amongst such projects, *Flora*

Europaea stands out as one that has been completed (at least to the stage of a first edition in five volumes, and revision of the first volume (Tutin 1993)). Most other projects are still incomplete, often making frustratingly slow progress because of lack of resources (both financial and human).

Most Floras are hard copy only, but checklists are increasingly available on websites. The increasing acceptance of electronic 'publication' is leading to re-consideration of appropriate ways to make plant information available. For example, several volumes of the *Flora Iberica* are now available on CD-ROM (http://www.rjb.csic.es/floraiberica/principa.htm) as well as in hard copy. The *Flora of New South Wales*, which was published as four volumes (Harden 1990–93), has since had new editions of the first two volumes but will in future probably only be updated electronically on the web (Tim Entwisle, pers. comm.). This electronic approach has advantages in terms of reducing publication costs, reducing time for publication, and increasing ease of updating. However, it is not universally accepted yet because of the problems many users face in getting adequate access to electronic data sources (including using Floras in the field), and unclear procedures for safely archiving electronic publications (see, for example, the electronic report by a working group of the American Association for the Advancement of Science, the International Council for Science and UNESCO on defining and certifying electronic publications in science at http://www.aaas.org/spp/dspp/sfrl/projects/epub/define.htm).

Global Species Databases

Compiling a checklist of species known to occur in a region has always been a first step to producing a Flora treatment for that region. Recently, of course, this compilation has been done electronically and increasingly these checklists have been made available on websites (Table 1 and websites listed therein). In addition, there has been a move in the last decade to go further and compile authoritative species databases for particular plant groups worldwide or over a large region by international cooperative efforts by specialists, for example, for legumes, cycads and grasses (Table 1). As pointed out in Froese and Bisby (2000), key features of complete global species databases are:

- They cover one taxon worldwide.
- They contain a taxonomic checklist of all species within that taxon.
- They deal with species as taxa, and contain synonymy and taxonomic opinion.
- They have an explicit mechanism for seeking at least one responsible / consensus taxonomy, and for applying it consistently.
- They cross-index significant alternative taxonomies in their synonymy.

The *Global Plant Checklist* database and the *Species Plantarum Project* are two projects of the International Organization for Plant Information (IOPI) that aim to bring together all these sources of systematic and geographic information on plant species, with a broad global network of collaborators to coordinate the editing of each plant family for the Checklist and Flora of the World, respectively. This specialist network is a key element in producing an up to date, authoritative list and, just as importantly, maintaining the quality of that list, as emphasized by several speakers at the seminal symposium 'Designs for a Global Plant Species Information System' held in Delphi in 1990 (Bisby et al. 1993) and by many others since then. Electronic access to data assembled in these and other projects will be facilitated by the *Species 2000* initiative, which will also tap into the worldwide systematic resources to validate the data. The advantage of these global species databases, of course, is that they are not an end in themselves: thanks to advances in information technology, they provide a way for all kinds of users to access electronically information of any kind about any of these organisms. These lists are the skeleton or backbone of what will be a vast, distributed electronic information system about all organisms, which is what the world needs to understand, conserve and manage its biodiversity.

Tools for Systematic Botanists

Production of Floras and species databases, and collaboration generally amongst systematic botanists has been aided greatly by various useful compilations relating to resources and sources of information, notably *Taxonomic Literature Edition 2* (Stafleu and Cowan 1976–1983), commonly known as 'TL-2'), *Index Kewensis* (compiled by the Royal Botanic Gardens Kew since the 1890s), the *Index Nominum Genericorum* (a collaborative project of the International Association for Plant Taxonomy (IAPT) and the Smithsonian Institution – see http://www.nmnh.si.edu/ing/ for details) and *Index Herbariorum* (currently maintained by New York Botanical Garden on behalf of the International Association for Plant Taxonomy). Another very useful compendium describes all known Flora treatments for all parts of the world (Frodin 1984).

Many of these tools have also been made available recently (or are being made available) in electronic form. *Index Kewensis,* for instance, is now on-line as the major global component of the *International Plant Name Index* (http://www.ipni.org). IPNI differs from the global species databases discussed above in being a list of published plant names rather than an edited list of taxa.

Some new electronic tools have sprung up as well, particularly dynamic, self-subscribing lists of workers and institutions. The *Plant Taxonomists Online* is one such list of workers, which can be found at http://www.unm.edu/~museum/herb/links.htm along with links to other useful indexes. Another useful on-line 'index to indexes' is the *Internet Directory for Botany* at http://www.botany.net/IDB/. The most comprehensive list of those working in IAPT-registered herbaria is the *Index Herbariorum*, available in hard cover or on the web from the New York Botanical Garden (http://www.nybg.org/bsci/ih/ih.html).This includes herbaria with collections of algae, lichens and fungi as well as 'true' plants, i.e. all organisms covered by the International Code of Botanical Nomenclature.

Regional lists are available covering systematists studying not just plants but all biota, such as:

- the *Australian Biological Resources Study Directory* (accessible along with other useful indexes at http://www.environment.gov.au/abrs/ABRS-Directory.html)
- the *Biodiversity Information Network - Brazil* (BINbr; accessible along with other useful indexes through the Base de Dados Tropical, Campinas - http://www.bdt.org.br/databases).
- the *Taxonomic Resources and Expertise Database* (TRED; http://www.nbii.gov/datainfo/syscollect/tred/) covering taxonomic specialists in all biota of the USA and Canada; its companion database, the *Directory of Research Systematics Collections* (DRSC; http://www.nbii.gov/datainfo/syscollect/drsc/index.html), covers natural history collections in the region.

In addition, the Expert Center for Taxonomic Identification in the Netherlands has set up a register for all biologists (the *World Taxonomist Database* at http://www.eti.uva.nl/database/WTD.html). As with the other lists of systematists mentioned above (except for *Index Herbariorum*), coverage is patchy because it is left to individual systematists to register themselves.

Conclusion

As outlined above, systematic botanists have widely accepted the benefits of collaborating internationally and of using electronic resources for Flora and database projects and for tools useful for these projects. This puts these systematists in a good position to tackle the botanical problems outlined in the Global Taxonomy Initiative, as long as adequate funding and support is provided.

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Public Domain Image Databases for Taxonomic Research and Education: A Case Study, Protist Image Database

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Abstract

DNA databases compiling research resources (i.e., sequence data) are now indispensable for genome sciences. Accordingly, databasing vast amount of taxonomic resources, most of which are specimen's images and relevant descriptions, is highly promising for taxonomic research and education.

But, in contrast to the DNA databases, it is almost impossible to centralize varied taxonomic resources into a few databases. Thus, taxonomy databases will grow as a distributed public domain database (Green, 1994), where each database should be maintained as a "volunteer database" by individual researchers.

Protist image database have been constructed as such volunteer database aimed to provide protist images and other related information as research and educational resources via the Internet. Currently more than 18,000 images and their taxonomic descriptions covering 401 genera and 1398 species can be used by downloading from our web site (URL: http://protist.i.hosei.ac.jp/Protist_menuE.html). In addition, we have been consulting or assisting other volunteer databases on taxonomy of various organisms.

In the course of these activities, we found that the Internet lacks both quality-control and preservation systems essential for scholarly communication. To establish volunteer databases as academic resources, they must be qualified and preserved by public organizations just like journals stored in public libraries.

Keywords: distributed public domain database, volunteer database, biological images, taxonomy, protists,

Introduction

Biology, especially taxonomy, relies on activity of compiling a large amount of observational experiences, most of which should be recorded as images (photo copies or drawings). However, only a small part of those images have been published on academic journals due to page limitation, and the remainings have been unused and finally scrapped after retirement of researchers. If such images (and their relevant descriptions) were databased and opened for public uses on the Internet, those databases will promote biological, especially taxonomic research and education just like present-day DNA databases.

But, in contrast to the DNA databases, it must be impossible to centralize such large amount of images with various sizes and formats into a few databases. Thus, the biological image databases will inevitably grow as a distributed public domain database (Green, 1994), where each database should be maintained as a "volunteer database" by individual researchers.

Needs for image databases in protist taxonomy

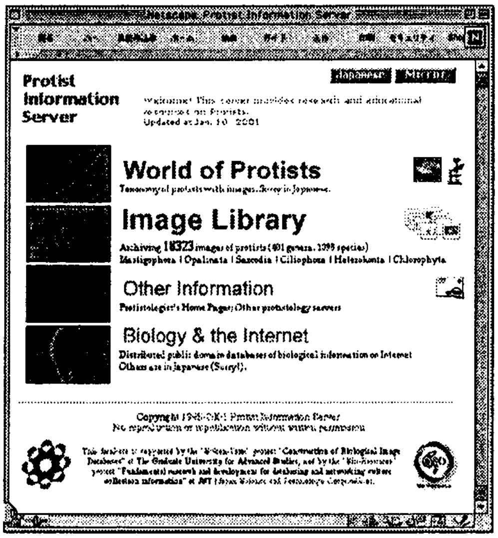
We have been constructing "protist image database" as one of those volunteer databases since 1995 (Fig.1, URL: http://protist.i.hosei.ac.jp/Protist_menuE.html). After publicizing our databases on the Internet, we found that image databases will play an important role for protist taxonomy. Because, as many protist species lack "type specimens" due to the difficulties of their preservation, protist taxonomy have mostly relied on drawings and their descriptions, causing confusions or inefficiency of species identification. In this situation, databases compiling images of many protists will partly, if not all, compensate the lack of type specimens by helping identification of species and serving as resources for taxonomic research in this group.

Furthermore, many protist species are cosmopolitan, i.e., their distributions are worldwide. This means that many species will be found in samples collected even at small local area. Therefore, to identify protist species, we must always carry a large taxonomy guidebook describing all known species of protists, though it is actually impossible.

Thus, databasing protist images and their taxonomic descriptions and publicizing such databases through the Internet will help people who want to know the species name of protists as well as protist taxonomists themselves.

Basic features of Protist image database

Protist image database was originally aimed to collect images (photo copies) and other



Protist Information Server

Welcome! This server provides research and educational resources on Protists.
Updated at Jan. 10 2001

World of Protists

Taxonomy of protists with images. Sorry in Japanese.

Image Library

Archiving 18323 images of protists (401 genera, 1398 species)
Mastigophora | Opalinata | Sarcodina | Ciliophora | Heterokonta | Chlorophyta

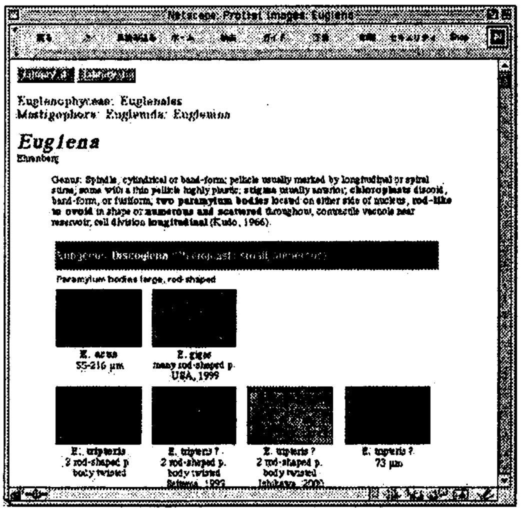
Other Information

Protistologist's Home Pages; Other protistology servers

Biology & the Internet

Distributed public domain databases of biological information on Internet
Others are in Japanese (Sorry!).

Fig. 1 Protist Image Database, English menu
URL; http://protist.i.hosei.ac.jp/Protist_menuE.html



Euglenophyceae: Euglenales
Mastigophora: Euglenida: Euglenina

Euglena
Ehrenberg

Genus: Spindle, cylindrical or band-form; pellicle usually marked by longitudinal or spiral striae; some with a thin pellicle highly plastic; stigma usually anterior; chloroplasts discoid, band-form, or fusiform; two paramylum bodies located on either side of nucleus, rod-like to ovoid in shape or numerous and scattered throughout; contractile vacuole near reservoir; cell division longitudinal (Kudo, 1966).

Paramylum bodies large, rod-shaped

E. acus
55-216 µm

E. gigas
many rod-shaped p.
USA, 1999

E. tripteris
3 rod-shaped p
body twisted

E. tripteris ?
2 rod-shaped p.
body twisted
Saitama, 1993

E. tripteris ?
2 rod-shaped p.
body twisted
Ishikawa, 2001

E. tripteris ?
73 µm

Fig. 2 A sample of "genus" webpages
In this webpage, names of species belonging to a genus, *Euglena* are listed with their representative thumbnail images.

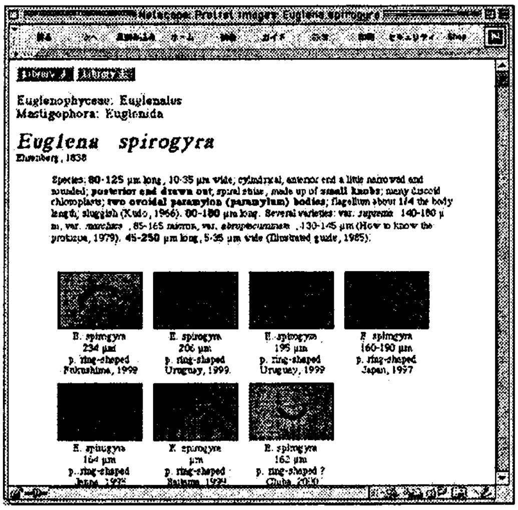
research resources which have been kept and unused by us and other researchers (mostly protozoologists). Thus, our database firstly became consisting of images of a limited number of species which are used in laboratories, such as *Paramecium* or *Amoeba*.

However, after publicizing the database we found most users are not protistologists but researchers in other fields or non-researchers, i.e., school teachers or people working at Water Service or at companies concerning environmental assessment, and so on, and they all want to know basic taxonomy of protists.

Therefore, we have shifted the main purpose of our database from collecting mere research resources to compiling resources on protist taxonomy (i.e., images of many protists collected from field and their relevant descriptions from many references). At present, more than 18,000 images and their taxonomical descriptions covering 401 genera and 1398 species can be used by downloading from our web site.

All images are basically presented by each cell (specimen) and classified according to taxonomic order (species, genus, family, etc.). For example, in a "genus" webpage, names of species belonging to the genus are listed with their thumbnail images (Fig. 2), where the species names are linked to each "species" webpage. In the "species" webpage, thumbnails of specimens belonging to the species are listed (Fig. 3), which finally lead to basic "specimen" webpages containing many images of each specimen (Fig. 4).

In our database, images are mostly digitized from 35 mm reversal films using PhotoCD service. Each image consists of five graphical files (JPEG files) with different magnifications, i.e., thumbnail-image files of 96 x 64 pixels, and its enlarged-image files of 192 x 128, 384 x 256, 768 x 512, and 1536 x 1024 pixels. The smaller files are provided for observing images on the monitor which has low resolution (usually 72 dpi) and the larger ones for printing which



Euglenophyceae: Euglenales
Mastigophora: Euglenida

Euglena spirogyra
Ehrenberg, 1838

Species: **80-125** µm long, 10-35 µm wide; cylindrical, anterior end a little narrowed and rounded; **posterior end drawn out**; *spiral striae, made up of* **small knobs**; many discoid chloroplasts; **two ovoidal paramylon (paramylum) bodies**; flagellum about 1/4 the body length; sluggish (Kudo, 1966). **80-180** µm long. Several varieties: var. *suprema* 140-180 µm, var. *marchica* , 85-165 micron, var. *abruptacuminata* , 130-145 µm (How to know the protozoa, 1979). **45-250** µm long, 5-35 µm wide (Illustrated guide, 1985).

E. spirogyra
234 µm
p. ring-shaped
Fukushima, 1999

E. spirogyra
206 µm
p. ring-shaped
Uruguay, 1999

E. spirogyra
195 µm
p. ring-shaped
Uruguay, 1999

E. spirogyra
160-190 µm
p. ring-shaped
Japan, 1997

E. spirogyra
164 µm
p. ring-shaped
Japan, [illegible]

E. spirogyra
µm
p. ring-shaped
Saitama, [illegible]

E. spirogyra
162 µm
p. ring-shaped ?
Chiba, 2000

Fig. 3 A sample of "species" webpages
In this webpage, specimens belonging to a species, *Euglena spirogyra*, are listed with their thumbnail images. Species names under the thumbnails are linked to each speciemen's webpage (Fig. 4).

Euglenophyceae:
Euglenales
Mastigophora: Euglenida

Euglena spirogyra
Ehrenberg, 1838

Species: **80-125** µm long, 10-35 µm wide; cylindrical; anterior end a little narrowed and rounded, **posterior end drawn out**; *spiral striae, made up of* **small knobs**; many discoid chloroplasts; **two ovoidal paramylon (paramylum) bodies**, flagellum about 1/4 the body length; sluggish (Kudo, 1966). **80-180** µm long. Several varieties: var. *suprema* 140-180 µm, var. *marchica* , 85-165 micron, var. *abruptacuminata* , 130-145 µm (How to know the protozoa, 1979). 45-250 µm long, 5-35 µm wide (Illustrated guide, 1985).

Euglena spirogyra , large paramylon grains, 234 µm long, µm wide, posterior end drawn out, sluggish, 2 oval paramylon rings, x 400, x 640, Oct. 1999, Shirakawa, Fukushima Pref., collected by H. Shimizu, photo by Y. Tsukii.

Fig. 4 A sample of "specimen" webpages
By clicking on thumbnail images listed, users can select four types of images with different magnifications (see Fig. 5)

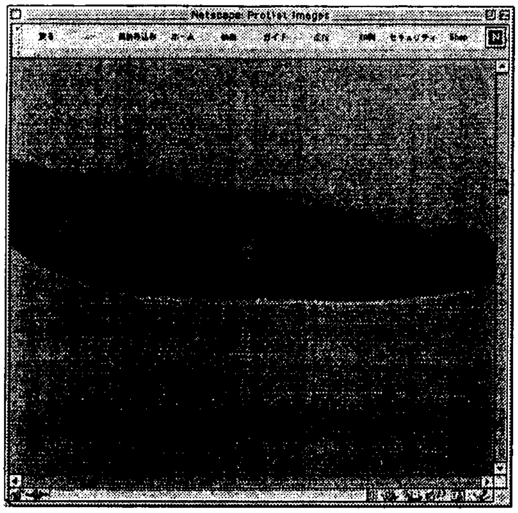


Fig. 5 A webpage showing an enlarged image of *Euglena spirogyra*
This image is in size of 768 x 512 pixels. By clicking thumbnail images, users can select other images of different sizes, 192 x 128, 384 x 256, and 1536 x 1024 pixels

usually require higher resolutions (300 or 600 dpi or more) (Fig. 5). These sets of image files with various magnifications will be a essential requisite for academic resource databases.

Our database presently consists of totally about 110,000 files (90,000 graphical files and 20,000 text files in html format), which occupy about 3.2 G bytes on our server machine.

Contributors and Collaborators

We are not only providing our own images through the Internet, but also accepting contributions of images from users who are working on protists (URL, http://protist.i.hosei.ac.jp/PDB/contributors_E.html). We are also welcoming other types of user's collaborations, i.e., comments or corrections on our webpages and help for identifying species name of images which have been unidentified by ourselves. These cooperations between database managers like us and its users will serve as quality-control system in volunteer databases.

How people are using our database

In addition to the user's contributions and collaborations mentioned above, we are accepting various requests or questions from users via e-mail (protist@i.hosei.ac.jp). Requests from users are for permission of use of images in their webpages or in printing (mostly textbooks or CD-ROM), or at poster presentations or in papers (e.g. master thesis). Others are requests for species identification or supplying various strains of protists or questions on culturing protists, etc.

On one hand, we have been distributing CD-ROMs copying a part of our database upon user's requests with no charge (in Japan only; version 1 was pressed 1,000 copies in 1995, version 2 pressed 5,000 copies in 1996 and version 3 pressed 10,000 copies in 1998). Our CD-ROM contains only one type of enlarged-image files (768 x 512 pixels) because of smaller capacity of CD-ROM (640 M bytes). However, as number of images increased, a single CD-

Table 1 The state of CD-ROM distribution

Group	No. of Users	No. of CD
Researchers at	263	1598
University	167	
Other Institutes	56	
Private Company	40	
Teachers at	168	4372
High school	I 98	
Middle school	40	
Primary school	9	
Others	20	
Company, etc.	46	105
Misc.	65	556
Undergraduate students	29	
High school students	5	
Others	31	
Unkowns	87	216
Total	629	6847

(2001.1.29)

On receipt of requests by e-mail, we asked user's occupations and for what purposes they want to use our CD-ROM.

ROM became insufficient to contain all images even if limited the enlarged-image files for only one type. So, we are now planing for the distribution of our database contents on DVD-ROM.

Our CD-ROM distribution service has various benefits for both researchers making databases and its users. For the researchers, as CD-ROM can be treated like printings in library, CD-ROM publishing would be a best choice for preserving database contents under present conditions that there is still no public organizations for preserving voluntary-delivered (or self-published) information, which will be discussed later. And then, it may lead to an evaluation for our databasing activity as scientific career. For users, as the databases containing many image files are tend to big size, off-line access using CD-ROM is better than on-line access through low-speed computer network.

Currently, our CD-ROM (version 3) has been distributed to more than 600 people, and the number of CD-ROM distributed reached about 7000 (Table 1). To save distribution costs, we are asking users to cooperate for secondary distribution, so that the 600 users helped us to distribute 7000 CD-ROMs to other users. Of the 7000 CD-ROMs, about 4400 CDs were distributed by 168 school teachers to their colleagues within their communities at prefecture- or city-level.

Consulting other volunteer databases

Beside constructing our own database, we have been consulting other volunteer databases (Tsukii et al., 1995). Since 1997, we have been working on a project, "Construction of Biological Image Databases" (or shortly "Soken-Taxa project", URL; http://taxa.soken.ac.jp/) at the Graduate University for Advanced Studies, where we are consulting or assisting construction of image databases on various organisms as follows:

1. Japanese Ant Color Image Database
   URL; http://taxa.soken.ac.jp/Ant.WWW/INDEXE.HTML
2. Marine Mammal Stranding Database
   URL; http://svrsh1.kahaku.go.jp/index.htm
3. Mammalian Crania Picture Archive
   URL; http://1kai.dokkyomed.ac.jp/mammal/en/mammal.html
4. Mouse Image Database
   URL; http://mouse.miyazaki-med.ac.jp:591/mouse1/
5. Morning Glories Database
   URL; http://taxa.soken.ac.jp/Asagao/Yoneda/menu.html
6. Makino Type Specimen Database
   URL; http://wwwmakino.shizen.metro-u.ac.jp/database.htm

Recently, many other volunteer image databases on taxonomy of various organisms are arising here in Japan.

Research on support systems for volunteer "bio-resource" databases

In addition to those consultations for other volunteer databases one by one, we are now developing more generalized supporting systems for databasing and publicizing biological research resources. Since 1997, we have joined another project, "Fundamental research and development for databasing and networking culture collection information" (shortly "Bio-Resource project", URL; http://bio.tokyo.jst.go.jp/index.htm) at JST (Japan Science and Technology Corporation).

In this project, we have developed various support systems for biologists to make databases by themselves, which are accessible through the Internet. Those systems are:

1) Optimized procedures for digitizing and assembling still images into a database; 2) Systems for making on-line movie databases, including optimization for the techniques of digitizing movies, methods for compression and decompression of the movies, and construction of the server for the movie databases, etc.; 3) A method for making WWW-browsable "digital image book" which will make easier to read rare but important books or papers.; 4) Editing manuals for the maintenance and the management of the databases, which will be published by printing and web pages (Tsukii & Kihara, 1999).

In the course of these activities, we gradually became aware of an important defect of the Internet with regard to scholarly communications, which make researchers to hesitate publicizing their own resources on the net. The defect is lack of public systems for qualifying and preserving information voluntary-delivered (or self-published) by researchers on the Internet.

Printing vs Internet

One of the basic features of academic information is that they are permanently preserved at public organizations such as university libraries. Before the Internet era, information produced by researchers was written on papers as manuscripts, and then submitted to journals, where the information was qualified by peer review system. After the qualification, the information was publicized worldwide via printing. Though most journals bought by individuals will be eventually lost, those bought by public institutions (e.g. university libraries) will be kept for long time to serve as references for researchers and others in future.

In other words, academic information publicized by printing have been in a well-established social system, i.e., 1) production of information by researchers, 2) their publicization (publication) by publishers after quality control, and 3) their preservation by librarians (Fig. 6).

On the other hand, the Internet as a "new media" is basically different from printing as a "mass media", that is, researchers, or actually anyone, can be both "producers" and "publishers" of their information through the Internet. This will promote information exchange not only within scientist community but also between scientists and other people. However, there is at present neither quality-control nor preservation systems for those information, except for genome sequences.

In case of genome sciences, all sequence data are centralized into a few computers and maintained by specialists, where the quality control is ensured by the cooperation between DNA database centers and journal publishers where researchers submit their papers analyzing their sequences. And the sequences data will be permanently preserved by the DNA database centers with government supports. This quality-control and preservation system for genome information functions like those of printing (journals), and evaluates sequencing works by genome researchers as their scientific career.

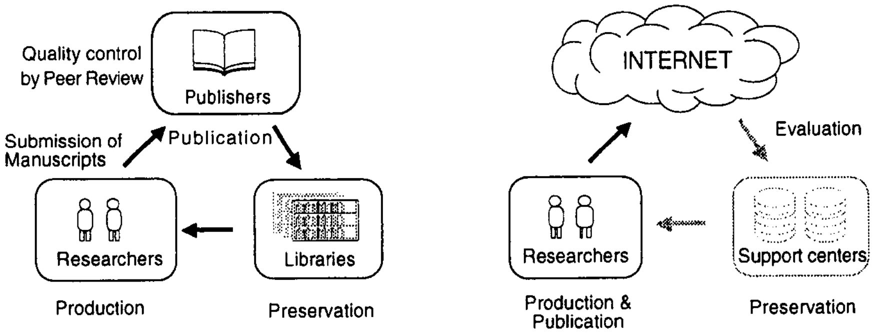


Fig. 6 Printing vs Internet
In printing, academic information is in a well-established system; production of the information by researchers, quality-control and publicization by journal publishers, and permanent preservation by university libirarians.
In contrast, in the Internet, researchers are able to not only produce but also publicize their information. But, there is still no public organizations ("Support centers" in this figure) for qualifying and preserving such information, so that information publicized on the net can not be at present used as academic resources.

Contrary, centralization of other biological resources such as images is actually impossible as already mentioned, and therefore, they should be databased and publicized on the Internet by researchers themselves. However, the Internet does not have systems for qualifying and preserving such voluntary-delivered information. This situation makes researchers unwilling to publicize their own resources via the Internet, because their works can not be evaluated as scientific career.

Public organization for quality-control and preservation of the voluntary-delivered biodiversity resources

To establish volunteer databases as academic resources, therefore, they must be qualified and permanently preserved by public organizations like journals stored in public libraries (Fig. 6). For example, databases or any other information publicized through the Internet by individuals or its groups (mostly researchers) can be qualified by a committee authorized by academic society or its alternatives. If they are qualified to have enough value as research and/or educational resources, the committee should issue "accession codes" for the database contents and, at the same time, the contents should be backuped by public organizations (e.g. "Support centers" in Fig. 6). When the original databases were updated, only the updated files should be added to the backup files by the centers. On this system, the "accession codes" can be used as references in papers similar to accession numbers in genome databases, and by checking the codes, users can access to the backuped contents even after the original databases (or web sites) disappeared from the net due to retirement of researchers or some other reasons.

These quality-control and preservation systems will be needed for all kinds of academic resources voluntary-delivered on the Internet. Establishing these systems are urgent especially in taxonomy where vast amount of biodiversity resources are demanded to be databased and opened for public uses.

Acknowledgements

Our research on databasing and publicizing of biological resources through the Internet is supported by the Bio-Resource project, "Fundamental research and development for databasing and networking culture collection information" (1997-2001) at JST (Japan Science and Technology Corporation) and by the Soken-Taxa project, "Construction of Biological Image Databases" (1997-1999) at The Graduate University for Advanced Studies. This work was also supported by a grant 07558052 (1995-1996) from the Ministry of Education, Culture, Sports, Science and Technology of Japan.

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Tsukii, Y., and Kihara, A (1999) Research on the support system for databasing bio-resource information., In: Proceeding of JST Symposium "*Fundamental research and development for databasing and networking culture collection information*", pp. 53-59, abstracts in English.

Appendix

July, 1999

Program

Oral Presentation

Date	Speaker	Organization	Country	Subject	time
14-Jul	**Opening Ceremony**				
	Chair: Hideyuki Shimizu (Japan)				
	Yohichi Gohshi	Center for Global Environmental Research, National Institute for Environmental Studies	Japan	Opening address	9:00- 9:10
	Hisao Shikano	Environmental Agency of Japanese Government	Japan	Biodiversity data and information accessible worldwide	9:10- 9:20
	Biological Diversitiy : Value of Information for 21st Century -DAY 1-				
	Plenary Lecture: Global Biodiversity and its Information				
	Makoto M. Watanabe	Species 2000, National Institute for Environmental Studies	Japan	Netwark approach to make biodiversity information accessible worldwide -As an example of microorganisms-	9:20- 9:40
	Frank A. Bisby	Species 2000 , University of Reading	UK	Species 2000: a global architecture for the Catalogue of Life	9:40-10:10
	Poster Display/*Coffee Break*				10:10-10:40
	Chairs: Hiroya Kawanabe (Japan) and Edgar F. Westrum Jr. (USA)				
	John Rumble Jr.	National Institute of Standards	USA	Developing Data and Database Standards in Science: Some challenges and how CODATA can help meet them.	10:40-11:00
	Motonori Hoshi	Tokyo Institute of Technology	Japan	Towards an Integratative Biology.-A new program for better understanding of living organizms-.	11:00-11:20
	Takuya Abe	Center for Ecological Research, Kyoto University	Japan	DIWPA activity and International Biodiversity Observation Year (IBOY)	11:20-11:40
	Haruo Katakura	Hokkaido University	Japan	The "GaiaList 21" Project	11:40-12:00
	Ebbe Nielsen	Australian National Insect Collection	Australia	The Global Biodiversity Information Facility (GBIF)	12:00-12:20
	Poster Session and Database Demonstration/*Lunch*				12:20-13:50
	Session 1:Distributed Nautre of Biodiversity Information				
	Chairs: Frank A.Bisby (UK) and Kwang-Tsao Shao (Taiwan)				
	Joan Thorne	Species 2000, BIOSIS UK	UK	Zoological Record -a bibliographic service and names resource	13:50-14:10
	Gary Waggoner	U.S. Geographical Survey	USA	The Integrated Taxonomic Information System (ITIS)	14:10-14:30
	Motomi Ito	Chiba University	Japan	Flora of Japan Database for Integrated Information of Japanese Native Vacular Plants	14:30-14:50
	Nicolas Bailly	Museum national d'historie naturelle	France	Systematic databases, taxonomic referentials, and validation of data in the museum national d'histoire naturelle, Paris,	14:50-15:10
	Satoru Miyazaki	WDCM	Japan	From Linking to Integration of Biological Databases	15:10-15:30
	Coffee Break				15:30-16:00
	Session 2:Accessibility of Catalogue of Names				
	Chairs: Karen Wilson (Australia) and Haruo Katakura (Japan)				
	Catalina Ranola	Species 2000, ICLARM	Philippines	Species 2000 Annual Checklist in CD-ROM	16:00-16:20
	Richard White	Species 2000, University of Southampton	UK	Species 2000 Dynamic Checklist with Added SPICE	16:20-16:40
	William Piel	Institute of Evolutionary and Ecological Sciences, Leiden University	Netherland	TreeBASE: A database of phylogenetic information	16:40-17:00
	Poster Session and Database Demonstration / *Coffee Served*				17:00-18:30
	Mixer				19:00-21:00
15-Jul	**Biological Diverstiy : Value of Information for 21st Century -DAY 2-**				
	Session 3: Global Species Databases				
	Chairs: Richard White (UK) and Hideaki Sugawara (Japan)				
	Karen Wilson	Species 2000, Royal Botanic Garden in Sydney	Australia	A Master List of the World's Plant Species	9:00- 9:20
	Kwang-Tsao Shao	Academia Sinica	Taiwan	Current Status of Fish database in Taiwan and its Future Perspective	9:20- 9:40
	Ashok Kolaskar	Species 2000, ATCC	USA	Universal Virus Database ICTVdB	9:40-10:00
	Dicky Yu	Species 2000, TAXA-Information System	Canada	Taxapad 1999 with the Ichneumonidae catalogue	10:00-10:20
	Jiri Komarek	University of South Bohemia	Czech Rep.	Several problems to the cyanobacterial database	10:20-10:40
	Coffee Break				10:40-11:10

Date	Speaker	Affiliation	Country	Title	Time
	Session 4: Regional Biodiversity Information and Related Studies				
	Chairs: Kunio Iwatsuki (Japan) and Marakot Tanticharoen (Thailand)				
	Dennis Gordon	National Institute of Water and Atmospheric Research	New Zealand	Species 2000: New Zealand-The challenge of biodiversity assessment, with special emphasis on the marine environment	11:10-11:30
	David Boufford	Harvard University Herbaria	USA	Biodiversity of the Hengduan Mountain Region, China	11:30-11:45
	Richard H. Ree	Harvard University Herbaria	USA	Diversity of *Pedicularis* in the Hengduan Mountains Region, China	11:45-12:00
	Barbara Becker	ZADI- Info Centre Genetic Resources	Germany	Federal Information System Genetic Resources (BundesInformationssystem Genetische Ressourcen, BIG)	12:00-12:20
	Poster Session and Database Demonstration / *Lunch*				12:20-13:50
	Chairs: Makoto M. Watanabe (Japan) and Susono Saono (Indonesia)				
	Endang Rahayu	FNCC Gadja Mada University	Indonesia	Culture Collections of Microorganisms Networking in Indonesia	13:50-14:10
	Juncai Ma	Inst. Microbiol., Chinese Academy of Science	China	Microbial Information Network of China (MICRO-NET)	14:10-14:30
	Morakot Tanticharoen	National Center for Genetic Eng. Biotech.	Thailand	BIOTE [Thailand] Culture Collection : Microbial Resources and Information	14:30-14:50
	Coffee Break				14:50-15:10
	Chairs: Othman Sahir (Malyasia) and Motomi Ito (Japan)				
	Lillian Chua Swee Lian	Forest Research Institute Malaysia	Malaysia	Conservation of Biological Diversity in Malaysia-Current Status of Plant Resource Information	15:10-15:40
	Volodymyr Domashilinets	Ministry of Environmental Protection and Nuclear Safety of	Ukraine	Perspectives of GIS for Wildlife Inventory and Monitoring in Ukraine	15:40-16:00
	Susono Saono	Indonesian Research Institutes - LIPI	Indonesia	Indonesia-Japan Collaborative Study on the Biodiversity of Lactic Acid and Acetic Acid Bacteria in Indonesia	16:00-16:20
	Ashok Kolaskar	University of Pune	India	Diversity in Animal Viruses-Virus Identification on WWW	16:20-16:40
	Poster Session and Database Demonstration				17:00-17:50
16-Jul	**Asian-Oceanian Scene** (Parallel Sessions of Biodiversity and CODATA/DSAO Task Group)				
	Session A : National and Regional Reports from Asian and Oceanian Countries				
	Chairs: Motonori Hoshi (Japan) and Dennis Gordon (New Zealand)				
	Tatsuo Sasaoka	Biodiversity Center Japan	Japan	The National Survey on the Natural Environment in Japan	9:00- 9:15
	Shang-Shyng Yang	National Taiwan University	Taiwan	How the Biodiversity Issue is Handled in Taiwan	9:15- 9:30
	Asep Sunjaya Adhikerana	Center for Research and Development of Biology, National Institute of Science	Indonesia	Empowerment of Indonesian Biodiveristy Information Resources	9:30- 9:45
	Salim Javed	Centre for Wildlife& Ornithology, Alighrh Muslim University	India	Developing Natural Resource Information Network for Planning and Prioritizing Biodiversity Conservation: Avian Database Perspective	9:45-10:00
	Yaruo Hu / Juncai Ma (as proxy)	Chinese Academy of Science	China	An Introduction to the Chinese Biodiversity Information System (CBIS)	10:00-10:15
	Coffee Break				10:15-10:45
	Chairs: Ebbe Nielsen (Australia) and Juncai Ma (China)				
	Sun-Hwa Hahn	KORDIC	Korea	Biodivesity in Korea and KORDIC	10:45-11:00
	Ben Richardson	Western Australian Herbarium	Australia	FloraBase, an Integrated Information System for Western Australia	11:00-11:15
	Sahir Othman		Malaysia	DWNP programmes consistent with national biological diversity strategy and action plan	11:15-11:30
	Junko Nehashi	Japan Science and Technol. Corp. (JST)	Japan	Constructing Informational Infrastructure for Bio-Resource --Prototyping Bio-Resource databases--	11:30-11:45
	Session B: CODATA/DSAO Task Group				
	Chairs: Akira Tsugita (Japan) et al.				
	Tetsuya Maeshiro	ATR Human Information Processing Research Labs.	Japan	The Structure for Self Organized Knowledge in Hyper Brain Computers with Learning and Thinking Functions	
	Hiroyuki Sato et al.	Japan Science and Technol. Corp. (JST)	Japan	Directory Database of Research and Development Activities (ReaD)	
	Kazutoshi Tanabe	National Inst Material Chemical	Japan	Development of Chemical Safety Database	

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Program

Oral Presentation

		Krishan Lal	National Physical Laboratory	India	Precise and Accurate Data in Advanced Areas of Materials Science:Biaxial Stress in Thin Film-Substrate Single Crystals	
		Toshihiro Ashino et al.	RACE The University of Tokyo	Japan	Knowledge Sharing with Modular Simulation Technique	
		Yoshiyuki Kaji et al.	Japan Atomic Energy Research Institute	Japan	JAERI Material Performance Database (JMPD) - Present Status and Examples of Utilization -	
		Jing-Zhi Yu et.al.	Institute for Materials Research, Tohoku University	Japan	Factual Materials Database for Non-Equilibrium and Metastable Phases	
		Mitsutane Fujita et al.	National Research Institute for Metals (NRIM) etc.	Japan	Material Data System and Data-Free-Way on Internet	
		Ying Chen, et.al.	Japan Science and Technology Corporation (JST)	Japan	A web-based data system for electronic structures by first principles approach	
		Yuri Kotliarov, et.al.	Japan Science and Technology Corporation (JST)	Japan	Crystallographic data quality control -- application of graph theory	
		Chieko Nakabasami, et.al.	Faculty of Regional Development Studies, Toyo University	Japan	Knowledge Representation of Technical Papers in Metallurgy from Various Perspectives in Context	
		Edger F. Westrum Jr.	University of Michigan	USA	CODATA/DSAO from a privileged perspective-*Quo Vadis* ?	
		Tsuguchika Kaminuma	National Institute of Health Sciences	Japan	Linkage of Data on Chemicals, Life and Environment	
		Suthat Fucharoen	Mahidol University	Thailand	Thalassemia in the Next Millennium	
		Takashi Kunisawa	Science University of Tokyo	Japan	Patentability of discovery in the EU Patent Directive	
		Akira Tsugita	JIPID Science University of Tokyo	Japan	Proteome Today and Future	
	Closing Remark					
		Chair: Makoto M. Watanabe (Japan)				
		Gen Ohi	National Institute for Environmental Studies	Japan		

Program

Poster Presentation

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2	Manabu Kajita	Yamashina Institute for Ornithology	Japan	Phylogenetic status of the Lidth's Jay *Garrulus lidthi* among the genus *Garrulus*, Aves	401
3	Nicholas Lander	Western Australian Herbarium, Department of Conservation & Land Management	Australia	Max - A species editing program for Windows 95/98/NT	401
4	Fabio Moretzsohn	University of Hawaii	USA	*TaxonBank*, a new online database for taxonomic research	401
5	Shubha Nagarkar	University of Pune	India	Metadata and metadata standards in Biodiversity	401
6	Kazuki Shimura	Japan Science and Technology Corporation	Japan	Linkage of data on chemicals, life and environment	401
7	Yasuhisa Abe	Forestry and Forest Products Research Institute	Japan	A small database on cultural characters of tropical wood-decay fung	401
8	Osamu Tadauchi	Entomological Laboratory, Kyushu University	Japan	Species information database KONCHU on Japanese, East Asian and Pacific insects on INTERNET	401
9	Hideaki Sugawara	WFCC-MIRCEN World Data Centre for Microorganisms (WDCM), National Institute	Japan	Evolution of genes, genomes and species	401
10	Yoshikazu Ikeda	Biodiversity Center of Japan	Japan	The functions of Biodiversity Center of Japan	401
11	Yuzo Ito	Biodiversity Center of Japan	Japan	The National Survey on the Natural Environment in Japan	401
12	Kousei Otoi	Biodiversity Center of Japan	Japan	The Japan Integrated Biodiversity Information System(J-IBIS)	401
13	Hiroshi Kanda	National Institute of Polar Research	Japan	Database system of the herbarium moss specimens from polar regions	401
14	Enrique Wulff-Barreiro	Marine Sciences Institute from Andalusia,Spanish Council for Scientific Research. ICMAN (CSIC)	Spain	Archive's renewable value: Electronic insights in the past record. The biological memory of the ecosystem for the	401
15	Koji Sugimura	CGER,National Institute for Environmental Studies	Japan	Development of a database of bryophytes in Okunikko area	401
16	Hideyuki Shimizu	CGER,National Institute for Environmental Studies	Japan	Has bryophyte diversity affected by atmospheric environment? -Some field and laboratory researches	401
17	Ryuichi Suda	Fukuoka Institute of Health and Environmental Sciences	Japan	The flora and vegetation of Okino-shima and Orono-shima Islands, northern Kyushu,	401
18	Siti Aisyah	Institute Biological Sciences University Malaya	Malaysia	Methods in monitoring biodiversity of tropical marine fungi in Malaysia	402
19	Dantsey Koffi Edinam	Point Local National de la biodiversite Ministere de L'Environment et de la Production Forestiere	Togo	State of the biological plant life diversity of Togo and preservation measures	402
20	Abdoulaye Gaye	ICSU/CODATA	Senegal	Taxonomy background in Senegal	402
21	Daniel A. Lagunzad	Institute of Biology, The University of the Philippines	Philippines	Measuring and monitoring biodiversity changes in a tropical forest primarily managed for timber production	402
22	Yevgenija Lanovenko	Institute of Zoology, Tashkent	Uzbekistan	Monitoring of bird biodiversity changes in Uzbekistan(Central Asia)	402
23	Chutamas Pholpunthin	Prince of Songkla University	Thailand	Biodiversity of insects at Ton-Nga-Chang Wildlife Sanctuary, Southern Thailand	402
24	Souwalak Phongpaichit	Prince of Songkla University	Thailand	Biodiversity of freshwater hyphomycetes at Ton-Nga-Chang Wildlife Sanctuary, Southern Thailand	402
25	Elmurod Shernazarov	Institute of Zoology, Tashkent	Uzbekistan	The Aral Sea crisis and avian biodiversity	402
26	Tsutomu Hattori	Forestry and Forest Products Research Institute	Japan	Host specificity of wood decay basidiomycetes in a tropical rainforest of Malaysia	402
27	Toru Katoh	International Research Center for Japanese Studies	Japan	Molecular phylogeny of Drosophilidae based on the Adh gene sequences	402
28	Abdul Kadir Abu Hashim	Dept. Wildlife and National Parks, Malaysia	Malaysia	DWNP Scientific vertebrate reference collection	402
29	Yoshitaka Tsubaki	National Institute for Environmental Studies	Japan	Within-species diversity in a Japanese damselfly: life history differences in the two male forms of *Mnais costalis*	402

Program

Poster Presentation

No.	Presentater	Organization	Country	Subject	Room
30	Herwint Simbolon	Research and Development Center for Biology	Indonesia	Dipterocarpaceae in Gunung Berui, West Kalimantan, Indonesia: Species diversity, and its growth	402
31	Shunsuke Mawatari	Graduate School of Sciences, Hokkaido Univ.	Japan	Museum specimens play a leading role in the animal taxonomy in Japan - a case of Dö derlein Collection in Europe -	402
32	Tokushiro Takaso	Iriomote Station, Tropical Biosphere Research Center, University of the Ryukyus	Japan	Exploration of plant biodiversity in Iriomote Island, Okinawa, with a natural subtropical forest in Japan - current status and prospect	402
33	Ryuhei Ueno	National Institute for Environmental Studies	Japan	Taxonomic information of chironomids in Japan and related data in ecology, limnology and medical zoology	402
34	Weiduo Si	University of Newcastle upon Tyne	UK	Bacterial diversity in an Antarctic soil as analysed by 16S rDNA cloning	402
35	Tom Lyons	University of Newcastle upon Tyne	UK	Relationships between ozone resistance and climate in European populations of *Plantago major* L.	402

Program

Workshop on Biodiversity Research and Information in Asia Oceania

Day 1 March 22 (Wed.) 2000 10:00-17:00

10:00 **Opening Address** Prof. Yohichi Gohshi (*NIES, Japan*)

Session I: Topics related to desertification and biodiversity

Chairman Dr. Hideyuki Shimizu (*CGER/NIES, Japan*)

10:10 **Vegetation-ecological Aspects of Desertification**
Prof. Kazuhiko Takeuchi (*Graduate School of Tokyo University, Japan*)

10:30 **Diversity of Plant Species in Ulan Buh Desert Area in Inner Mongolia of China**
Dr. Yong Guang Han (*Dengkuo Country Center for Agriculture and Forestry Development, China*)

10:50 **Variation of Plant-Diversity in the Established Community for Combating Desertification**
*Dr. G. Y. Qiu[1], Dr. Kazuo Tobe[1] and Dr. Hideyuki Shimizu[2] ([1]*NIES, Japan,* [2] *CGER/NIES, Japan*)

11:10 **Changes in Plant Diversity with Acceleration of Desertification: A Case Study of Some Desertified Areas in China and Sudan**
Prof. Shinobu Inanaga[1], *Ms. Ping An[1] and Dr. Imad Ali[2] ([1]*Tottori University, Japan,* [2]*ARC, Sudan*)

11:30 **Discussion**
Commentator: Prof. Atsushi Tsunekawa (*Graduate School of Tokyo University, Japan*)

12:00 *Lunch*

Session Ⅱ: Topics related to tropical rainforest and biodiversity

Chairman: Dr. Shunsuke Mawatari (*Graduate School of Hokkaido University, Japan*)

13:30 **International Programme of Biodiversity Science (DIVERSITAS): Its History and Present Status**
*Prof. Hiroya Kawanabe[1] and Tohru Nakashizuka[2] ([1]*Lake Biwa Museum, Japan,* [2]*Centre for Ecological Research, Kyoto University, Japan*)

13:50 **The Effect of Forest Disturbance on Avian Community Structure at Two Lowland Rainforests in Peninsular Malaysia**
Dr. Hisashi Nagata (*NIES, Japan*)

14:10 **Estimation of Gene Flow in the Tropical-rainforest Tree Neobalanocarpus Heimii (Dipterocarpaceae)**
Dr. Akihiro Konuma (*NIES, Japan*)

14:30 **Monitoring of Forest Dynamics in Indonesia: Growth of Fagaceae Species in Sub-mountain and Mountain Forests of West Java**
*Dr. Herwint Simbolon[1] and Prof. Eizi Suzuki[2] ([1]*Graduate School of Hokkaido University, Japan,* [2]*Kagoshima University, Japan*)

14:50 **Biodiversity of Xishuangbanna, Yunnan, China**
Dr. Liang Yang (*Yunnan Environmental Monitoring Center Station, China*)

15:10 **Discussion**
Commentator: Dr. Yan Hong Tang (*NIES, Japan*)

15:40 *Coffee Break*

16:00 **Tour through NIES facility** (Aquatron, Phytotron, Pedotron, Experimental farm)

17:00 *Mixer*

Program

Workshop on Biodiversity Research and Information in Asia Oceania

Day 2 March 23 (Thu.) 2000 9:00-12:45

Session Ⅲ: National / Regional Report of biodiversity

Chairman: Dr. Hideyuki Shimizu (*CGER/NIES, Japan*)

9:00 **Introductory Remarks on Species 2000 Asia Oceania**
Prof. Makoto M. Watanabe (*NIES, Japan*)

9:15 **Species 2000 Annual Checklist: Overview and Status in March 2000**
Dr. Rainer Froese (*ICLARM, Philippines*)

9:30 **Species 2000 in the Americas - Symposium and Result**
Dr. Karen Wilson (*Royal Botanic Gardens Sydney, Australia*)

9:45 **Chinese Biodiversity Information System in 2000**
*Mr. Juncai Ma, Dr. Keping Ma and Dr.Liquiang Ji (*Chinese Academy of Sciences, China*)

10:00 **Biodiversity Research and Development in Thailand**
Prof. Sutat Sriwatanapongse (*National Center for Genetic Engineering and Biotechnology, Thailand*)

10:15 **Several Databases for Biodiversity Built Up by KORDIC, Korea**
*Dr. Soon-Chan Hong, Dr. Tae-Joong Kim and Dr. Young-Hwa Cho (*Korea Research and Development Information Center, Korea*)

10:30 *Coffee Break*

11:00 **The Sumatran Tiger and the Sumatran Elephant: the Indonesian Species 2000**
Dr. Sugardjito (*The Indonesian Institute of Sciences, Indonesia*)

11:15 **Biological Diversity Research and Information in Malaysia**
Dr. Elizabeth Philip (*Forest Research Institute Malaysia, Malaysia*)

11:30 **Biodiversity and Information in Malaysia**
Dr. Burhanuddin Mohd (*Department of Wildlife and National Parks, Malaysia*)

11:45 **Biodiversity Survey and Information in Japan**
Mr. Tatsuo Sasaoka (*Biodiversity Center of Japan, Japan*)

12:00 **Species 2000: New Zealand - Benefits, Lessons, and Intended Outcomes**
Dr. Dennis Gordon (*NIWA, New Zealand*)

12:15 **Discussion**
Commentators: Prof. Kawanabe (*Lake Biwa Museum, Japan*)
Prof. Mawatari (*Graduate School of Hokkaido University, Japan*)

12:45 **Closing Address** Prof. Makoto M. Watanabe (*NIES, Japan*)

* Person who make a presentation.

Joint Forum: Taxonomy Initiatives for Biodiversity Conservation in an IT Era
Date: January 13th-14th, 2001
Venue: National Science Museum, Shinjuku Branch. 3-23-1 Hyakunincho Shinjuku, Tokyo 169

Day 1: January 13, 2001					
Session 1					
	Case Study in Fishes towards Global Scale Data Integration				
	Chair: Keiichi Matsuura / John R. Paxton				
	9:00	-	9:20	Rudy Reyes	Approaches and preliminary results of integrating fish databases
	9:20	-	9:40	Peter Ng	"The state of freshwater fish taxonomy in Southeast Asia"
	9:40	-	10:00	John R. Paxton	"Status of Australian Fish Taxonomy and Fish Collections, Databases and
	10:00	-	10:20	Kwang-Tsao Shao	"Integrate Fish Databases of Taiwan for Research and Educational Use"
	10:20	-	10:40	Keiichi Matsuura and Hiroshi Senou	"Fish database in Japan with special reference to fish-image database and its role in biodiversity study"
	10:40	-	11:00	Coffee Break	
Session 2					
	Biodiversity Information Activities in Asia Oceania				
	Chair: Hideyuki Shimizu				
	11:00	-	11:20	Motomi Ito	"Flora Japonica"
	11:20	-	11:40	Tadasu K. Yamada	"Marine Mammal Stranding Database and It's Future"
	11:40	-	12:00	Li-Qiang Ji	"An Introduction of Chinese Biodiversity Information System"
	12:00	-	12:20	Kazuo Koyama	Biodiversity data sharing for better conservation planing
	12:20	-	12:40	Junko Shimura	"Bacteriology Insight Orienting System"
	12:40	-	14:00	Lunch	
Session 3					
	Expectation on Informatics to Study Biodiversity				
	Chair Junko Shimura				
	14:00	-	14:20	Takashi Kunisawa	"Plastid Phylogeny Inferred from Gene Order"
	14:20	-	14:40	Hirobumi Suzuki	"Genetic diversity, geographic differentation and artificial disturbance in the Japanese firefly, Luciola cruciata (Coleoptera, Lampyridae)."
	14:40	-	15:00	Dennis Gordon	"Towards a Biosystematics Strategy for New Zealand"
	15:00	-	15:20	Hiroshi Tobe	Plant Taxonomy Researches in an IT Era: Current Status and Perspectives in
	15:20	-	15:40	Coffee break	
Session 4					
	What taxonomists Can Do and Should Do in IT era				
	Chair Makoto M. Watanabe / Shunske Mawatari				
	15:40	-	16:00	Karen L. Wilson	Systematic Botanists and International Collaborative Projects
	16:00	-	16:20	Tohru Nakashizuka	
	16:20	-	16:40	Ebbe Nielsen	Global Biodiverisity Information Facility
	16:40	-	17:00	Makoto M.	Global Taxonomy Initiative
	17:00	-	17:20	Shunsuke Mawatari	"How to promote taxonomy?"
	17:20	-	17:40	General discussion on overall sessions	
	18:00	-	19:00	CODATA DSAO Business Meeting	
	18:30	-	End	Mixer (PYOB ; 3,000 yen/person)	

Day 2: January 14, 2001					
The Union of Japanese Societies for systematic zoology in Japanese					
	Symposium : Interfaces between present-day society and taxonomy Organizers				
	Organizers: Haruo Katakura, Shunsuke Mawatari				
	10:00	-		Masahide Kubota	Official Certificate for Taxonomy Skills in Japan
		-		Yuji Tsukii	Joint Forum: Taxonomy Initiatives for Biodiversity Conservation in an IT EraDate: January 13th-14th, 2001 Venue: National Science Museum, Shinjuku Branch. 3-23-1 Hyakunincho Shinjuku, Tokyo 169
		-		Tomomi Kaneko	Environment Assessment and Taxonomy
		-	12:00	Motoki Hoshi	JSPS research grant for studies in biodiversity
Species 2000 Asia Oceania Working Group Meeting (Pre-register necessary)					
	13:30	-	17:00	Discussion on Future Plan / GTI in Asia Oceania	