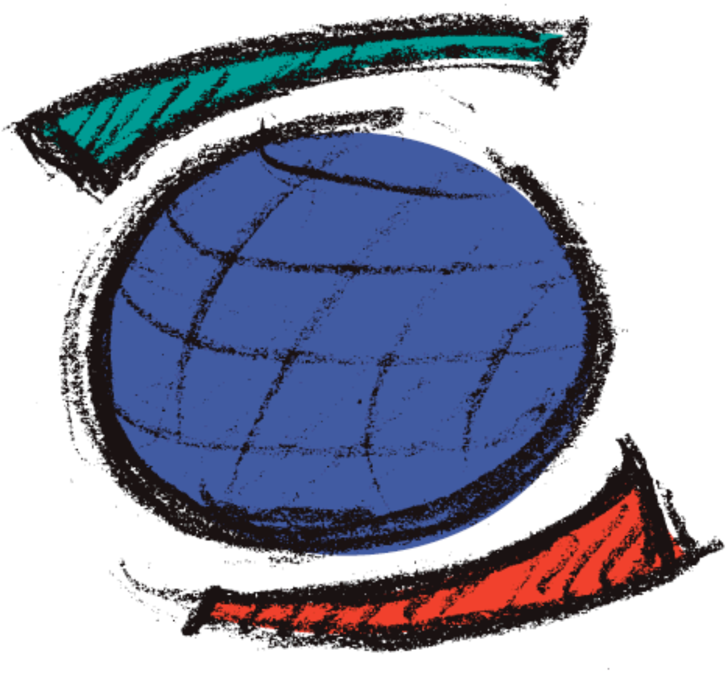

BIODIVERSITY RESEARCH – SAFEGUARDING THE FUTURE

> *"We do not inherit the earth from our ancestors,*
> *we borrow it from our children"*
> *Navajo Proverb*

Outcomes and recommendations of the CBD - COP 9 Associated Meeting
Bonn, May 2008

Editor: Jessica M. Reeves

Organized and supported by IUBS, German Science Foundation (DFG),
Deutsche Bundesstiftung Umwelt, DIVERSITAS, Museum Koenig, Nees Institute

Foreword

The fossil record informs us that the diversity of the Earth's biota has always been in a state of flux. There are many drivers for this change in biodiversity, and most of these are inextricably entwined; they include climate change, volcanic activity, extraterrestrial bombardment, and species migration/dispersal. It is generally a culmination of events that results in major changes – where evolution or introduction of new taxa outcompetes established endemics. Recently however, the impact of humanity has altered the balance of natural systems within the biosphere. Humans have over-fished, over-harvested, over-logged and over-utilised the Earth's resources, with an outcome that many taxa have become, or are soon likely to become, extinct.

There is balance required; but this balance, between feeding a vast and still growing human population, whilst ensuring that the needs of humanity do not compromise those of nature, is elusive. Up to the present, *Homo sapiens* has failed to demonstrate that it is capable of thinking, and then implementing the measures appropriate to ensure a viable global environment – for it is not simply what humanity takes from nature, it is what humanity returns to nature that has put many ecosystems at risk.

The collection of papers herein provides us with a snapshot of global biodiversity as at May 2008. Importantly, many of the writers are enthusiastic about showing the link that clearly exists between diversity in nature and human fulfilment. Humans are not *apart* from nature, rather *we are a part of it*. The fundamental postulate, encompassing "the singularity of life and interconnectedness of all organisms", is one that we, as individuals, must continue to be cognisant of, as well as reinforcing the concept with colleagues and even more importantly, with our political representatives.

This report, appropriately entitled "Safeguarding the Future", is published in mid-2009, a year during which we also reflect upon the life and influence of Charles Darwin – born 200 years ago on February 12th, 1809. The closing words in Darwin's seminal work "On the Origin of Species by Means of Natural Selection" give us reason to both stand in awe of the beauty of nature and of its great diversity.

> *There is grandeur in this view of life... from so simple a beginning endless forms most beautiful and most wonderful have been, and are being, evolved.*
>
> (Charles Darwin, 24th November, 1859)

We must ensure that there is wide recognition that without biological diversity, our lives would not only be very much the poorer, they would probably not be sustainable. Drops in biodiversity are now sufficiently extensive, and occur often enough, for us to recognise that there is much wrong with the natural environment. The loss of one species is a concern, the loss of many, an indication that whole ecosystems are in crisis. Humanity, through overuse and pollution of natural resources, is largely the orchestrator of this degradation. Clearly it is our moral duty to mitigate our behaviour... action is required, now.

John Buckeridge
President, International Union of Biological Sciences

RMIT University, Melbourne, Australia
21st July, 2009

Contents

President's Address

High-Level Segment of the 9th Conference of the Parties to the Convention on Biological Diversity (CBD)

Bonn (Germany) 28-30 May 2008

Conclusions of Minister Gabriel, President of COP-9

The High-Level Segment of the 9th Conference of the Parties to the Convention on Biological Diversity (CBD) took place in Bonn (Germany) on 28-30 May 2008. It was chaired by Mr Sigmar Gabriel, Federal Minister for the Environment, Nature Conservation and Nuclear Safety of Germany. 157 countries participated in the High-Level Segment, 80 of which were represented at ministerial level, 37 on Deputy Minister or State Secretary level. The meeting was also honoured by H.E. Dr. Angela Merkel, Federal Chancellor of Germany; H.E. Dr. Srgjan Kerim, President of the General Assembly of the United Nations; H.E. Stephen Harper, Prime Minister of Canada; H.E. Jose Manuel Barroso, President of the European Commission; H.E. Achim Steiner; Executive Director of the United Nations Environment Programme and Dr. Ahmed Djoghlaf, Executive Secretary of the Convention on Biological Diversity. The High-Level Segment was honoured by a welcome message from H.E. Ban Ki- Moon, Secretary General of the United Nations, which was read out by H.E. Achim Steiner. Representatives of international intergovernmental organizations, parliamentarians, local communities, business, youth, non-governmental organisations and Indigenous and local communities have also participated.

In my opinion this High-Level Segment has fully achieved the main objectives l had in mind when inviting you:

- Giving the necessary guidance at relevant stages of COP-9 negotiations in order to help negotiators to reach agreement on key topics,

- Providing a new impetus to the further development and implementation of global biodiversity policies,

- Showing the world which concrete steps countries are taking in order to halt or significantly reduce the loss of biodiversity.

I summarize our discussions as follows:

1. We underlined that biological diversity constitutes the indispensable foundation of our lives and of economic and social development. We stressed the fundamental importance of biodiversity for human livelihoods and the crucial role of biodiversity in poverty eradication and the achievement of the Millennium Development Goals. The economic relevance of biodiversity was highlighted by the presentation from Pavan Sukhdev with findings of his study "The Economics of Ecosystems and Biodiversity". However, all of us were aware that human-induced extinction of biodiversity is still advancing at a dramatic pace. Having only two more years to reach the target agreed by the heads of state and government in Johannesburg to significantly reduce the loss of biological diversity by 2010, we acknowledged the urgent need for concrete action at international, national and local levels.

2. Our meeting has been instrumental for COP-9 to achieve significant progress on key topics such as:

   - The sustainable production and use of biofuels in relation to biodiversity. The role of the CBD was confirmed. A concrete process until COP 10 was agreed.

   - The establishment of networks of protected areas and the related Life Web Initiative,

- Forest biodiversity with a special focus on addressing the potential threat of Genetically Modified trees
- Marine biodiversity with a special focus on addressing the potential threat of oceans fertilization
- The cooperation between the CBD and the United Nations Convention to Combat Climate Change.

3. In order to provide a new impetus to protect biodiversity we considered it important to take due account of and strengthen:

The role of local authorities
In order to achieve the objectives of the CBD it is essential that the local authorities undertake specific initiatives to implement relevant objectives of the different programmes of work of the CBD within their respective areas of competence. Local authorities should also participate in the development of national policies for the implementation of the CBD. The IDCN's Countdown 2010Initiative has an important role to play in promoting this.

The role of Indigenous and local communities
Indigenous and local communities should meaningfully participate in decision making processes affecting them. International, national and local authorities and organisations should take due account of the UN Declaration on the Rights of Indigenous Peoples when developing and implementing relevant initiatives for fulfilling their commitments under the CBD. The COP should agree on elements of a code of ethical conduct to ensure respect for the cultural and intellectual heritage of Indigenous and Local Communities and should promote the effective participation of Indigenous and Local Communities in the CBD's decision and policy-making concerning the use of their traditional knowledge.

The importance of young people
We must conserve and sustainably use biological diversity for the benefit of present and future generations. Children, and the children of our children, have the right to grow in a healthy environment where the choices provided by nature are preserved. Our education and awareness precondition our patterns of production and consumption, the CBD should therefore give a priority to the implementation of the CBD's Programme on Communication, Education and Public Awareness.

The Contribution of Non-Governmental Organizations
The civil society represented by the NGOs has an essential role to play in the efforts towards achieving the objectives of the CBD. This helps to raise the awareness of the public and decision makers on the importance of biodiversity and the challenges ahead. They are facilitators and are involved in implementing biodiversity projects on the ground. It is therefore important to listen to their voice and to facilitate their participation in decision making processes affecting biodiversity both at international and at domestic levels.

The role of the business community
We recognized that a re-linking of biodiversity, climate change, economics and poverty eradication is necessary to adequately address these global challenges. The business community should seize opportunities provided by biodiversity and should also integrate biodiversity concerns within its operations. The Business @ Biodiversity Initiative will provide a forum for further enhancing the engagement of the business community towards the objectives of the CBD.

The High Level Segment of COP-10 should take this issue again in order to review progress achieved.

The understanding of the economic significance of the global loss of biological diversity
We considered it important to analyse the global economic benefit of biological diversity and its ecosystem goods and Services, the costs of the loss of biodiversity and the failure to take protective measures versus the cost of effective conservation. The outcomes of a global study should be submitted for consideration to COP-10 and to the General Assembly of the United Nations.

The rôle of science
There is the need to strengthen the science-policy interface of the Convention. An international mechanism for providing scientific advice (IMoSEB) should be established in order to enhance the quantity and quality of scientific information available to institutions and organisations at different levels.

4. We are aware that for achieving the 2010 target it is essential to take urgent and strong actions, the High Level Segment warmly welcomed specific commitments announced during the different sessions by Parties.

Bonn Agenda on Global Biodiversity

Having only two years left to meet the 2010 target set by heads of states and governments in 2002 at the WSSD in Johannesburg, the German CBD Presidency will be guided by a clear roadmap to COP10. We will do our utmost so that the decisions taken by COP 9 are implemented comprehensively and in a timely fashion. We will enhance cooperation and team-spirit amongst parties and bodies of the CBD. We will try to bridge gaps inside the CBD-family and to others outside. We will also try to convince those countries, still outside the CBD to join and make the Convention the real global one for all life in all countries on earth!
Our "Bonn Agenda on Global Biodiversity" of the German CBD Presidency will have a special focus on the following issues:

1. **Access and Benefit Sharing**
   Finalising the ABS-Regime promptly to be adopted at COP 10 will be the key task of the German CBD-Presidency. The negotiation process is well designed by COP 9-decisions, with a number of working group meetings both on political and on scientific expert level. I will invite ministers from all regions of the world to form a high level group of Friends of the Presidency to give political guidance on the CBD process with special focus on ABS – whenever it is needed.
2. **LifeWeb Initiative**
   The Protected Areas Programme of Work will be assessed at COP 10. Key to this is the enhanced management of existing protected areas and the establishment of additional ones to fill the gaps in the global net of protected areas. COP 9 welcomed the LifeWeb Initiative as one tool to assist in implementing the Programme of Work. Many parties announced that they want to be involved in this Initiative. The German CBD Presidency will - in cooperation with the CBD Secretariat and other institutions - facilitate to make the LifeWeb Initiative a vital one. We want to make the LifeWeb Initiative an effective tool to protect our precious forests.
3. **Mobilizing financial resources**
   Appropriate financing of all three pillars of the CBD is vital. The German CBD-presidency will pay special attention to enhance cooperation between CBD, GEF and other funding institutions

and mechanisms. We will continue our efforts to establish new and innovative funding mechanisms on all levels.

4. **The Economics of Ecosystems and Biodiversity**
   Under the leadership of Pavan Sukhdev we will continue our work on the Economics of Ecosystems and Biodiversity. We will provide a comprehensive report before COP 10 which will allow a comparison of the cost of action with the cost of non-action on Biological Diversity.

5. **Beyond 2010**
   A thorough assessment of the 2010 target is necessary. Together with other institutions we will analyse to what extent we have reached the 2010 target. We want to understand why (or why not) countries or regions were able to meet the challenge. We will follow the invitation of the President of the United Nations General Assembly to cooperate in the preparation of a special Session of UNGA on Biodiversity.

6. **Global Biodiversity Governance**
   The CBD has achieved a lot since the World Summit in Rio de Janeiro in 1992. Regarding our enormous challenge of holding the loss of biodiversity, we have to assess whether the approach, the governance and the way we work is efficient and appropriate. We will start a discussion inside the CBD, with other Partners in the UN and with those who might have an outside view on our convention.

   Biodiversity needs an effective science-policy interface. We will support the Imoseb Process and all efforts to synergize with other relevant processes like MEA.

General Introduction

Sciences are vital to the achievement of the objectives of the Convention on Biological Diversity (CBD), by *inter alia* conducting basic biodiversity-related research, including taxonomy and ecosystem research, and providing a range of benefits. To give science a voice amidst the political discussions of the CBD-COP and to provide science-based arguments for the promotion of biodiversity and conservation research, an associated meeting was organized in March 2006 to prepare recommendations for the CBD-COP 8.

The success of the COP 8 Associated Meeting "BIODIVERSITY – THE MEGASCIENCE IN FOCUS", held in Curitiba, Brazil (15-19 March 2006), prompted the German participants to suggest a follow-up conference in conjunction with the CBD - COP 9 in Bonn, Germany (May 19-30, 2008).

The recommendations and outcomes of the Curitiba conference were circulated by the secretariat of the CBD on the second day of the CBD-COP.[1]

The Curitiba conference dealt with three major themes:

I. **"Biodiversity and Systematics"**
II. **"Benefit Sharing and Bioethics"**
III. **"Sustainability"**

In the continuation of the discussions of the CBD - COP 8 Scientific Conference these themes are now expanded and new aspects are added.

Background
Symposium I: "**Acceleration of Biodiversity Assessment and Inventorying**":

The Workshop on Biodiversity and Systematics in Curitiba identified the need for increased support for taxonomic research that would in turn enhance the generation of information needed for the protection of biodiversity. These recommendations are in accord with the Darwin Declaration[2] and the Buffon Declaration (Buffon Symposium, Paris, 2007).

The lack of rapid tools for species identification and the incompleteness of species information in databases is still a severe impediment for conservation measures, the assessment of habitat quality and species richness, the discovery of natural resources, and the observation of climate change and land use effects. Species inventories for nature reserves, national parks and other conservation areas are virtually non-existent.

Currently, for the vast majority of species changes in the composition of local communities can not be monitored. While the necessary technology is available, the required databases, infrastructure, and manpower are not.

Databases with species information required by taxonomists, ecologists, policy makers etc. already exist. They are, however, incomplete and need continuous input of data. Species catalogues like *ITIS* and *Species 2000* now include 1 million species, but further support is required. Furthermore, species names

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[1] Outcomes and recommendations of the meeting on "Biodiversity – the Megasceince in Focus", Curitaba, 15-19th March 2006. 8th United Nations Environment Programme, Conference of the Parties on the Convention of Biological Diversity, (UNEP/CBD/COP/8/INF/46), page 5. (21 March 2006; see also http://www.cbd.int/doc/?mtg=cop-08)

[2] Information Document Inf. 28 of the 4th United Nations Environment Programme, Conference of the Parties on the Convention of Biological Diversity (UNEP/CBD/COP/4/INF/28), 1998.

must be linked with geographical, genetic, and ecological data. The Encyclopedia of Life (*EoL*) combines such records in a single platform, while *BOLD* and *Genbank* contain entries with DNA barcodes and other genetic information.

The symposium specifically emphasizes

- the adaptation and development of technology to accelerate efficient and cost-effective inventorying at species level.

- the essential long-term support for biodiversity databases

Background
Symposium II: "**Biodiversity: Functions and Uses**":

Biomimicry increasingly attracts the interest of industry and sciences as a powerful tool to develop engineering products and process solutions from biological models. This means, that properties, functions and processes of organisms are examined and transferred onto technical products or systems. Products or systems created this way include features which were optimized by millions of years of evolution. They often provide new and so far unknown solutions for technical issues.

Access and benefit sharing (ABS) has been a major subject of the COP 8 associated meeting in Curitiba (2006). ABS supports the property rights of source countries that possess species rich habitats and traditional knowledge, but also enables co-operation in commercial and in non-commercial research. Now, the Curitiba recommendations require the development of actual steps in the real world.

- Some governments are still hindering basic research, including activities of their own scientists. National research communities usually need the co-operation of international science networks and, for example, loans of specimens for non-commercial scientific analyses.

Benefits of genetic resources and living species can only be generated and shared if users and potential users are encouraged to explore and use these resources in a sustainable way.

The manifold functions and uses of biodiversity and their scientific assessment are also the subject of this symposium. The symposium addresses:

- the numerous services biodiversity provides to the ecosystem and ways to secure the sustainable provision of such services by means of regulations and economic incentives,

- the amazingly important role that nature plays as a model for technical innovations and

- the importance and benefits of genetic resources and the critical role that regulation of access and benefit sharing plays in this regard.

Background
Symposium III "**Biodiversity Changes: The 2010 Target and Beyond**":

Biodiversity research and management are limited by a lack of observation data describing at adequate resolution and specificity the change in biodiversity. Major themes are:

- Prioritized tasks for a Global Biodiversity Observing System

- Definition of the desired spatial and temporal resolution with special regards to the 2010 goal and beyond

- Definition of the desired data and products with special regard to modelling the consequences of climate change and environmental change

- Development of a strategy for its implementation and funding

It is clear that decisions should be based on knowledge produced by the worldwide scientific community, who must also work to understand the requirements of policy-makers and society as a whole. The aim of the COP 9 associated meeting is: to focus on advances and new viewpoints that result from current scientific research, to highlight measures that are necessary and feasible, to discuss the impact of the recommendations of the Curitiba conference, to remind the COP delegates and the general public of the existing recommendations and to formulate further pressing tasks that require actions, changes of attitudes, more consideration from policy makers and legislators, and investments.

Summary of recommendations of the COP 8 Associated Meeting (Curitiba 2006)

Biodiversity and Systematics:

- Taxonomic inventories, species discoveries and descriptions, and national inventories must be accelerated (recommendations # 1, 2, 3), biological inventorying (# 7) must be scaled up
- Increase of taxonomic expertise and work-force (# 4)
- Expansion of natural history collections (# 5)
- Improvement of information flow between natural history institutes (# 6) and development of large scale informatics infrastructures for biodiversity information (# 8) that offer interactive tools for species identification and monitoring (# 9) and provide global access to biodiversity information (# 17)
- Improvement of public outreach activities (# 10)

Benefit Sharing and Bioethics:

- Build and maintain trust between partners and governments (# 11), streamline the ABS process (# 12), facilitate non-commercial research and exchange of material required for basic science (# 19)
- Scientists should engage in capacity building and co-operations (# 16)
- Scientists must be involved in proposal evaluation (# 13), and should also be informed about the aims of ABS regulations and best practice (# 14)
- Scientists involved in basic and applied biological research must accept and follow regulations and recognise bioethical concerns (# 15), and countries are encouraged to take measures against illicit use of biological resources (# 17)

Sustainability

- Biodiversity research must be more integrative and predictive (# 20) and respond to social needs, considering the interface of human activities with biodiversity (# 21)
- A global network of co-operations and standardized methods is needed (# 21)
- Conservation efforts require capacity building, education, and institutional infrastructure (# 22)
- Develop mechanisms for remuneration of providers of ecological goods and services, adjusted to specific regional conditions (# 23, 24)
- Biodiversity-related research projects should involve indigenous and local communities and stakeholders (# 25) and promote conservation and development of traditional knowledge (# 26)
- User fees demanded for resource use and environmental degradation should be adequate to pay for conservation measures (# 27) and payments must be up-scaled to a global level to address the severity of the problem (# 28); institutions must be created to implement these payments (# 29)
- Climate and biodiversity objectives should be integrated to combat global warming (# 30)

Recommendations from the pre-COP9 scientific conference:

Recommendations Pre-COP9

“Biodiversity Research — Safeguarding the Future”

(Official COP 9 information document 51[3])

The conference “Biodiversity Research — Safeguarding the Future” brought together global scientific expertise to address the current global biodiversity crisis. Convened by the International Union of Biological Sciences (IUBS) and DIVERSITAS, 258 scientists from 36 countries met in Bonn during the week prior to the COP9 of the CBD to prepare a statement to enrich the discussions on the CBD agenda. This document presents the conclusions of their work.

The scientific consensus

Despite the best of intentions to reduce the rate of biodiversity loss by 2010, available scientific evidence clearly shows that the dramatic global decline in biodiversity is generally accelerating; this emphasises the urgent need for intensified political action by the CBD. Biodiversity provides crucial goods and ecosystem services and constitutes our long-term life-support system.

Global monitoring systems have been established for weather, climate change, and earthquakes; a comparable system is urgently needed for biodiversity. This will strengthen the evidence base for action and enable a predictive capacity to guide and facilitate the implementation of a wide range of management strategies. In addition, the full benefits that societies derive from biodiversity should be effectively incorporated into national accounting and policies. Achieving these goals will require new scientific endeavour and improved science input to policy.

Recommendations

To address the urgent need to reverse the dramatic global biodiversity decline, the scientific community here convened recommends that governments:

- Establish an integrated global biodiversity observation network by complementing, expanding, and linking national and regional monitoring systems to provide effective information on ecosystems, species, and genes, and the services they collectively provide.
- Intensify support for the 2010 target and build on current progress to support stronger targets and improved indicators beyond 2010.
- Account for the values of the ecosystem services provided by biodiversity and internalize them in relevant policies and decisions.
- Increase investment in a wide range of tools and technologies, including citizen-science schemes, to accelerate biodiversity description, identification, inventory and monitoring.
- Increase efforts to make biodiversity information universally available through technological innovations, particularly the transfer of legacy information to countries rich in biodiversity.
- Formulate streamlined and simplified rules for purely scientific open-access research in the proposed International Regime for Access and Benefit Sharing (ABS), to avoid unnecessary impediments to the generation of knowledge which serves CBD objectives.
- Enhance the effectiveness of the science-policy dialogue through full use of scientific expertise by CBD bodies, including SBSTTA, and through establishing a dedicated assessment body for biodiversity.
- Recognise the role of biodiversity in mitigating the negative effects of global change and employ sound biodiversity management accordingly.

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[3] See http://www.cbd.int/cop9/doc/

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Abstracts of the Presentations

Oral Presentations

Symposium I:
Acceleration of Biodiversity Assessment and Inventorying

P.0

Addressing Future Challenges in Biodiversity Science and Policy - A UNESCO Contribution

W. Erdelen [1]

[1] United Nations Educational Scientific and Cultural Organization, Natural Sciences Sector

No abstract provided

P.1

A world where Biodiversity counts

M. Walpole [1]

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Biodiversity loss is occurring at an unprecedented rate, yet our ability to chart that decline, let alone do anything about it, remains severely under-developed. The task is hampered not only by gaps in taxonomic knowledge, but also by a lack of sufficient attention to monitoring biodiversity change over time and by our inability to show convincingly what difference biodiversity loss will make to society and human wellbeing. A range of global initiatives are attempting to answer policy-relevant questions, often on impractically short time-frames, which marginalise the role that science can play. Real progress will demand better integration of science and policy over the longer term, incorporating both immediate priority research questions and sustained assessment and monitoring initiatives. In a world where biodiversity counts, biodiversity science must count for much more than it currently does.

T I.1

Present situation of Brazilian biodiversity studies

C.R. Brandao [1]

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The Brazilian scientific community organized the international conference "Biodiversity – The Megascience in Focus" prior to COP8 in Curitiba, which produced recommendations presented to COP delegations. The aim has been to enhance biodiversity studies, to meet CBD objectives. Our reading of Brazilian official politics is that it is focused on benefit sharing and failed to attend to other components of CBD, except for the recent efforts by Brazilian Federal and state governments. The proposal for a law to regulate collection and transport of organisms, access to molecular information and the protection of traditional knowledge, guarantees the rights of planters, fishermen, and traditional communities, while imposing heavy regulations to basic research. This is based on the false principle that research may negatively affect the environment and may risk the rights of communities. We seek a positive agenda, with compensation measures and, in case of legal transformation of ecosystems, previous surveys. We believe there is no need to sign contracts in case of research aiming products with commercial potential; the existing regulations to launch new products guarantees benefit sharing.

Meanwhile the Brazilian biodiversity is under severe risk. We surveyed what is known and evaluated our capacity to apply names to organisms. We know where and to which groups of organisms to concentrate collecting efforts and in which fields to focus the attention of new scientists. It is time to act.

T I.2

Biodiversity conservation and sustainable development: feasible solutions to real challenges, the case of Mexico

R. Medellin [1]

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Megadiversity, OECD, oil exports, poverty, population growth. All these terms and subjects apply to Mexico. This makes the country an interesting case study to follow closely and learn from its mistakes and achievements. Mexico has been ranked number 5 in the world because of its very rich biological diversity. At the same time, it has been a member of the OECD since 1994, ranks fifth in oil production, 40% of its people are below poverty line, and is number 13 in population. Additionally, very recently Mexico stopped being the head of the mouse (among the richest of the poor countries) to be the tail of the lion (the poorest of the rich countries). Challenges and opportunities abound in Mexico. So over the past 10 years, Mexico has initiated a series of policy-driven programs to understand its biodiversity, use it sustainably and mainstream its benefits. Among them, the Mexican Commission of Biodiversity has put the country at the leading edge in the knowledge of its biodiversity, the Secretary of the Environment has launched innovative programs to benefit land owners from biodiversity conservation initiatives and environmental NGOs have undergone significant growth and impact in the country. Many shortcomings are still to come, but lessons abound to continue pursuing a brighter future. Despite efforts such as CONABIO's, assessing biological diversity, even from supposedly well-known groups such as mammals, is a critical necessity. Many taxa are only superficially understood. Beyond that, monitoring and assessing ecosystem services, such as declining pollination, is also a top priority. We are still in time to gather data on all aspects of biodiversity so that we are optimally prepared to slow down the extinction pulse, to maximize biodiversity benefits and to ensure the vital ecosystem services it provides, but we must act now.

T I.3

Accelerating global taxonomy - the *Solanum* Planetary Biodiversity Inventory experience

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The pace of taxonomic research is not keeping up with demand for taxonomic information – creating what is known as the “taxonomic impediment”. Many solutions to this problem have been proposed, ranging from the purely technological to largely people-centred. The National Science Foundation of the US government established the Planetary Biodiversity Inventory programme in 2002 with the aim to accelerate taxonomic research with a series of "mission[s] to an (almost) unknown planet”. Projects funded by the PBI programme were to be global in scope, focused on the species-level taxonomy of a monophyletic group, undertake new research and to be presented on-line. Here we will discuss our own PBI project “PBI *Solanum*: a worldwide treatment” in terms of its success in accelerating work on the taxonomy of one of the largest genera of flowering plants and in terms of the use of this sort of model for accelerating taxonomy in general. Speeding up scientific research can cause problems as well as providing solutions. We will particularly explore issues associated with working as large dispersed teams, presenting taxonomic information on-line and with the maintenance of such in-demand information for the long-term.

T I.4

Networks by Design: Recommendations for a Global Biodiversity Monitoring Program

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On a global scale, climate change and land use change are accelerating at a rapid rate, with potentially serious threats to biodiversity as well as to its emergent ecosystem services. Nonetheless, little is known about the mode or tempo of response by the abundance or distribution of organisms and how such changes will affect patterns of biodiversity at multiple spatial scales. Consequently, a synoptic network of biodiversity monitoring sites is required at the global scale. Sites should be deployed and configured so as to evaluate temporal trends in hierarchical aspects of biodiversity (e.g., alpha, beta, and gamma components), especially in regions of the globe that are predicted to experience heightened change in the next few decades. A number of extant (e.g., US-LTER) and emerging (e.g., NEON) national networks, as well as international networks (e.g., CI-TEAM) provide important insights regarding the nature of a global biodiversity network and its potential to act as an early warning system of the well-being of the earth’s biota.

T I.5

iBats: Global acoustic monitoring of bat biodiversity

K. Jones [1]

[1] Institute of Zoology, Zoological Society of London, UK

Biodiversity is being lost at an unprecedented rate in human history as the world population continues to grow and use a greater share of global resources. We urgently need to evaluate the effect of human development on our biodiversity and the benefits we obtain from ecosystems (e.g., clean water, flood and disease control, climate stability). However, basic information on how species abundances and distributions change in response to development are lacking for most areas and species. Bats show the potential to be useful biodiversity monitoring indicator species as they are distributed globally, use a wide range of landscapes and play an important role in ecosystem functioning (controlling insect populations, pollination and dispersing seeds) and their population declines reflect changes in climate, water quality and agricultural practices. Here I present an innovative method for monitoring bat biodiversity at national and international scales to generate data on changes in bat species distributions and abundances to evaluate the impact of global change on biodiversity. Specifically, I develop methods for collecting acoustic transects of bat ultrasonic echolocation calls along roads and demonstrate the feasibility of this approach with preliminary results from annual surveys carried out between 2005-2007 in the United Kingdom and Eastern Europe.

T I.6

DNA barcoding for biodiversity assessment

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DNA barcoding, i.e. taxon identification using a standardized DNA region, has received much attention recently and is being further developed through an international initiative. The now well-established Consortium for the Barcode of Life (CBOL; http://barcoding.si.edu/), an international initiative supporting the development of DNA barcoding, aims to both promote global standards and coordinate research in DNA barcoding. For animals, the gene region proposed for the standard barcode is a 658 base-pair region of the gene coding for the mitochondrial (mt) cytochrome *c* oxidase 1 (COI). For plants, the target is chloroplast (cp) DNA, but the situation is controversial, due to the relatively low sequence variation of this genome. With more and more DNA sequences allowing species identification accessible in databases and new sequencing technologies dramatically expanding available sequencing power, we anticipate that DNA barcoding techniques will be increasingly used by ecologists for biodiversity assessment. They will be able to not only identify a single species from a specimen or an organism's remains using the standardized approach, but also determine the composition of complex source material. For example, the use of very short DNA fragments that persist in the environment will allow an assessment of local biodiversity from soil or water. In my talk, I will emphasize the perspectives offered by the analysis of environmental samples.

T I.7

Activities on species conservation and DNA barcoding as one of the ways of monitoring species in Korea

C-B. Kim[1]

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Biodiversity research in Korea, with emphasis on species conservation, has been systematically well organized and documented even though it is far from comprehensive. Since 1959, the major taxonomic works have been published in the Illustrated Encyclopedia of Fauna & Flora of Korea by the national repository for biodiversity, the National Institute of Biological Resources. In spite of the continuing efforts of taxonomic specialists, drastic species loss and introduction of foreign species have occurred following the global tendency. In a complementary manner to the traditional approaches it was decided to incorporate DNA barcoding. Since 2006, four barcoding projects, supported by government funding, have been initiated in Korea. The Korean Bioinformation Center has developed a database system for Korean barcode data in collaboration with BOLD. Even though a barcoding centre *devoted* to barcoding activities does not exist, an infrastructure for collection, molecular biology laboratory capacity and bioinformatics for the barcode data is well established. Finally, we hope to share barcode activities with other countries as a way of safeguarding future biodiversity.

T I.8

Impacts of Global Climate Change on Tropical Ecosystems: Recent findings and debates

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[1] Smithsonian Tropical Research Institute, USA

Global climatic and atmospheric changes could potentially have wide-ranging effects on tropical ecosystems and their biota. Some possible changes are relatively well understood, others are not and many are subjects of active debate. I will highlight the various kinds of global-scale changes that have been hypothesized or putatively demonstrated for tropical forests. These include deleterious impacts of global warming on cool-adapted biotas at higher elevations, increasing effects of pathogens and declining primary productivity in lowland forests as a result of higher plant-respiration rates. Another potential category of change, which might arise from increasing atmospheric CO_2 concentrations, involves increasing forest productivity from CO_2 fertilization, elevated forest dynamics and non-random changes in plant-species composition. A third category of change, around which there is great uncertainty, concerns the effects of global warming on rainfall regimes and storm intensity in the tropics. Any of these changes could potentially interact with, and exacerbate, the effects of rapid forest loss and disruption in the tropics.

T I.9

KeyToNature: new tools for teaching and learning biodiversity

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After Gutenberg, information useful for identifying organisms was printed on paper. The constraints of a paper-printed text have forced most authors to organise information according to the hierarchical scheme of biological classification. Classification and identification, however, belong to two different operational processes. Supraspecific taxa often need “difficult” characters; hence the classical identification tools are intrinsically “difficult”. However, several programme packages were developed in the last decades, which enable the rapid and easy creation of interactive identification tools which are not necessarily based on systematics. Such tools, having high educational content, are much more user-friendly than the traditional paper-printed keys and can be easily adapted to different educational levels. Their introduction into the educational world will overcome one of the most serious gaps in biodiversity education: the lack of identification tools adapted to user-specified needs. The new tools require the connection of different - presently scattered - databases, including those concerning images, sounds, textual descriptions, thesauri of scientific and common names, etc. - KeyToNature (http://www.keytonature.eu) is a three-year project started in 2007, funded by the EU Commission under the eContentplus programme. The project joins the experience of 14 partners from 11 European countries, including leading centres in biology, pedagogy, education and information technology. It aims at achieving a common approach in teaching biodiversity, mainly focusing on identification, improving the searchability and usability of existing digital contents for the emergence of a European educational service related to teaching and learning biodiversity with novel, advanced, powerful approaches, filling a serious gap. The new technologies raise a series of novel issues and problems, which require solutions. The main objectives of KeyToNature are to: 1) Increase access and simplify use of e-learning tools for identifying biodiversity, 2) Address interoperability among existing databases for the creation of identification tools, 3) Optimise educational efficiency and increase quality of educational contents, 4) Add value to existing identification tools by providing multilingual access, 5) Suggest best practices against barriers that prevent the use, production, exposure, discovery and acquisition of the digital contents required for designing the identification tools. A selection of primary and secondary schools and university courses in the EU will be involved in testing, using and accessing the educational products of KeyToNature. International data standards will be used to make existing e-contents more accessible, usable and exploitable in formal education, both for face-to-face and distance learning.

Symposium II:
Biodiversity: Function and Uses

Ecosystem Services: Provision, Regulation & Support

P.2

Ecosystem Services: Human use of biodiversity functions

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No abstract provided

T IIa.1

Biodiversity & Marine Resources

J. McGlade[1]

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No abstract provided

T IIa.2

Biodiversity and Infectious diseases

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Understanding the ecology and evolution of infectious diseases remains one of the grand challenges in environmental science. Emerging infectious diseases are a threat to biodiversity and their role in species extinction are only recently been realised. Traditionally, it was held that the complex interactions between pathogens and their hosts are the principal driving force of emerging pathogens. Recent evidence suggests that non-host environments and social behaviour may play even more important roles. Indeed, changes in biodiversity at every level, from genes to ecosystems, contribute to infectious disease transmission. Thus quantitative and qualitative relationships between anthropogenic stressors, changes in disease host or vector biodiversity, infectious disease transmission from permissive to non-permissive hosts, all impact on the emergence of infectious disease. In my contribution, I examine the role of environmental and social factors that contribute to diversity change, the population dynamics of animal reservoirs, vectors of disease and the processes whereby infectious diseases emerge and spread.

TIIa.3

Biodiversity, Carbon storage and Trace gas release

D. WALL [1]

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Research on carbon cycling and the relation to biodiversity is at the forefront of understanding how ecosystems will respond to global changes. While much of the research has concentrated on aboveground plant production, there has been considerable research belowground. Soils contain a large volume of carbon (1500Gt) and the balance of C storage and CO_2 release to the atmosphere is dependent to a large degree on the activities of soil biota. Key questions include: Is soil biodiversity important for soil carbon dynamics? Can soil biodiversity loss affect the functioning of ecosystems and the services they provide to humans? Soil biodiversity (animals, microbes) provides ecosystem services such as soil aeration, soil formation, erosion control, nitrogen transformation, waste recycling, bio-control of plant and human pests and soil fertility. At smaller scales, studies of low diversity (< 10 species) show a positive diversity-function relationship, whereas those with greater diversity (>10 species) often show no relationship between diversity and ecosystem function, indicating low diversity ecosystems have less redundancy. A global experiment of >30 sites showed that soil animals increased decomposition rates in temperate and wet tropical regions and suggests loss of a species, abundance or biomass could impair decomposition of litter. Additionally, numerous studies show some taxa (earthworms, termites) are more influential in ecosystem function than others.

Nature as a model for technical applications and innovations

P.3

Biomimetic diversity

J. VINCENT [1]

[1] Mechanical Engineering, University of Bath, UK

We are at a very early stage in appreciating the ways in which biological organisms solve the technical problems of existence. Our current technical problems are related to climate change, energy consumption and generation, water conservation and, crucially, the development of materials with which we can realise novel technologies which will ameliorate these problems. In nature we have answers to these problems from animals and plants living on the environmental edge. These are the most exposed to ecological pressures and so the most vulnerable. We know that these organisms provide novel insights for new biochemistries. Their utility as a reservoir of inspiration for other technologies has hardly been explored. We are investigating them both physiologically (e.g. water capture mechanisms) and theoretically (the role of information in materials processing).

T IIb.1

Biomimetics: Industrial innovation driven by nature

R. BONSER [1]

[1] Centre for Biomimetics, University of Reading, UK

Protection of intellectual property can be regarded as an essential for realising the value of inventions; however, it is costly and may indicate some degree of confidence in a commercial return on this investment. Recent analyses of patenting trends reveal a consistent level of growth in patents containing aspects of biomimetics, or design inspired by natural systems. This may imply that natural systems are increasingly providing the basis of commercialiseable technologies in the marketplace.

T IIb.2

Nature inspired technology: tapping into biodiversity

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[2] Hochschule Bremen, Bionik-Innovations-Centrum (B-I-C), Germany

This talk will present two points of views of bionics. First, we will present the approach and results of an EU-wide effort to design MEMS (Micro-Electronical-Mechanical Systems) for fluid flow measurements inspired from crickets hairs. The continuous back and forth dialogue from insect physiology and ecology to the technological implementation was a key to the design of a successfully functioning new measurement device. We also learned a lot of new biology, driven by questions stemming from the engineer's corner. In terms of returns, however, technology was the sole winner. If time permits, other sensors inspired by insects, designed with a similar spirit, will be presented. In the second and smaller part of the talk, the work done on anti-fouling paints for ships inspired from sharkskin will be discussed. The increased fuel consumption by large tankers and the highly toxic paints requires urgently better technology. Hence, a biomimetic solution would make a lot of sense, both in economic and ecological terms. The reasons for such a successful implementation of a biomimetic approach will be exposed and hints for increasing the number of win-win solutions will be presented.

TIIb.3

Do we need the Sacred Lotus Flower? – A Case Study in Biomimicry

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Biodiversity stands for life and its diversity, the only quality specific to our planet. In millions of years some 10 million species evolved a vast variety of fascinating functions and abilities, which provide a wealth of information for technical innovations. Loss of species means loss of information. One of some 300 000 plant species is the Sacred Lotus. Without having any serious economic value it only plays a role in Asian religions as a rather obscure esoteric symbol of purity. Do we really need this species? Over the last three decades, our analysis of the Lotus leaf surface revealed its surprising secrets. Like most biological interfaces it is not flat and smooth, but exhibits a most intriguing geometry of micro- and nanostructure with water repellent abilities. Even submersed in water the leaf remains absolutely dry for days. Dirt and other contaminants do not adhere to the surface and are washed off by rain drops. Lotus was proven to possess a novel self-cleaning mechanism based on specific physicochemical properties of its surfaces. It was successfully transferred to biomimetic technical products like facade-paints. Today, some hundred thousands of buildings with self-cleaning lotus surfaces exist worldwide. The economic and ecological benefit of bio-inspired materials cannot be overestimated. Bionic applications and biomimicry are further unexpected values of biodiversity. Lotus is only one example out of millions of species, providing an immense archive of potential innovations.

Regulations of Access and Benefit Sharing

P.4

Access and Benefit Sharing: the current debate on regulation in perspective

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Both the Convention on Biological Diversity (CBD) and the more specialist regime of the FAO International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA) endorse the sovereign rights of States over their genetic resources and consequent authority to regulate access and benefit sharing (ABS) although each of these treaties accomplishes these objectives in different ways.

The CBD regime seeks to strike a balance between a State's authority to regulate access to genetic resources and its obligation to facilitate access by others to those resources. When it comes to access to genetic resources under Article 15 CBD the emphasis is on each individual Contracting Party granting access on 'mutually agreed terms' and based on 'prior informed consent', which is a clear indication that access is most likely to be granted on the basis of bilateral agreements.

Likewise Article 15 CBD calls for the sharing in a 'fair and equitable' manner of the results of research and development as well as the benefits arising from commercial and other forms of utilisation of genetic resources. The only caveat to this is that developing countries should enjoy priority access to biotechnologies based on their genetic resources on 'a fair and equitable' basis while transfer of technology to developing countries for the purposes of conservation and sustainable use of biological diversity should proceed on 'fair and most favourable terms'.

In theory, Contracting Parties to the CBD enjoy a wide discretion as to how to regulate ABS and this has already led to a variety of national and regional regulatory developments, which cover a broad spectrum of both statutory and contractual rights, such as bio-prospecting arrangements between governments and individual entities. The scope of national and regional access legislation may also extend to the regulation of traditional knowledge, including the prior consent of local and indigenous communities for access to genetic resources and their subsequent utilisation. Even so, Article 15 CBD makes it clear that national ABS legislation does not cover ex situ collections of genetic resources acquired before the entry into force of the CBD and this has particular significance for collections of seed germplasm, most of which are held in national agricultural research centres or NARCS, agricultural research stations, marine biological institutes, botanical gardens and similar institutions.

In practice, Article 15 CBD is the unsatisfactory outcome of compromise between States and many issues remain unreconciled. Moreover, it is unclear as to how the ABS regime will operate in practice and whether it can meet the pace of agricultural and biotechnological research and development in the real world. To that end work has been going on since 1995 to elaborate and negotiate an international ABS regime while ensuring the effective participation of indigenous and local communities in the process (Article 15 and Article 8(j) CBD). This initial work culminated in the 2002 Bonn Guidelines on Access to Genetic Resources and the Fair and Equitable Sharing of the Benefits Arising out of their Utilization (Bonn Guidelines). The Bonn Guidelines are a set of voluntary, non-binding provisions aimed at guiding Contracting Parties, which are countries of origin of genetic resources, on ways to implement the CBD's articles on ABS and serving as a model for private contracts and other arrangements. Following the January 2008 meeting of the ABS Working Group, agreement has been reached on a five-part framework for further negotiations on an international ABS regime, which will include coverage of fair and equitable sharing of benefits, access to genetic resources, compliance issues, traditional knowledge and genetic resources as well as capacity building. Matters such as the long-term sustainability of the planned international ABS regime, including an appropriate funding mechanism, have not yet been dealt with.

The specific regulation of access and benefit sharing of plant genetic resources for food and agriculture (PGRFA), which remain outside the scope of the CBD, has proceeded along a different, but at times parallel track to that of the CBD. Under the previous legal framework for plant genetic resources the sharing of PGRFA, and knowledge derived from their conservation, were the guiding principles and were of particular importance for scientific research and the transfer of technology. The ITPGRFA follows the lead of the CBD in being more sovereignty-based whilst also seeking to balance the need for conservation of PGRFA against their sustainable utilisation. However, it is precisely in this latter context that the ITPGRFA breaks new ground and has moved ahead of the CBD in establishing an ABS regime, the most important aspect of which is the establishment of the Multilateral System of Access and Benefit-Sharing' (the Multilateral System).

A consequence of a policy reversal in the field of PGRFA, which has seen crop germplasm pass from the domain of common heritage of humankind to that of national sovereignty over biological resources, the ITPGRFA continues to recognise this sub-species of plant genetic resources as a common concern of humankind and the fact that all countries depend to some extent on PGRFA which originated elsewhere. Just like the provisions regulating access under the CBD, Parties retain full authority to regulate their own PGRFA but where the ITPGRFA differs from the CBD is that it places strict limitations on the ability of Contracting Parties to restrict access to that PGRFA from other states. Moreover, while the ITPGRFA covers all genetic material for food and agriculture, states that are Parties to it are under a *de minimis* obligation to guarantee access to the genetic material of 35 crop genera and 29 forage species that are in the public domain and are considered essential for global food security and human nutrition.

In terms of an ABS regime, the Multilateral System's provisions on access under Article 12 of the ITPGRFA are both complex and sophisticated. Access to PGRFA in the Multilateral System is limited solely to the conservation and utilisation of essential crop germplasm for the purposes of research, breeding and training for food and agriculture. However, there are different levels of access, dependent upon whether the crop species is in the public domain, whether it is listed in the Annex I crops and forages, whether it is forms part of an *in situ* or *ex situ* collection and in the latter context whether the species is found in one of the ex situ CGIAR collections. Benefit sharing under Article 13 ITPGRFA is regulated on the basis that all crop germplasm accessed acquired through the Multilateral System is to be shared equitably through one of four mechanisms: exchange of information; access to and transfer of technology; capacity-building; and the sharing of monetary and other benefits arising from commercialisation.

TIIc.1

Transaction Costs in ABS procedures

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In the past years less ABS agreements have been signed than expected. High transaction costs in ABS procedures are named as one main reason for this. Model contracts are one of the measures under discussion. Basis to this discussion has to be an in depth understanding about the realities of transaction costs in ABS procedures. Theoretical and Empirical research on transaction cost indicates that the transaction characteristics and the transaction environment determine the efficiency of organizational solutions. Three large groups of transaction can be differentiated in ABS: direct provider-user transactions; transactions between providers and intermediaries and intermediaries and users. We assume that there are significant differences in transaction costs and organisational solutions for these groups. Especially transactions with the participation of intermediaries are highly relevant for a successful ABS implementation and yet are not at all analysed from a transaction cost perspective. Research in this area needs to systematise the experiences and solutions of stakeholders in genetic resources transactions under ABS requirements concerning transaction costs and transaction environment. Only with this information will it be possible to assess the suitability of model contracts for different sorts of transaction.

TIIc.2

Access to genetic resources and benefit sharing: Undoing or tightening the knot

E.C. Kamau [1]

[1] University of Bremen, Germany

The Convention on Biological Diversity (CBD) entered into force on December 29, 1993 with only three objectives. Article 1 states that, "*[T]he objectives of this Convention, (...), are the conservation of biological diversity, the sustainable use of its components and the fair and equitable sharing of the benefits arising out of the utilization of genetic resources*". More than a decade later, realising these objectives has proved to be a nightmare. From the observation of an international workshop held in Bremen by the Research Centre for European Environmental Law (FEU) of the University of Bremen in February 15/16th 2008, a balance between the interests of provider and user countries (or of the traditional and modern sectors within countries) is far from being reached. Departing from this thought, crucial issues of ABS are discussed with the aim of finding amicable solutions. They include: ensuring and facilitating prior informed consent for the use of knowledge, coping with the special features of disseminated traditional knowledge, tailoring and streamlining access to genetic resources as such, designing schemes of benefit sharing, triggering user countries' benefit sharing obligation under Article 15.7 of the CBD. The talk concludes with a reflection on the need for promoting "cross-fertilisation of legal transplants" as a valuable source of law development equal to "vertical" development through international harmonisation.

Symposium III:
Biodiversity Change – The 2010 Target and Beyond

The loss of biodiversity and approaches for a sustainable world: A state of the art assessment

P.6

Taking the pulse of biodiversity: a vision for a Global Biodiversity Observation Network

R.J. SCHOLES [1]

[1] DIVERSITAS vice chair, and CSIR-NRE, Pretoria, South Africa

It is common cause that the information systems relating to global biodiversity trends are currently inadequate for the purposes of detecting and managing the rapid and far-reaching changes that are occurring in the current era. A large group of biodiversity data providers and users, under the auspices of the Global Earth Observation System of Systems (GEOSS) and the leadership of DIVERSITAS and NASA, have been in discussion on how to put a sufficient system into place. At this time it seems technically feasible to do so, although many details remain to be worked out. The envisioned system would be strongly focussed on satisfying user needs. The core of the system would be observations on the state and condition of biodiversity, at the gene, species and ecosystem levels, but the system would also contain indicators of drivers of biodiversity change, impacts of the change and measure of the effectiveness of the responses. Some of these indicators would come from other GEOSS areas, taking advantage of the synergies provided by an integrated system. The system would need to be able to provide useful information at several scales, ranging from the sub-national to the global and for the immediate past as well as modest projections into the future. For these reasons, the observation system must contain integrated models. Most of the technical elements of such a system already exist, but are not yet linked into a seamless whole. To do so will take a high level of co-operation between a large number of players, including both national agencies and international non-governmental organisations. This will involve additional costs (modest in relation to the investments already sunk into observation systems), but will yield disproportionately large benefits.

T IIIa.1

Approaches to biodiversity planning in a changing world

G. MACE [1]

[1] Centre for Population Biology, Imperial College London, UK

Plans for biodiversity management at local to global scales will be more effective if the goals are set to meet societal needs and if targets are realistic in relation to known trends in direct and indirect drivers of change. Both direct evidence from biodiversity sampling and indirect evidence from observed and modelled information on drivers can be used to focus the targets to be relevant and achievable.

T IIIa.2

Challenges and approaches in (a/the) mega-diversity country(ies) of the south.

J. SOBERON [1]

[1] Division of Ornithology, University of Kansas, USA

To conserve and manage their biodiversity, the megadiverse countries face a number of daunting challenges. One of the most frustrating is the lack of detailed knowledge upon which to base decisions and provide society with elements to demand answers. In this presentation I will analyze this problem from the perspective of scaling of the data and the process of knowledge transferring to decision makers. I will present some experiences that show that certain problems can be faced using available information. Monitoring, specifically, can be addressed using combinations of tools, like Ecological Niche Modelling and data (remote sensing and primary biodiversity databases) previously almost unavailable to many developing countries.

Change of ecosystem functions and services

TIIIb.1

Pollinators as critical ecosystem service providers: the biodiversity of species interactions

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Plant-pollinator interactions are fundamental to the sustainable functioning of the majority of terrestrial ecosystems: they are essential for the reproduction of most plant populations and are directly or indirectly responsible for significant levels of trophic movement of energy and nutrients. The Convention on Biological Diversity has mainly considered the economic importance of pollinator conservation in relation to the agricultural services highlighted by the Sao Paulo Declaration. It is important to recognise, however, that biotic pollination is a critical aspect of biodiversity that has a value far in excess of its significance to crop pollination. There is an urgent need to develop a toolbox of standardised survey and statistical methods to allow rapid assessment and monitoring of plant-pollinator interactions, using historical surveys as a baseline for comparison where possible. Ecosystem monitoring should be undertaken to assess the role of landscape complexity, anthropogenic disturbance and climate change on pollinator diversity in order to develop indices of current and future habitat quality. Meeting the targets of 2010 and beyond requires us to go further than taxonomic inventories and consider changes to, and extinctions of, species interactions.

T IIIb.2

Conservation genetics: from species to habitats

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[2] Inst. for Animal Health, UK
[3] Biodiversity Institute of Ontario, Canada

Conservation genetics, as does conservation in general, falls into the two broad areas of the identification and preservation of endangered species and the identification and preservation of biodiverse habitats. Most research has been in the first area, with hard-won findings on the importance of genetic variation in population management, but genetics promises to be at least as important in the second great aim. Molecular phylogenies have long been proposed as an important approach that has been shown to capture conservation worth and evolutionary distinctiveness better than simple species richness and avoids common problems in defining species identity and boundaries. Progressively faster and cheaper DNA sequencing and the rise of DNA barcoding are making the phylogenetic approach to habitat conservation widely applicable. Barcoding was seen initially as a means to species discovery and to species identification, but it now holds promise as a resource-efficient means of estimating the evolutionary history preserved by different sets of reserves. Initial indications are that biodiversity assessment using the short cox1 sequence usually used in barcoding animals reliably reflects the picture from longer sequences. The phylogenetic approach not only infers evolutionary history via barcoding, but in synergy with morphology, will speed species discovery and the subsequent expansion of general biological knowledge.

Towards an integrated biodiversity observation system

T IIIc.1

A Global Biodiversity Observation Network: What Do Satellites Have to Offer?

W. Turner [1]

[1] Earth Science Division, NASA, USA

Satellite data typically come to us at spatial resolutions too coarse to detect two of the three key elements of biodiversity (i.e., genes and species). Nonetheless, many see satellite imagery as a vital component of a biodiversity observation network. What do satellites actually have to offer the biodiversity research community, limited in both resources and time? Do satellite products justify the funds, time and effort required to use them effectively in biodiversity research? Recent developments are converging to make satellite data and related products an integral part of any strategy to understand, monitor and conserve biodiversity across spatial scales. Rapid growth in the number and variety of sensors on orbit is giving us unique looks of the Earth at new spatial resolutions, wavelengths and repeat times. The widespread availability of geopositioning devices has enabled field researchers to put their *in situ* data into a broader context while the revolution in geographic information systems has provided platforms to overlay site-based biodiversity data with satellite information. The Web allows us to move digital information around the world. We may also be entering a time of greater political integration in the realm of Earth observation. All of these are positive signs. Yet, it is still necessary for the tools to work. My talk will focus on remote sensing solutions to the challenge of understanding biodiversity and how it is changing over time.

T IIIc.2

Techniques & targets: The present potential and the future role of projections & predictions

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No Abstract.

T IIIc.3

Observatories and exploratories: German interdisciplinary approaches to realise biodiversity changes and understand their functional consequences

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The Millennium Ecosystem Assessment 2005 clearly shows the interactions between biodiversity, ecosystems and people. To detect changes in biodiversity, to unravel their drivers and causes and to assess their consequences, interdisciplinary collaboration of scientists from life sciences, geosciences, social sciences and economics is necessary. Beyond that, research into biodiversity changes requires combined research activities on the same areas or regions, long-term perspectives of research and funding and a database, that allows handling of a great variety of data sets in easy accessible formats. Efforts have been made worldwide towards those goals, e.g. in the ILTER programme. However, there are many plans, few conclusive results and even less ecological experiments. Nevertheless, politicians and stakeholders call for scientifically sound and workable scenarios as decision support information. German approaches tackling the problems associated with biodiversity changes or losses will be briefly presented, such as the BIOLOG/BIOTA-programme, the Exploratories-programme and some other relevant research projects. Although some of them are now running for up to 10 years and have accumulated a wealth of mainly scientific data, development of reliable guidelines and their implementation remains a major problem.

TIV.1

Experiences from implementing CBD in the local context; Restoring *Satoyama* and urban biodiversity through citizens' participation in Higashiyama, Nagoya Aichi

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As a potential city for hosting the 10th meeting of the Conference of the Parties (COP10), Nagoya designed a plan for urban biodiversity. Despite its size of 2.2 million residents, Nagoya has two unique ecosystems: tidal flats and urban forests within its area. Historically the city struggled to balance urban pressure and resource needs against conservation of its urban biodiversity. Increasing pressure by residents is a threat to neighbouring urban forests, and conservation of biodiversity is aimed at designing sustainable use patterns for these ecosystems. Based on past experience, the current plan targets the restoration of its urban forests by facilitating the participation of local residents. As part of the plan, urban forests are categorized into five areas based on human uses: *Satoyama*, animal watching, environmental education, cemetery and waterfront. *Satoyama* translates as "forest areas that exist between residential and mountainous regions" and these forests once supplied fuel and daily commodities for local communities. The challenge with the current plan is to translate conservation and sustainable methodologies into reality and this is two of the three key objectives of the Convention on Biological Diversity (CBD). Restoring *Satoyama* is regarded as one model in achieving such objectives. In this paper, examples of citizens' participation will be discussed.

Poster Presentations

Symposium I

P I.1

Plazi.org: A service to provide access to the content of the published taxonomic literature

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Access to taxonomic literature is a vexing problem in a biodiversity crisis, and the rapidly developing World Wide Web (WWW) allows unlimited sharing of all this information. This highly structured, >100 million pages of printed and increasingly electronic documents of taxonomic literature covering the world's species, includes an often unique source of information. Through its structure, this corpus is predestined for machine reading and data mining. The Biodiversity Heritage Library and animalbase.de, as well as taxon based services like antbase.org are increasingly providing access to the old printed record; however, for a large part of new literature it is assumed that they fall under copyright protection and thus are not accessible for open access. The Plazi.org association aims at developing and building technologies to transform legacy documents into semantically enhanced, machine readable documents, providing a repository or archive for species descriptions, exploring the legal issues and collaborate with partners to make all the taxonomic publications open access. Tools already developed include a taxonomy specific XML mark-up schema (TaxonX), a dedicated XML editor (GoldenGate), a repository (Dspace) for marked-up publications, and a dedicated server to provide access to the descriptions enhanced with Life Science Identifiers for names, specimens, and legacy publications. The system provides over 3,700 descriptions and is supported from GBIF, US-NSF and German DFG.

P I.2

Freshwater fungi: Biodiversity research before they vanish?

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Freshwater fungi are a phylogenetically heterogeneous group predominantly found on organic matter in lotic ecosystems. They are key players in the carbon cycling and energy flow of aquatic habitats. Human impairment of nature results in a dramatic decrease of natural and near-natural aquatic habitats. In particular, the amphibian ecosystems seem to be sensitive to changes in climate. Climate change scenarios include the increase in summer droughts in Europe. Two effects of low rainfall are already apparent: The premature leaf fall and the fragmentation of streams into small pools. As the leaf litter degradation is part of the global carbon cycle, the ecological function of microorganisms directly involved, should be well understood. However, our knowledge of freshwater fungal diversity, life cycles, community dynamics and individual functions in ecosystems remains poor in comparison to other fungal groups such as phytopathogens. Most publications on freshwater fungi concern ecologically aimed studies based primarily on identifying and counting fungal spores. However, the revealed data give an incomplete picture of diversity, disregarding substrate specificity, sporulation conditions and microbial interactions of freshwater fungi. Furthermore, the lack of taxonomic expertise leads to misidentification of freshwater fungi. We overview the knowledge of freshwater fungal diversity research to date and advertise the need for future studies in both: diversity assessment and functions.

P I.3

International collaboration between taxonomists in All Taxa Biodiversity Inventories

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"All Taxa Biodiversity Inventories" (ATBIs) are long term efforts by large numbers of taxonomists to identify and document the total biodiversity of a given area in the most efficient way possible. The EU-funded "European Distributed Institute of Taxonomy" (EDIT: Work Package 7 "Applying Taxonomy to Conservation") organizes such inventories as concept for international taxonomic collaboration. The principal objectives are to enhance the relation between taxonomists and other users of taxonomic information, to accelerate the processes of taxonomic science through the worldwide web and to overall transform taxonomy into an integrative science. In 2007 the first ATBI started in the French/Italian Mercantour and Alpi Marittime natural parks and during the first 3 months over 40 scientists from six EU countries visited the parks with support from EDIT. These participating scientists documented a broad spectrum of taxonomic groups that included conspicuous organisms such as butterflies and birds, but also less conspicuous groups such as diatoms, bryophytes (mosses and liverworts), tardigrades (water bears) and parasites of the park's mammal species. First results underline the high biodiversity of the region, which is, however, locally affected by impacts from anthropogenic activities, for example, high intensity of livestock grazing. Records and specimens collected in the framework of EDIT's ATBI activities are being made available online for participating researchers and conservation management to maximize re-usability of the results. For 2008, field work will be scaled up in the Mercantour / Alpi Marittime parks involving specialists from many additional European institutions. Furthermore, the EDIT ATBI concept will be promoted for implementation in nature reserves elsewhere in Europe (e.g., the Slovakian Carpathians) as well as in biodiversity rich countries outside Europe. In the Mercantour / Alpi Marittime parks, the first EDIT "Summer School in Taxonomy" will take place in 2008 to which students can subscribe for courses in biodiversity field recording and collection techniques.

P I.4

Biodiversity in the deep sea – adding the largest piece to the puzzle

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The Census of Marine Life, an international megaproject involving several hundred scientists from over 80 nations, is a visionary project to assess the diversity of life in the oceans of the world which cover about 70% of the Earth's surface. Several ocean realms were identified which have been sampled according to carefully designed plans with standardised methods to ensure better estimates of the species richness of the ocean and to learn more about the scale with which to assess biodiversity in different parts of the ocean, e.g., coastal waters or the deep-sea basins. One of the so-called field projects of the Census, CeDAMar, assesses the diversity of abyssal plains and basins. During more than ten cruises to areas in the southern Atlantic, the Southern Ocean and the eastern Pacific, stations were sampled with a large array of gear to collect qualitative and quantitative data on organisms ranging from bacteria to whales. Sedimentological and biogeochemical data are used to relate distributional patterns of selected taxa to ecological parameters. Molecular genetics are used to reveal evolutionary processes that might drive biodiversity in the deep sea. All projects of the Census are entering their synthesis phase, preparing products to be presented to the scientific community as legacies which are hoped to foster further research beyond 2010 when the Census in its current form ends. Among these legacies are OBIS, a portal to marine data bases, and EOL, the Encyclopedia of Life.

P I.5

Mitochondrial DNA Variation in the invasive North American beaver (*Castor canadensis*) in Tierra del Fuego (Argentina) and spatial analysis in the control of populations.

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The North American beaver *Castor canadensis* was introduced in Isla Grande of Tierra del Fuego, Argentina, in 1946 as a potential source of wild fur. The species showed a growth capacity reaching close to 100,000 individuals from an original founder stock of 25 females and 25 males. Beaver adapted rapidly to its new environment and became an invasive species providing an excellent model of a successful adaptation of introduced population to a new habitat. In this study, we used polymorphic mitochondrial (mt) DNA to evaluate genetic variation in the introduced Tierra del Fuego beaver population. Nucleotide variation in partial sequences of the main non-coding region DL (521 bp) were analyzed. Our study has allowed us to identify 7 different mtDNA lineages in the invasive population indicating an absence of gene flow that could be explained by a halt of the original expansion of the 50 founder beavers from rivers and watershed network of Isla Grande since the time of its introduction. This approach will help to understand the effects of genetic change on the survival ability and reproductive success of invasive species and also have important implications for the management of invasive species.

P I.6

Primate biodiversity: characterization, mechanisms, and conservation

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Although primates represent one of the most diverse mammalian orders, which currently include about 700 species and subspecies, their taxonomic status and phylogenetic relationships are far from being resolved. Moreover, more than 40 taxa have been discovered and described within the last 15 years. Since 62% of all primates are endangered, they represent important flagship-species for initiating conservation activities in regions of high biodiversity. The aim of this research initiative is to better understand the causes and mechanisms contributing to primate biodiversity. Using a comparative approach, we are studying eight genera, representing the main radiations of primates in South-east Asia (*Presbytis, Nomascus, Macaca),* Madagascar *(Cheirogaleus, Microcebus, Lepilemur, Propithecus),* Africa (*Papio*) and South America *(Saguinus*). Specifically, we address three interrelated aims and questions. 1. Characterization of biodiversity: How many taxa exist in these primate groups? Genetic traits, biogeographic and morphometric data are being used to characterize different taxa, identify evolutionary independent units and clarify their phylogenetic relationships. 2. Causes and mechanisms of diversity: Which specific processes may have caused speciation and radiation within the groups? How do primates in the macro-geographic regions differ in this respect? 3. Conservation: By delineating taxa, we can help determine effective conservation units for primates and conservation priorities.

P I.7

From sugarcane plantations to primary rainforest: Ants in the Kakamega Forest area (Kenya)

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Ants are highly abundant and important elements of tropical ecosystems and perform a variety of ecological functions. In particular, they are among the most important predators in natural and agricultural ecosystems. However, up to now it is scarcely known if human caused environmental degradation affects the diversity, composition and ecological function of rainforest ant communities. In our newly established project within the framework of the BIOTA East Africa project we investigate how habitat degradation affect ant communities and try to evaluate patterns and consequences for ecosystem functions. The study was done in the Kakamega Forest, Kenya, and the surrounding agricultural area. We set up 27 transects along a degradation gradient (primary and secondary forest, extensively and intensively managed farmland). The ant sampling was performed by using 2 standard methods for the collection of ground-dwelling ants: Winkler litter extraction and pitfall trapping. However, up to now only 50% of the pitfall traps have been processed and analysed, so that we present our first results. We tested if ant species richness and species composition differed among the habitats and we found significant differences in both. Our preliminary results suggest that extensively managed farmland habitats may sustain a high number of ant species. Nevertheless, the conservation value of farmland habitats for the ant fauna of East African rainforests seems to be rather low, as many ant species depend on forest habitats.

P I.8

Beyond economic efficiency in biodiversity conservation

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The paper aims to explain the importance of the democracy stance as compared to the efficiency stance in order to deal with complexity in biodiversity conservation. While the efficiency stance refers to the realm of relatively simple systems, individual rationality and instrumental values, the complexity stance transcends these boundaries into the realm of complex systems, social rationality and intrinsic values. We argue that the task of biodiversity conservation is impossible to achieve in merely economically efficient ways, because (a) it is impossible to come to a (fully informed) complete account of all values, not only because it is costly but also because (b) moral values are involved which (by their nature) exclude themselves from being accounted for and (c) biodiversity conservation can be regarded as an end in itself instead of only a means towards an end. The point we raise is, that in order to cope with biodiversity conservation we need to apply valuation methods which are from the complexity stance, take better account of intrinsic values and feelings, as well as consider social rationality. Economic valuation methods are themselves ‘value articulating institutions’ and as biodiversity conservation confronts us with the complexity of social-ecological systems, the choice of the ‘value articulating institutions’ needs to consider their ability to capture instrumental and intrinsic values of biodiversity. We demonstrate a method, based on cybernetics, which is able to take into account the issues raised.

P I.9

Rapid assessment of fungal diversity using genetic fingerprints

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Fungi are of great ecological and economical value. However, the knowledge about fungal diversity, especially in the tropics, is still scant. Due to the proceeding destruction of old growth tropical rainforests and the associated loss of plant hosts and capable habitat, a loss of fungal diversity is expected. Old growth forests are often replaced by secondary forests. The successional dynamics of fungal diversity in these secondary habitats is unknown and therefore even the magnitude of the expected loss in fungal diversity can not be evaluated. As a first step, a rapid assessment of fungal diversity in secondary forest sites of different successional age is necessary to direct the conservation and restoration of fungal biodiversity. Our study is part of the SOLOBIOMA project, a German-Brazilian co-operation with its focus on the Atlantic rainforest in the Brazilian state of Paraná. This rainforest is known to be a biodiversity hotspot and also one of the most endangered rainforests in the world. The aim of the study is an assessment of fungal diversity in forest sites of different successional age. We use ARISA, a genetic fingerprinting method, which is appropriate for a quick assessment of fungal diversity with a high resolution and reproducibility. On the basis of length variability of a given, non-coding DNA region (ITS) operational taxonomic units are defined, which are used for further diversity analyses. First experiences and results with this method are presented.

P I.10

The EU Project ALARM: Assessing Large-scale Risks for biodiversity with tested Methods.

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Based on a better understanding of terrestrial and freshwater biodiversity and ecosystem functioning, research will focus on assessment and forecast of changes in biodiversity and in structure, function and dynamics of ecosystems. This relates to ecosystem services and includes the relationship between society, economy and biodiversity. In particular, risks arising from climate change, environmental chemicals, biological invasions and pollinator loss in the context of current and future European land use patterns will be assessed. There are an increasing number of case studies on the environmental risks subsequent to each of these impacts. This yields an improved understanding on how these act individually and affect living systems. Whereas the knowledge of how they act in concert is poor and ALARM will be the first research initiative with the critical mass needed to deal with such aspects of combined impacts and their consequences. Risk assessments in ALARM will be hierarchical and examine a range of organisational (genes, species, ecosystems), temporal (seasonal, annual, decadal) and spatial scales (habitat, region, continent) determined by the appropriate resolution of current case studies and databases. The ALARM consortium combines the expertise of 68 partners from 35 countries. ALARM encompasses 7 SMEs as full partners with central responsibilities and with a share of >10% of the project resources. Total project costs are 22 Million Euro.

P I.11

Documenting and Explaining Biodiversity: Insights and Prospects from Danthonioid Grasses (Poaceae)

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Species level phylogenies are a valuable tool for explaining processes underlying changes in biodiversity, globally and locally. For >200 years the temperate grass subfamily Danthonioideae has been the focus of active research and the number of recognised species, currently 288 distributed worldwide, is still growing. Real advances in our understanding of species diversity, however, have only been made recently, due to increases in the availability and power of molecular and analytical techniques and due to collaborative research efforts. Molecular phylogenetics has shown non-monophyly of several genera, e.g. pampas grasses, *Cortaderia*, and the African *Merxmuellera*. The need for a reliable nomenclature has thus led to a reconsideration of generic delimitation criteria. Molecular clock and likelihood optimisation methods have allowed us to infer the origins and spread of this group in time and space. Only in a phylogenetic context can we infer just how frequent intercontinental dispersal has been. Global species diversity and distribution today are the result of several such events, originating in southern Africa (~15 Mya). While local species richness in some areas chiefly results from repeated immigration (Drakensberg), in others it is attributed primarily to *in situ* diversification (Cape). The importance of taxonomy, for the continued documentation and communication of biodiversity and of phylogenetics, in explaining dynamicity of biodiversity globally and accumulation of biodiversity locally, is evident.

P I.12

Diversity of Baboons – Genes, Vocalizations, and Social Behaviour

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The taxonomic status and phylogeny of the genus *Papio* is a current subject of speculation. Although baboons are a well-studied genus the number of species within the genus is debated and the phylogenetic relationships among the taxa are widely unknown. For the assessment of genetic diversity contact zones of different taxa are of special interest. Thus we focused our study on southern Africa where, according to different sources, two to six taxa meet. Using different genetic markers (mtDNA, nDNA, Y-chromosome) we aim to clarify the genetic relatedness between taxa and elucidate the evolutionary mechanisms that led to the current pattern of genetic clades. Genetic material was extracted from faecal samples we collected in different regions of southern Africa. First results confirmed the proposed genetic distinctiveness of the Kinda baboons (*Papio cynocephalus kindae*) in Zambia and narrowed the southern border of this taxa down to less than 100 km. Furthermore, at least two genetically distinctive forms of Chacma baboons (*P. ursinus*) occur, a south-western and a north-eastern clade. We conducted a detailed study of baboon vocalizations and social behaviour in Namibia, the western habitat border. Our aim is to compare these results with the data we will collect from a Mozambican population as representatives of the easternmost Chacmas. The combined results will shed light on the forces that caused and influenced the ongoing process of speciation in the genus *Papio*.

P I.13

Sulawesi: Island between the Realms – Biodiversity Research in Central Indonesia

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The majority of earth's biodiversity occurs in the tropics. Indonesia, with its thousands of islands, is one of the megadiversity countries of the world bridging Asia, Australia and the Malay Archipelago. Sulawesi (formerly known as Celebes) lies right in the centre of this vast archipelago. Due to its exceptional geographic position between these distinct faunal regions, Sulawesi, together with the Lesser Sunda Islands in the south and the Moluccas in the east, represents a zoogeographic transitional region called Wallacea. Thus, Sulawesi's fauna comprises an assemblage of typical Oriental and Papua-Australian species. In addition, because of long periods of isolation in its geological history, Sulawesi is characterized by a high degree of endemism (e.g., >40% in butterflies) embedded in a complex biogeographic setting. Despite the investigations of numerous famous scientists of the 19th and 20th century such as P. Bleeker (fish, amphibians, reptiles), G. A. Boulenger (fish, amphibians, reptiles), L. Martin (butterflies), G. G. Musser (rodents), F. and P. Sarasin (fish, invertebrates), E. Stresemann (birds) and M. Weber (fish), recent fieldwork on Sulawesi reveals several new records for that island as well as many more undescribed species of fish, amphibians, reptiles and butterflies. Thus, the peculiar fauna of Sulawesi is still far from being completely inventoried and further systematic investigations are urgently required to fill these gaps.

P I.14

Characterisation and valorisation of grapevine cultivated in a coastal oasis.

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The oasis of Chénini (southeast Tunisia) presents a wealthy genetic diversity. The grapevine is one of the oldest fruit trees cultivated in this oasis. The valorisation and the conservation of this threatened inheritance remains a preoccupation of the oasis peoples. Eight local varieties have been collected for description based on pomological and chemical characteristics of its fruits and leaves. This characterization showed that most of these varieties present a good adaptation to environmental conditions and an acceptable quality of fruit (low acidity and high sugar content). Vitamin C is present as a trace in these varieties (3, 22 - 6, 69 mg/100g). Uses for the studied grapevines could be as follows: Mguergueb, Miski, Sawoodi and Khalt for grapes, the Medina and Bezzoul Kalba Akhder for table wine and Akhal for dry grapes. These varieties need particular attention and valorisation to carry out genetic improvement.

P I.15

Development of a European Environmental Risk Assessment Toolkit (RAT) for biodiversity and ecosystems

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ALARM (Assessing LArge-scale environmental Risks for biodiversity with tested Methods), an Integrated Project funded under the European Union's Framework Programme 6, aims to develop methods to predict risks to a range of aspects of biodiversity associated with the combined action of key drivers such as climate and landuse change, environmental chemical pollution, biological invasion as well as loss of pollinators. Such risk assessments should account for interactions between drivers and reflect natural variability and qualitative and quantitative uncertainty in our knowledge. An important challenge in communicating biodiversity risk assessment is therefore how to present such a complex and uncertain picture across scientific disciplines and to policy makers, politicians and the wider public. Here we describe the initial development of a European Risk Assessment Toolkit (RAT) by the ALARM consortium which aims to provide an interactive tool to allow users to explore uncertain multiple and varied biodiversity risk assessments generated at the European scale by the ALARM project. The aim is to provide access to individual risk assessments, but to also allow sets of results to be grouped together according to a user defined criterion (e.g. all measures of aquatic environments), enabling end-users to build-up more complete pictures of areas of particular concern.

P I.16

Taxonomy and Biogeography of tamarins (genus *Saguinus*, Hoffmannsegg 1807)

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The tamarins of the genus *Saguinus* (family Callitrichidae) represent one of the most diverse primate radiations. So far, about 30 taxa have been described from Amazonia, but detailed information on their taxonomic status, phylogenetic relationships, biogeography and the mechanisms of speciation is still lacking. The general aim of this study is to clarify the taxonomy and internal relationships within the genus *Saguinus*. Therefore, several molecular markers, including mitochondrial, autosomal and gonosomal markers, will be applied. Two expeditions to the Peruvian Amazon (an area of high tamarin diversity) are conducted to collect faecal samples from different wild tamarin populations. For the non-Peruvian taxa tissue samples of museum specimens and captive animals will be used. Taxonomic data will be combined with biogeographic evidence to analyse the biogeography and speciation of *Saguinus* and to develop a model for tamarin radiation throughout Amazonia in the Pleistocene and to explain the complex extent tamarin diversity and distribution. This may also provide general evidence for speciation processes and the role of riverine barriers and Pleistocene refugia in Amazonia, one of the biodiversity hotspots of the planet. An additional outcome of the study could be the detection of tamarin taxa in certain parts of Northern Peru, which are unknown to science so far.

P I.17

Phylogeny and biogeography of the Asian leaf monkey (Colobinae) genus *Presbytis*

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With more than 50 previously described taxa (Groves 2001), the Asian leaf monkeys (Colobinae) of the genus *Presbytis* represent one of the most diverse genera within the Old World monkeys (Cercopithecoidea). Although many studies on the taxonomy of *Presbytis* have been carried out during the last three decades, the phylogenetic relationships within the genus and the current biogeographic patterns of distribution are still disputed and controversially discussed. Almost all previous studies are based on anatomical features, particularly pelage colouration and the very few molecular genetic data are heavily based on captive animals. The main objectives of this study are therefore to clarify the taxonomy, phylogeny and biogeography of *Presbytis* using molecular genetic analysis and bioacoustic data. In an initial field survey, faecal samples for DNA extraction have been collected from selected wild populations on Java and Sumatra. Male loud calls were recorded with the use of a playback experimental design. Phylogenetic reconstructions will be based on maternal, paternal and biparental genetic markers. Structure analysis of the loud calls will be applied and used as an additional parameter to supplement the phylogenetic reconstructions. The results of this study will contribute to a better understanding of the process of speciation and biodiversity in colobine monkeys and provide important information for the assessment of the conservation status of the genus.

P I.18

Phylogeny, taxonomy and distribution of crested gibbons (genus *Nomascus*)

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Currently, several classification schemes based on morphology, fur colouration and genetics are available, but no consensus of crested gibbon taxonomy exists and the distribution areas of different taxa are not well defined. All gibbon taxa are endangered at different levels, knowledge about their taxonomic classification and their exact distribution zones is a major issue for crested gibbon conservation. The present study is set up to clarify the taxonomy of crested gibbons and to elucidate their exact distribution zones. Therefore, an approach will be used in which acoustic, morphological and genetic data will be combined. Call parameters from acoustic signals will be extracted and analysed in combination with already published data. In order to detect hybridization or introgression, genetic studies will include maternal, paternal and biparental marker systems. As the maternal inherited marker, the complete mitochondrial cytochrome b gene and the hypervariable region I of the mitochondrial D-loop will be sequenced. To obtain paternal and biparental data, partial sequences from the genes coding for the testis-specific protein on the Y-chromosome and von Willebrand factor will be generated, respectively. Based on the expected results, it will be possible to 1) clarify the taxonomy of crested gibbon taxa, 2) depict their exact distribution zones, 3) reconstruct phylogenetic relationships among them, 4) reconstruct biogeographic patterns leading to their current distribution, and 5) detect possible hybridization zones.

P I.19

Decline of ant-following birds in African rainforest fragments: patterns and causes

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In the tropical rainforests of Africa and America, specialized insectivorous birds follow the swarm raids of army ants and prey on insects which are flushed by the ants. In a Congo-Guinean rainforest in western Kenya, I studied the consequences of habitat fragmentation on African ant-following birds and analyzed if their response is related to the availability of army ant colonies in habitat fragments. Similar to ant-following birds in the Neotropics, most specialized ant-followers totally disappeared or strongly declined in small forest fragments. My data suggests that the decline of these birds is best explained by a decrease in the size of forest fragments and by the loss of *Dorylus wilverthi* army ants from small forest fragments. Even though a second army ant species, *Dorylus molestus*, compensated the decline of *D. wilverthi* in terms of mean abundance, it can not functionally compensate it because the daytime activity of the former, but not of the latter species, is depending on high humidity conditions. Consequently, in the dry season, specialized ant-followers in small fragments missing *D. wilverthi* colonies suffer from food scarcity due to a cessation of army ant foraging. My study elucidates that a subtle alteration of the species composition in fragmented rainforests may have large ecological consequences.

P I.20

Phylogeographic approach in two species of armadillo from Argentina: *Chaetophractus villosus* and *Chaetophractus vellerosus* (Dasypodidae, Xenarthra).

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Living xenarthrans are representatives of the initial South American mammalian stock. This order is the second offshoot of the placental tree, after the rise of Afrotheria and represents one of the four major placental clades. Armadillos are the oldest and most diverse xenarthran lineage, with about 21 extant species, 14 of which are present in Argentina including *Chaetophractus villosus* and Chaetophractus *vellerosus*. The phylogenetic and phylogeographical aspects of these species have not been elucidated thus far; consequently, analysis of molecular markers, such as the Control Region (CR) of mitochondrial DNA, has been proposed to study molecular evolution of these armadillos. The CR has three components: two lateral hypervariable domains, namely ETAS (extended termination associated sequences), CSB (conserved sequence blocks) and a Central Domain (CD), which evolves, in terms of mutation rates, as any mitochondrial gene. Particularly, variable regions of ETAS and CSB are used for population structure and phylogeography studies. Sixty nine CR sequences were analyzed and 17 haplotypes for the Control Region were identified for the first time for genus *Chaetophractus*, constituting a novel contribution for the elucidation of Xenarthran molecular evolution. This study has important implications in biodiversity and species conservation.

P I.21

Biodiversity Characterization of *Ephedra* in Lahul & Spiti (India)

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The relative difference in responses of growth forms to habit conditions are useful in determining the relative status of build-up of diversity and adaptation of the different species. The Gymnosperms represent the most primitive type of seed plants. They have their own implication because of attractive foliage, ecological, economical and therapeutic values and grand appearance providing splendour to the hills, at higher elevations and are closely associated with the life of human beings. Living Gymnosperms in the world comprises about 70 genera and 750 species. Indian boundaries encompass only 48 species and 10 varieties under 15 genera, growing in wild state in different environmental habitats. *Ephedra* is such a taxon that grows in extreme conditions in hot and cold deserts in India. The monitoring of *Ephedra* in Lahul & Spiti region (alt 3600 m) exposed its value in ethnobotany, medicine and ecology. It thrives in open, dry loose gravel soil, as well as rock crevices and road side cuttings in the high ranges of North West Himalaya. The stem possesses an active constituent (ephedrine), which is used to cure respiratory passage infections and tooth ache. Successful tissue culture practices will be an invaluable contribution for rapid propagation and for *in vitro* conservation in this regard. The present paper emphasizes diversity, systematic studies including variation in populations, reproductive behaviour of Indian Ephedras to realize a way of sustainable utilization and bioprospecting by extensive field explorations. An attempt has been made to solve the disputed taxonomy considering morphological markers and the combination of characters in Lahul and Spiti, which may be the additions to the existing data. The patterns of morphological variation within and among populations of *Ephedra* in the Western Himalayan region have been investigated. Populations of *E. intermedia* collected from the various localities of Lahul and Spiti, depict contrasting results in the character states of habit, morphology of scale leaf, male and female strobilus. The major distinct characters included are shape, size, number, extent of connation of scale leaf at the nodal region on stem, bract, synangiophore with synangium in mature male strobilus and bract, colour of seed, degree and nature of coiling of micropyle in mature female strobilus. On this basis a new species *E. sumlingensis* Sharma & Uniyal has been established and much more needs to be explored for new inventions to come up in the near future.

P I.22

Towards a Global Assessment of Taxonomic Needs and Capacities: what taxonomists do we need where?

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The Global Taxonomic Initiative (GTI) is a cross-cutting issue of the UN Convention on Biological Diversity (CBD) and as part of its Programme of Work, has asked in 2002 for national, regional and global assessments of taxonomic needs and capacities (CBD/COP6/Decision VI/8). Whereas several national and regional assessments have already been undertaken, a global assessment is still pending. As an important contribution for a global assessment, information about the current state of knowledge of national biodiversity and taxonomic capacities is being compiled. The German GTI National Focal Point is contributing to the global assessment with a study analyzing the numbers of taxonomists and taxonomic resources in relation to the species numbers recorded and estimated per taxonomic groups and countries, also with a focus on species inventories of protected areas. As expected, preliminary results indicate that existing taxonomic knowledge and resources are distributed unequally among countries and taxonomic groups. Numbers of taxonomists and the relative state of knowledge about a countries' biodiversity are positively correlated, whereas numbers of taxonomists negatively correlate with the known or estimated actual species richness per country. Especially, tropical regions of Africa are in need of more taxonomic expertise, as are many parts of SE Asia. The state of knowledge of not especially prominent and unpopular groups such as micro-organisms, algae, fungi and several invertebrate taxa is generally poor.

P I.23

The EDIT network: Taxonomy to enhance capacities in conservation.

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The conservation of biodiversity requires not only a solid knowledge of existing organisms, but the ability to assess, identify and measure change as it happens. Taxonomy covers the whole of these techniques and scientific enquiries; to maintain good conservation, therefore, we need to develop and upgrade taxonomic practice and standards. The European Distributed Institute of Taxonomy (EDIT) is a European Commission-sponsored Network of Excellence aimed at starting to overcome the "taxonomic impediment" through collaboration, integration and a joint work programme (http://www.e-taxonomy.eu). It is made up of 22 major European scientific centres in taxonomy, along with Russian and US partners. Through EDIT we hope to build capacity globally and provide information and tools for use by all. The EDIT proposal is an initiative of the Consortium of European Taxonomic Facilities (CETAF) which since 1996 has been working for better integration of the taxonomic effort in Europe.

P I.24

Aquatic Biodiversity in Latin America

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Latin America is famous for harbouring many hot spots for biodiversity. However, very little is known about its aquatic fauna and flora. Information is scattered for different geographical regions and combined datasets about taxonomy and ecology of individual species are hardly available. This scarcity of knowledge is opposed to a fast dwindling diversity of aquatic species due to a large number of ecological impacts. An international team of editors have combined their efforts to compile the current state of knowledge in taxonomy *and* ecology, in order to produce a concise and affordable handbook for each group. Information on the ecology and status of the taxa (written in English) is combined with illustrated identification keys to families and genera, in both English and Spanish. Four volumes on Fish Parasites, Ephemeroptera, Simuliidae and Ceratopogonidae of South America are already available, other volumes on Plecoptera, Mecoptera and Neuroptera are close to be published. The series is an essential tool for standardizing and accelerating biodiversity assessments and monitoring, for training purposes and to identify lacunae for future research and conservation.

P I.25

Collections, Research, Data and Informatics - Integrating and Accessing Knowledge on Biological Diversity at the BGBM

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With a permanent staff of about 150 the BGBM is the largest German collection institution. The botanical garden is one of the three largest in the world with respect to species and accession holdings. The herbarium again counts among the top 20 worldwide, and the library has the most complete holdings of botanical literature in the German-speaking area. Since 2007, the BGBM DNA bank coordinates the establishment of a network of German DNA banks. The institution thus offers excellent access to taxonomic primary information which forms the basis for a wide array of research activities, ranging from biosystematics and the inventorying of phytodiversity to molecular genetics and applied conservation research. The BGBM's Biodiversity Informatics Department, which is one of the global leaders in its field, develops IT services and tools to integrate taxonomic and specimen data from multiple, disparate resources. The BGBM's objective is to communicate scientific knowledge of the plant kingdom and to increase awareness of the public to the threats the living world is facing today. The integration of biological knowledge, using voucher specimens and organism names, facilitates 'taxonomically intelligent' information and enables comparative biology. Thus, biodiversity knowledge can be used more readily by researchers and decision makers in applied contexts – such as the study of climate change effects on the conservation of species and habitats as well as questions of health and well-being of humans.

Symposium II

P II.1

Livelihood demand and its implication on the alpha and beta diversity of tropical rainforest in southwestern Nigeria

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This study examines the demand placed on the diversity of tropical rainforest by the interaction of local communities with forest estates in their bid to secure a livelihood. The linkage between poverty and environmental degradation is investigated and the implications of these for the biodiversity forest communities are discussed. The implicit relationship between the socioeconomic status of rural communities and biodiversity loss was established. The need to meet the livelihood requirements of the rural poor, especially in developing countries, so as to secure maximum value from forest biodiversity is recommended.

P II.2

The effect of diversity on light mediated changes in phytoplankton production and stoichiometry: A field experiment

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The functioning and sustainability of ecosystems may depend on their biological diversity. The proposal of Darwin that more diverse plant communities are more productive has received much attention and field and laboratory experiments show that more diverse communities can indeed be more productive. This effect may result from a more efficient resource use of more diverse communities. Here we use data from field experiments with algal communities from 42 lakes to show that the resource use efficiency of phytoplankton communities is related to their diversity. Increasing light levels resulted in a higher increase of carbon incorporation in more diverse communities. This coupling between biodiversity and ecosystem functioning was related to plant biochemistry. Taxonomic diversity was closely correlated with (biochemical) functional diversity. Highly diverse algal communities were able to absorb light at a broader range within the photosynthetic active radiation (PAR). This resulted in a stronger increase of photosynthesis with increasing light in species-rich algal communities. Additionally, the higher increase in photosynthesis and carbon assimilation with increasing light of species-rich algal communities resulted in higher phytoplankton biomass carbon to phosphorus ratios.

P II.3

Revealing genetic diversity and phylogeographic pattern of an inquiline gall wasp

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Gall wasps (Hymenoptera: Cynipidae) induce a wide diversity of highly complex galls on a variety of host plants. However, around 12% of known species have lost their ability to induce galls (Synergini) and develop as inquilines inside galls of other cynipids. *Synergus umbraculus* is the representative of the latter group and has been reared from oak galls of more than 30 gall wasp hosts. In contrast to the gall inducers, we know little about inquilines. Species identification is difficult, resulting in ambiguities in the taxonomy of *Synergus* genus. We examined (i) the genetic diversity within the species; (ii) the degree of genetic differentiation within and between populations, considering the possible effects of their hosts; and (iii) the large-scale phylogeographic pattern in the Western Palearctic. Based on sequences of three different mitochondrial and nuclear loci of 250 individuals, a remarkable degree of genetic differentiation was detected. Considering the orthologue sequences of other *Synergus* species, *Synergus umbraculus* can not be regarded as one uniform species since at least four cryptic species were found. Further analysis suggested that *S. umbraculus* does not depend on a particular host association. In the Carpathian Basin the effect of each sampled glacial refugium was observed.

P II.4

Evaluation of Functional Biodiversity in Tropical Agroforestry Systems - The Case of Tomé-Açú, Northern Brazil

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A multi-criteria evaluation protocol has been developed to evaluate the functional biodiversity of agroforestry systems. The approach combines productive, ecological and operational factors to describe the functional biodiversity and aims at the identification of supporting management decisions and interventions. The suitability of the evaluation protocol was tested with three groups of farmers which had been defined, based on the time of settlement, property size, technological know-how, organization and access to market: i) 'established', ii) formerly 'immigrated', and iii) recently arrived farmers ('newcomers'). The analyses reveal that the most relevant factors supporting functional biodiversity in agroforestry systems are (1) the farmers' preference for low impact techniques, (2) their adaptation capacity to environmental-social-political changes, (3) the diversification of the species composition on a plot, (4) the increase of the share of perennial species and (5) the financial profitability of the system. Concerning the differences among groups, the 'established' farmers are significantly different from the two other groups only in agricultural practices related to production. The newly developed multi-criteria evaluation protocol has proved to be feasible in a first instance. Nevertheless, its further validation, testing and adaptation as a monitoring tool is necessary.

P II.5

Globalization and management of phytogenetic resources by cocoa farmers' communities: Opportunities to promote agro and wild life biodiversity conservation in Southern Cameroon

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With the drop of cocoa prices and liberalization of economic and agricultural sectors in the 90th, Cameroonian cocoa farmers' strategies to maintain and increase their incomes shifted toward increasing integration/management of forest species, fruit trees and annuals in/outside cocoa agroforest. Based on the participatory rural appraisal with 45 rural communities in southern Cameroon, the study evaluated: (i) the phytogenetic resource preferences of farmers in view of diversifying and increase their income within and outside cocoa agroforests; (ii) the contribution mix of incomes between cocoa and other phytogenetic resources. Intensifying and diversifying non-cocoa phytogenetic resources inside agroforestry can help in minimizing ecological/economical risk and increase ecosystem services. Results from the exchanges with farmers are discussed in the perspective of biodiversity conservation within and outside cocoa plantations in the forest landscape. The study thus offers a good example of how trade-related policies in the agricultural sector (ex: Liberalization of the cocoa sector in Cameroon) can influence biodiversity management and conservation in the forest fringe.

P II.6

Faunal Diversity in Tiger Reserves of India

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The Convention of Biological Diversity (1992) to which the Government of India is a signatory, dwells a great deal on the need to document the biological diversity existing with in the Indian territory. The 28 Tiger Reserves of India encompassed by surrogate species (Tiger- a flagship species) should hold viable populations of other species in order to act as a robust conservation tool, but there are virtually no studies that have tried to measure the viability of background populations. By focusing on, and achieving conservation of that species, the status of many other species which share its habitat – or are vulnerable to the same threats. Documentation of faunal resources in Tiger Reserves therefore, focuses on developing 'indicators' to be used in the assessment which are reflected in a combination of ecological fundamentals, such as biodiversity, critical habitat and key ecological relationships; site-specific considerations, environmental stress and potential impacts. Assessments and documentations also provide biodiversity values that are recognized and taken into consideration in the planning and decision making process. Species diversity in itself, for example, is valuable because the presence of a variety of species helps to increase the capability of an ecosystem to be resilient in the face of a changing environment.

P II.7

Biodiversity as an important factor for mosquito control

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Mosquitoes can heavily affect human health, as they are vectors for various diseases (e.g. Malaria, West- Nile Virus). Climate change (particularly parameters like warmer temperature and heavy rainfalls) can potentially induce a geographic redistribution of mosquitoes and pathogens from lower to higher latitudes. Both microcosm and field studies have shown that mosquito larvae populations are strongly reduced, sometimes even non-existent, when a diverse community of food competitors have the potential to develop. Mosquito larvae are pioneer organisms and select preferentially as breeding sites temporary water bodies, characterized by low density of competitors or predators. An environment with low biodiversity may thus favour the development of mosquito larvae. This fact is important for the traditional use of chemical pesticides for mosquito control. Many pesticides affect non- target species and reduce biodiversity in aquatic biotopes. Although mosquitoes are also reduced by these insecticides, they will recover rapidly, as their antagonists disappear. For a long-term, effective and environmentally friendly mosquito control, it is necessary to complement the use of pesticide by the use of a biological approach.

P II.8

Does climate change increase the susceptibility of monoculture pine stands to outbreaks of mass reproduction of pathogenic (phytophagous) insects?

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For eastern parts of Germany and Poland summer temperatures are predicted to increase between 1.5 to 2 °C accompanied by a decline of summer precipitation of 10% to 20% over the next 50 years (Gerstengarbe *et al*, 2003). Forests are dominated by Scots Pine *Pinus sylvestris* (Brandenburg 83 %, Poland 63% of total of forested area), which is attributed to be one of the most adaptive species in areas with low precipitation, soil water and nutrient availability. Consequently, vast areas of eastern parts of Germany (Brandenburg) and Poland were afforested with Scots Pine and are presently pure, single age class stands. However, such homogenous stands are characterised by unfavourable factors such as low biodiversity and an enhanced susceptibility for pest attacks. Pure stands reveal unfavourable conditions for pest antagonists and provide ample food for verminous insects. It is not clear to what extend these mass outbreaks will increase for certain scenarios and neither do we know the cascade of associated environmental reaction, like potential elevated soil organic matter decomposition, which would be a feedback effect to climate change. In order to alleviate the consequences of outbreaks in forest stands and the associated monetary detriments, it is indispensable to take preventive measures, such as the transformation of existing species-poor forest stands into site-adapted, resilient management units which, in turn, will also be earmarked by a higher degree of biodiversity.

Gerstengarbe, F.W., Badeck, F., Hatterman, F., Krysanova, V., Lahmer, W., Lasch, P., Stock, M., Suckow, F., Wechsung, F., Werner, P.C., 2003. Studie zur klimatischen Entwicklung um Land Brandenburg bis 2055 und deren Auswirkungen auf den Wasserhaushalt, die Forst- und Landwirtschaft sowie bie Ableitung erster Perpektiven. PIK report 83. Potsdam.

P II.9

Access to genetic resources and benefit sharing – Good practice for academic research

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Whenever scientists intend to use organisms, or parts thereof, from abroad for their research purposes, they need to adhere to a specific code of conduct, as stipulated by the Convention on Biological Diversity (CBD). The Swiss Academy of Sciences has developed a brochure on Good Practice. It offers easy to understand information about the Access and Benefit Sharing system regarding basic research. It explains the necessary steps to take for obtaining access to biological resources for research purposes and sets out possibilities for benefit sharing within the academic context.

P II.10

Linking Development and Conservation: Lessons and Limitations

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The questionable conservation success and social aftermath of many protected area initiatives has given way to a series of community based approaches. These have tried to fuse economic development, sustainable resource use and biological conservation. Over the last few decades scholars have concentrated on trying to disentangle the factors that facilitate common resource management. Although these studies have identified a series of conditions for successful collective action, there is still relatively little quantitative data that successfully links social characteristics with conservation outcomes. We present the results from a meta-analysis linking social characteristics and institutional arrangements to conservation outcomes.

P II.11

Comparision of species diversity in protected and unprotected area of Chepeghli region in Markazi province (Iran)

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The Chepeghlin protected area comprising about 1000 hectares is situated in Markazi province near Arak. Plant diversity is one of the most important factors to show changes in ecosystems. In this study, three plants types were collected and species richness, diversity and equitability were applied to measure overall species diversity. The results indicated that *Astragalus eriostylus-Centaurea virgata* ecosystems have the highest diversity and *Astragalus eriostylus-Stipa hohenackeriana* the lowest. In this investigation, the effect of entering a protective regime was shown to be beneficial, although the differences between unprotected and protected parts of Chepoghli are not as great as expected. The enforcement of a protective regime needs a longer time to overcome short-term local effects.

P II.12

Understanding fragmentation effects on Tropical Forests

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Increasing demand for bio fuels may lead to even stronger human land use pressure in the tropics, with the consequence of massive habitat destruction and following habitat fragmentation, for example, within the Brazilian Atlantic Forest (Mata Atlántica), one of the biodiversity hot spots in the world. Already approximately 92% of the former Atlantic forest has disappeared within the last five centuries and the remaining forests are mostly highly fragmented. Although the fragmentation problem is well known and has global dimensions, its impact on dynamics and biodiversity of ecosystems is still not well understood. To improve the understanding of fragmentation on tropical forests we disentangle the single effects of several processes related to fragmentation on the dynamics of the system. We present simulation results from the individual-based forest growth simulation model FORMIND. Additionally we investigate the potential of external long distance seed rain for compensating the effects of fragmentation. Different levels of external seed rain reflect different degrees of isolation within the landscape, which is analyzed for tropical forest fragments of different size. FORMIND was adapted to the Mata Atlántica at the Plateau of Sao Paulo to the study sites Caucaia/Ibiuna and Morro Grande. From the background of the local recruitment dynamics and tree growth, we contribute to the understanding of how external seed rain and fragmentation act on tropical forest fragments of different size.

P II.13

Biodiversity in Change

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The poster will present the different activities of the long-term project “Biodiversity in Change” of the Academy of Sciences and Literature, Mainz. The project focuses on four main objectives:

- Global biodiversity mapping
- Rock outcrops & forest islands Diversity, dynamics and functional aspects.
- Life at the canopies Tropical epiphytic diversity in natural and anthropogenic influenced vegetation.
- Diversity & biogeography of the genus *Impatiens* in Africa and Madagascar.

P II.14

The Potential of Green Gene Technology in Biomass Production. Harming or Protecting the Environment - A legal examination

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The European Union and Germany have both set ambitious targets for renewable energies to represent a 20% share of all energies consumed by the year 2010. The use of biomass in fuel production will increase as well, due to the EU-Biomass-Action-Plan and National Acts governing the share of biofuel to be around 17 % in 2020. Relying on those targets, this lecture will illustrate how Gene Technology has the potential to intensify the cultivation of GM-Biomass-Plants. Necessarily, the lecture will, as well, provide an overview of the current cultivation and research of GM-Plants for biomass production, in both the International and European arenas. The rise in the use of biomass from agriculture and forestry is likely to put an additional stress on biodiversity. Therefore relevant European and German Laws, Acts, and Regulations such as the GMO-Release-Directive, the Biofuel-Directive or the German Gene Technology Act as well as similar draft laws, like the German Biomass-Sustainability-Ordinance and the Best-Practice-Guidelines for GMO Cultivation, will be reviewed and analyzed to determine their ability to protect biodiversity.

P II.15

Certification of Ethiopian wild coffee as an appropriate avenue for biodiversity conservation? A local level perspective

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The montane rainforests of Ethiopia are the worldwide origin of the *Coffea arabica* gene-pool. Until the present, they comprise naturally regenerating coffee populations with a high genetic diversity. Local people gather this wild coffee for income. Concurrently, the forests witness high deforestation leading to an irreversible loss of the wild coffee gene-pool and biodiversity. The poster concerns the question of certification of coffee cooperatives and unions, according to generic standards, can provide for the conservation of forest biodiversity. Empirical evidence is given that certification of wild coffee is in the given ecologic, socio-economic and institutional context, fraught with fundamental problems. The fulfilment and monitoring of certification standards requires stable value chains, know-how and trust between autonomous actors. These terms are hardly given in Ethiopia in general and the cooperative – union system in particular. In addition, higher prices for producers provide incentives to intensify forest coffee production at the cost of forest depletion. It is argued that the application of generic certification standards are not appropriate to promote conservation of forest coffee biodiversity. Instead, the development and implementation of a distinctive Ethiopian wild coffee certification standard is recommended that directly links consumer’s willingness to pay for biodiversity conservation with actual sustainable forest management projects on the local level.

P II.16

The effect of diversity on light mediated changes in phytoplankton production and stoichiometry: A laboratory experiment

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The availability of light may influence the biomass and the structure of phytoplankton communities and causes changes in the biochemical composition and in the rates of photosynthesis and respiration of phytoplankton. The combination of pigments in a species determines which part of the light spectrum the species can utilize for photosynthesis. Existing theory and experiments on phytoplankton competition for light predict competitive exclusion. As a result, species interact by shading each other, and only the strongest competitor for light survives. Communities with more species could use a greater variety of resource capture characteristics, leading to greater use of limiting resources (complementarity) and therefore greater productivity (overyielding). The accessory pigments in an algal species will determine its potential for utilizing a particular wavelength. Therefore, one can expect a wide range of physiological responses to variations in light quality. To investigate the effects of diversity on light mediated changes in algal stoichiometry (C:P ratios) we performed laboratory experiments as semibatch cultures. We used different algal communities of defined volume and composition and exposed them to different light intensities. Our results suggest that a strong relationship between diversity and light mediated changes in phytoplankton photosynthesis, production and biomass stoichiometry exists.

PII.17

Effects of land use and genetic variability of oaks on diversity of associated arthropods

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Differences in the chemical and physical traits of plants caused by both genetic and habitat characteristics may influence the diversity of associated arthropods. Oaks (*Quercus* sp.) are common trees in Germany which give habitat to many specialized arthropods. In the presented study we investigated the effects of oak genetic variability and land use of forest patches on the diversity of beetles (Coleoptera) and true bugs (Heteroptera). Arthropod communities were sampled using flight-interception traps in various forest patches in Bavaria (Germany), genetic variability of oaks was assessed from microsatellite loci. We present results on the relationships between the genetic variability of oaks and their associated arthropods. We also report on the effects of land use of forest patches on the species richness of true bugs and beetles.

P II.18

Characterization of microbial iron oxidizing biofilm populations of the Oder floodplain

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Natural floodplains play an essential role in the processing and decomposition of organic matter and in the self-purification ability of rivers, largely due to the activity of bacteria. The Oder floodplain is located in the Lower Oder Valley National Park and is characterised by an artificial water management, which includes flooding in winter time, while in spring time the water is actually pumped out. This results in contact of all soil systems in the park with highly pollutant water from the river Oder and subsequent deposition of the pollutants in the soil matrix. Due to the special geographical location of the Oder floodplain, the iron cycle plays an important role in this habitat. Anaerobic iron reduction in the floodplain sediments as well as iron oxidation and precipitation in the river Oder is mediated by microorganisms. As iron reduction is used for bioremediation in soil, only little is known about iron oxidizing bacteria and their role in degradation of organic substances, in particular of humic substances. The bacteria responsible for turnover processes and their role in iron oxidation of the Oder floodplain was characterised combining traditional cultivation techniques and molecular methods. For the investigation of the biofilms the DGGE method was used. The iron-oxidising bacteria were isolated, cultivated and phylogenetically analyzed. New developed CARD FISH probes on biofilms link our molecular data directly to the biofilm.

P II.19

CoCE - Conservation and Use of wild Populations of *Coffee arabica* in the montane Rainforests of Ethiopia

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[1] ZEF C - COCE Projekt, Zentrum Für Entwicklungsforschung, Univ. Bonn, Germany

The overall objective of this project component is to evaluate the role of certification of ‘wild’ forest coffee in Ethiopia with regard to its specific ecologic, socio-economical and institutional circumstances. This includes a desk study of certification standards that are potentially suitable for ‘wild’ forest coffee certification in Ethiopia, as well as the evaluation of already ongoing ‘wild’ coffee certification activities on site. Thereby, the socio-economic and ecological impacts and implications of certification on the local level producers’ side will be highlighted. In order to ensure the trustworthiness of the certified products and to lay the ground for marketing a coffee of origin, the genetic fingerprinting technique will be tested in practice. Based on these findings, the second objective focuses on the search for and development of realistic alternatives to the currently applied modes of ‘wild’ forest coffee certification.

Symposium III

P III.1

Towards an International Mechanism of Scientific Expertise on Biodiversity (IMoSEB)

D. BABIN [1]

[1] IMoSEB Initiative

The poster will present the consultative process towards an IMoSEB and the follow-up of this initiative.

P III.2

The Hidden Freshwater Biodiversity Crisis

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The Centre for Freshwater Biodiversity: Freshwater Biodiversity *sensu lato* is a key research focus of the Leibniz-Institute of Freshwater Ecology and Inland Fisheries, IGB, in Berlin, Germany (www.igb-berlin.de). More than 40 internationally recognized scientists deal with all aspects of freshwater biodiversity, from habitat to genetic diversity and from microbes to fish. Despite the increasing public awareness of the problem, few are aware of the catastrophic decline in freshwater biodiversity on both local and global scales. While Freshwater Ecosystems cover only 0.8% of our planets surface, they hold more than 10% of all animal species (about 126,000). More than 35% of all vertebrate species are restricted to freshwater habitats during at least part of their lives. Compared with terrestrial and marine species, there is already an over proportional rate of extinction and threatened freshwater animals, showing that the threats are real and acting today. The main human impacts that threaten freshwater biodiversity are water abstraction, pollution, invasive species, overexploitation, river fragmentations and flow modifications. Increasing needs for water already makes freshwater biota the most threatened part of biodiversity. Freshwater biodiversity will also be the first victim of climate change and extinctions are increasing especially in semiarid areas such as the Mediterranean biodiversity hot spot. Rivers, lakes, groundwaters, and wetlands offer a remarkably diverse array of natural functions and services to humans; more than any other ecosystem types. Despite their pivotal ecological and economic importance, freshwaters have been almost completely ignored in European and global biodiversity assessments. Therefore, they have not been of primary concern in policy making. Only recently did the EU take the initiative to improve this situation through the European Community Biodiversity Strategy (COM (98)42). Further, governments have set the ambitious target of halting biodiversity loss by the year 2010. The scientific community now faces the challenge of determining the critical factors responsible for loss and for providing the tools to assess the progress made toward this target. In fact, the patterns of freshwater biodiversity and the processes that maintain it at global and European scale are poorly understood for most freshwater groups. This poses a severe handicap for effective conservation planning of freshwater biodiversity as well as the human-related services that depend on it. Substantially increased efforts are needed to evaluate, complement, integrate, and analyse the quantitative data on freshwater biodiversity patterns, and on how freshwater biodiversity responds to environmental pressures at global, European, and local scale.

P III.3

Species Diversity of the two genera *Caulerpa* and *Caulerpella* (Chlorophyta, Bryopsidales) in the Vietnamese waters

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Caulerpa and *Caulerpella*, the two genera belonging to the phylum Chlorophyta, order Bryopsidales are distributed generously along the coast and islands of Vietnam. Based on the collected specimens, twenty-seven taxa belonging to the genus *Caulerpa* Lamouroux and one species of *Caulerpella* Prud'homme van Reine and Lokhorst are described and illustrated. The list of species includes: *Caulerpa brachypus, C. cupressoides, C. fastigiata, C. lentillifera, C. mexicana, C. microphysa, C. nummularia, C. peltata, C. racemosa, C. serrulata, C. sertularioides, C. taxifolia, C. urvilliana, C. verticillata, C. webbliana* and *Caulerpella ambigua.*

P III.4

Earth Observation for Monitoring Biodiversity in Central America

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[2] Nansen Environmental and Remote Sensing Center (NERSC), Norway
[3] Marine Spatial Ecology Lab (MSEL), University of Exeter, UK
[4] Collecte Localisation Satellites (CLS), France

The ESA DUE project "DIVERSITY" aims at defining, demonstrating and validating a number of geo-information products and services based on Earth Observation technology for supporting the implementation of the UN Convention on Biological Diversity. Based on the requirements of the project users (UNESCO, CBD, CCAD, Marviva) several products are generated for Central America and parts of the Caribbean:

1) A status map of worldwide drylands and their changes, based on existing land cover products.
2) Regional and local information on land cover, land cover changes and derived indicators in context with biological corridors.
3) Coral reef habitats and their changes across the Caribbean region, with hotspot areas in greater detail. In conjunction with related impacts on coral reef systems, water quality in the Caribbean Sea is monitored.
4) Mangrove maps and mangrove change maps using classification approaches on radar data.
5) EO based sea surface temperature, chlorophyll and surface currents are routinely provided and analysed for the Tropical East Pacific Ocean in order to determine how oceanic conditions influence migrations of marine animals in this area.

The general goal of the project is to establish sustainable biodiversity monitoring based on repeatable approaches and earth observation data from space. The experiences gained in the project can support the objective of developing a Global Biodiversity Observation System with respect to data and products specifications and priorities.

P III.5

Expansion of oil palm plantations and their impact on biodiversity and climate change in north-east Pará, Brazil

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Expansion of biofuel industries intensifies the existing competition for land surface between agriculture, urban areas and natural forests. In contrast to the well-known environmental effects of oil palm cultivation in south-east Asia, the consequences of oil palm plantation expansion in the Amazon basin have hardly been discussed, until now. In a new approach, we combined Landsat-ETM satellite images with QuickBird scenes. This method allowed us to distinguish very clearly between oil palm plantations and secondary vegetation. In addition to conventional land use classes, our classification identified the extension of palm oil plantations of almost 10% of the Bragantina region. This means that palm oil production seriously enters into competition with fallow-based agriculture systems of smallholders, which incorporate biodiverse secondary forest fallows. Thus, the increasing biofuel production accelerates deforestation and the loss of biodiversity and ecosystem functions. Our results support a governance scenario, which predicts a reduction by about two-thirds of watersheds, eco-regions and mammalian species. One of the main driving forces of biofuel development is the benefit of reduced GHG emissions. The assumption that biofuels produce lower emissions than fossil fuels has been disproved by several recent studies. But even a positive final result related to GHG's could not justify the destruction of forests and the consequences on biodiversity and ecosystems involved.

P III.6

Modelling the abundance of a keystone army ant species for a changing East African forest landscape over the past 90 years

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Tropical rainforests are rapidly declining, but the consequences for many taxa are little understood. The swarm-raiding army ant *Dorylus wilverthi* is considered a keystone species of Central African rainforests because a multitude of organisms (e.g. ant-following birds), directly or indirectly, depend on this ant. Using land cover information from 1913 to 2003 and an extensive data set on the abundance of army ants sampled over the course of four years, we estimated the consequences of forest clearance and fragmentation on the *D. wilverthi* population in the Kakamega Forest area, western Kenya. We found that the abundance of *D. wilverthi* strongly increased with increasing forest cover at a spatial scale of 1.6 km ($R^2 = 43\%$). Our model predicts that the landscapes will loose the army ant if the forest cover falls below 23%. Since 1913 the Kakamega Forest area lost ca. 32% of its cover and up until 1984 became increasingly fragmented. Spatial extrapolation of our regression results by a moving window algorithm suggests that the change in forest habitat over this time period led to a 45% decline of the population of *D. wilverthi*. It is interesting to note that the forest distribution is affecting the abundance and not just the proportion of forest cover. As only a small part of the forest is under protection, divided into four distinct areas, spatial modelling suggests that the size of two of the reserves would not be sufficient for long-term conservation of *D. wilverthi*.

P III.7

The Conservation Commons

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[2] Global Biodiversity information Facility (GBIF)
[3] IUCN-Canada
[4] IUCN
[5] Conservation International
[6] The Nature Conservancy
[7] University of Maryland, Maryland, USA
[8] Reference Centre on Environmental Information (CRIA)
[9] Plazi.org

Environmental degradation and habitat loss continue to accelerate. Solutions may be found to reverse this trend, but only with comprehensive data, information and knowledge on the conservation and sustainable use of biodiversity. Data access and knowledge sharing are not simple tasks, however. Difficulties abound. Much of the data, information and knowledge conservationists require is fragmented, difficult to find, or simply not accessible to the conservation community. This challenge is magnified in many developing countries where the consequences of the ever-widening "digital divide" impede conservation efforts at national, regional and global levels. The Conservation Commons is the expression of a co-operative effort of 69 non-governmental organizations, international and multi-lateral organizations, governments, academia and the private sector, which is responding to this challenge by seeking to break down barriers to access, more effectively connect practitioners to data and information assets, as well as to develop and adopt standards for integrating these assets to support the generation of knowledge and best practice. The purpose of the Conservation Commons is to ensure open access and fair use of data, information, knowledge and expertise on the conservation of biodiversity for the benefit of the global conservation community and beyond.

P III.8

Monitoring of Forest Ecosystem Biodiversity in Human-Impacted Zones Using GIS Technologies

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Maintenance of forest ecosystem biodiversity and sustainability under ever increasing human-caused environmental stresses is a high-priority task. Siberian boreal forests have been disturbed significantly by logging, fire, industrial pollution and natural disasters over the past fifty years. This resulted in a prominent ecosystem inbalance including changes of forest biodiversity and ecological functions. Our study was focused on monitoring the current state of forest ecosystems, their regeneration dynamics and biodiversity. The regional vegetation was classified using a topogenetic approach, i.e. by similarity of site conditions, forest community origin and development trends, rather than easily changeable outward features, such as vegetation species composition. A methodology of building computer vegetation dynamics maps based on the analysis of multispectral Landsat ETM+ images superposed on a digital relief model, and linked with ground observation data was developed using GIS called “Forests of Central Siberia”. The vegetation cover maps obtained as polygonal vector layers show the spatial distribution of vegetation regeneration series and stages under various site conditions. These maps allow, as a part of the GIS database, to estimate forest regeneration with an account of differences in ecological conditions. They are actually spatial vegetation models that reflect ecosystem diversity and can be helpful in fulfilling numerous ecological and monitoring tasks.

P III.9

Microclimate and tree community linked to the directional changes in lepidopteran larvae community due to fragmentation of tropical forest

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We investigated the effects of habitat fragmentation on leaf herbivory, larval density, species richness and diversity as well as composition of the herbivorous lepidopteran larvae community in a medium altitude tropical forest in Western Uganda. We looked at microclimate, size of fragment, isolation and tree community as possible explaining factors. We sampled ten Neoboutonia macrocalyx Pax. (Euphorbiaceae) trees on each fragment during dry and rainy season, four times in a year. The rates of herbivory, total larval density and species richness were significantly negatively affected by habitat fragmentation. Species diversity did not change, probably due to the influx of matrix species, as 28 % of the species were found only in the fragments. The dominance structure in the larvae communities had changed and all the communities in the fragments had experienced parallel changes in the community composition. None of the changes we observed were related to the size of the area or isolation. We found an indication of association between the larvae and the tree communities, but this only approached significance. The fragments were significantly drier during most of the day and hotter during the afternoons. Our results show that habitat fragmentation negatively affects larvae communities due to hotter and drier microclimate and changed tree communities. Reduced larval densities make the species more prone to extinction; thus the fragments cannot support viable communities in the long run.

P III.10

Climate Change and global plant diversity

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Little is yet known about the impact of global climate change on plant species distributions and species richness patterns. We modelled global contemporary species richness across 1,032 geographic regions worldwide based on environmental predictor variables according to the water-energy-richness hypothesis. The results are then applied on the contrasting A1FI and B1 global greenhouse gas emission scenarios used by the Intergovernmental Panel of Climate Change (IPCC), in combination with corresponding future climate surfaces from 5 global climate models per 110 x 110 km equal area grid. By 2100, the capacity for species richness per standard area decreases by 10.4% in the A1FI scenario in a global average, whereas it remains similar to today in the B1 scenario (+0.2%). Both scenarios indicate there is a strong deviance in the predicted changes amongst different geographic regions. Large proportions of species richness are likely to be no longer supported by future climate conditions, especially in many tropical and subtropical drylands, but also partly in the wet tropics, whereas the capacity for species richness may increase by more than 10% in Arctic and many temperate regions. However, any rapid shift in contemporary climate conditions that causes changes in the capacity for species richness may have negative impacts on contemporary floras due to species turnover and local extinction, resulting in possible changes of ecosystem functionality.

P III.11

NATURA 2000 sites under climate change - a challenge for nature conservation

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[4] University of Applied Sciences in Eberswalde (FHE) , Germany

The loss of biodiversity, including genetic diversity, species diversity and ecosystem functions threaten ecosystem services and the maintenance of biodiversity for future generations. The main reasons are land use change, climate change and pollution. The European Union had decided to implement a European network of protected areas, Natura 2000, to reduce the loss of biodiversity. The German Federal National Agency of Nature Conservation (BfN) funds a research project to assess the risk for specific nature conservation targets under climate change. The project aims at quantifying the risk for plants, animals and habitats. Management options are discussed with stakeholders, and political implications are specified. Nature conservation needs more space for dynamic processes and larger areas to allow adaptation to global change. Functional coherence has to be increased to allow for dispersal, including a management of the surrounding landscape. The legal framework had to be adapted to allow for dynamic processes without threatening the state that has been achieved for species and ecosystem conservation so far. On one hand, financial resources are needed to implement adaptive management. On the other hand, measures have to be implemented that acknowledge the fact that nature conservation areas contribute to climate change mitigation (e.g. forests, bogs) and to climate change adaptation (e.g. flood control, maintenance of genetic diversity, landscape cooling by evaporation).

Full Manuscripts

Observatories and Exploratories: German interdisciplinary approaches to realise biodiversity changes and understand their functional consequences.

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The Millennium Ecosystem Assessment 2005 clearly shows the interactions between biodiversity, ecosystems and people. To detect changes in biodiversity, to unravel their drivers and causes and to assess their consequences, interdisciplinary collaboration of scientists from life sciences, geosciences, social sciences and economics is necessary. Beyond that, research into biodiversity changes requires combined research activities taking place on the same areas or regions, long-term perspectives of research and funding and a database that allows handling of a great variety of data sets in easy accessible formats. Efforts have been made worldwide towards those goals, e.g. in the ILTER programme. However, there are many plans, few conclusive results and even less ecological experiments. Nevertheless, politicians and stakeholders call for scientifically sound and workable scenarios as decisions support information. German approaches tackling the problems associated with functional biodiversity, biodiversity changes or losses are briefly presented, such as the BIOLOG/BIOTA-programme, the Biodiversity Exploratories programme and some other relevant research projects in Germany and abroad. Some of them have been running for almost ten years or more (e.g. the Ecuador project), others have just started (e.g. the Biodiversity Exploratories or the China project) and therefore not much detail of results are presented. For more information, the reader is recommended to the respective web-pages.

Introduction

Research into biodiversity issues focuses on three major aspects, which are reflected by the three symposia of the PreCOP9-conference: Biodiversity as a product of evolution, biodiversity as a resource for humans, biological diversity and the functioning of ecosystems. The latter aspect, in particular the role of biodiversity for the ecosystem services has been addressed in detail by the Millennium Ecosystem Assessment (2005). Ecosystems circulate interior matter and energy mainly via food webs and exchange both with their surroundings, a feature that is known as “Self Supporting Ecosystem services”. However, the other ecosystem services which are of special importance for humans, the “Provisioning”, “Regulating” and “Cultural” services. e.g. productivity and carbon sequestration, mineralization, soil formation, water filtration, alleviation of erosion, or recreation are likewise connected with an ecosystem’s biological diversity. Loss of biological diversity as a possible consequence of global change may thus result in a deterioration of the ecosystem services to humans, a serious concern which is one of the major drivers for the enhanced activities in ecosystem and biodiversity research in our days. In that context, the question of the resilience of an ecosystem in response to human impact is gaining more and more importance.

To detect changes in biodiversity, to unravel their causes and drivers and to assess their potential consequences, interdisciplinary research collaboration of scientists from life sciences, earth sciences, social sciences and economics is necessary. Beyond that, such studies must be performed on the same areas or regions and they require a long-term perspective of research and funding. This is due to the complexity of the issue on the one hand and to the usually slow progresses of changes which must be differentiated from natural fluctuations of population sizes and abiotic factors. Both the complexity of the general research targets “ecosystem-related biological diversity” and the long time period expectedly result in huge amounts of data which demand new types of databases to handle the great variety of data in easy accessible formats.

Efforts have been made worldwide towards those goals, e.g. in the ILTER programme. However, implementation of such big ventures require many political and financial negotiations and, as a consequence, a long time. Areas must be selected and must be placed at researchers’ disposal for a long time period. Biosphere Reserves, National Parks, or otherwise protected areas, may suit this purpose which, however, may not always harmonise with the particular national regulations. As a consequence, not many multidisciplinary projects have come into action worldwide and knowledge about ecosystem-related biological diversity is still scarce. The following contribution presents a selection of several collaborative projects which have been implemented by German scientists in Germany as well as abroad and which are financed by the Federal Ministry of Education and Research or by the German Research Foundation. All projects deal with biodiversity in terrestrial ecosystems. In several of the projects, the main questions go beyond biodiversity and even may address socio-economic questions. Nevertheless, also in those, biodiversity plays a crucial role as an ecosystem parameter and is a major part of the research programme.

Whenever such a project is performed in a country outside Germany, CBD regulations, such as access to biological resources and benefit sharing, have to be respected. The projects reported here have clarified these issues with their counterparts and most of the individual subprojects are run in close collaboration. The examples presented here are invariably projects of non-commercial research in the sense of the ABS regime of the CBD (Laird & Wynberg 2008). Nevertheless, a variety of benefits have been achieved, which have particular relevance for the host countries. Apart from the production of data, capacity building, not only by training of researchers, but also by awarding them academic degrees is the most sustainable way to share the benefits of the research.

The individual projects and programmes

Table 1 Overview of research types and projects/programmes

Investigating biodiversity, biodiversity changes and functional biodiversity	The "classical" observatories (**BIOLOG /BIOTA**)
	The new **Biodiversity Exploratories**
Biodiversity in special ecosystems	Tropical forests margins (**STORMA**)
	A hotspot of tropical biodiversity (the "**Ecuador project**")
	Cultivated landscapes of Central Europe (**BIOLOG Europe**; the "**Göttingen Forest Project**")
Synthetic biodiversity: Investigating biodiversity functions in synthetic ecosystems	The **Jena experiment**: Grassland,
	The "**China project**": Woodland

Table 1 presents an overview of the comprehensive German collaborative research projects and their particular aims and traits. Few of these projects are observatories or exploratories only, in a pure sense. Most of them contain at least minor portions of the other category as well. Table 2 shows a comparison of the basic features of both types of ecosystem-related biodiversity research.

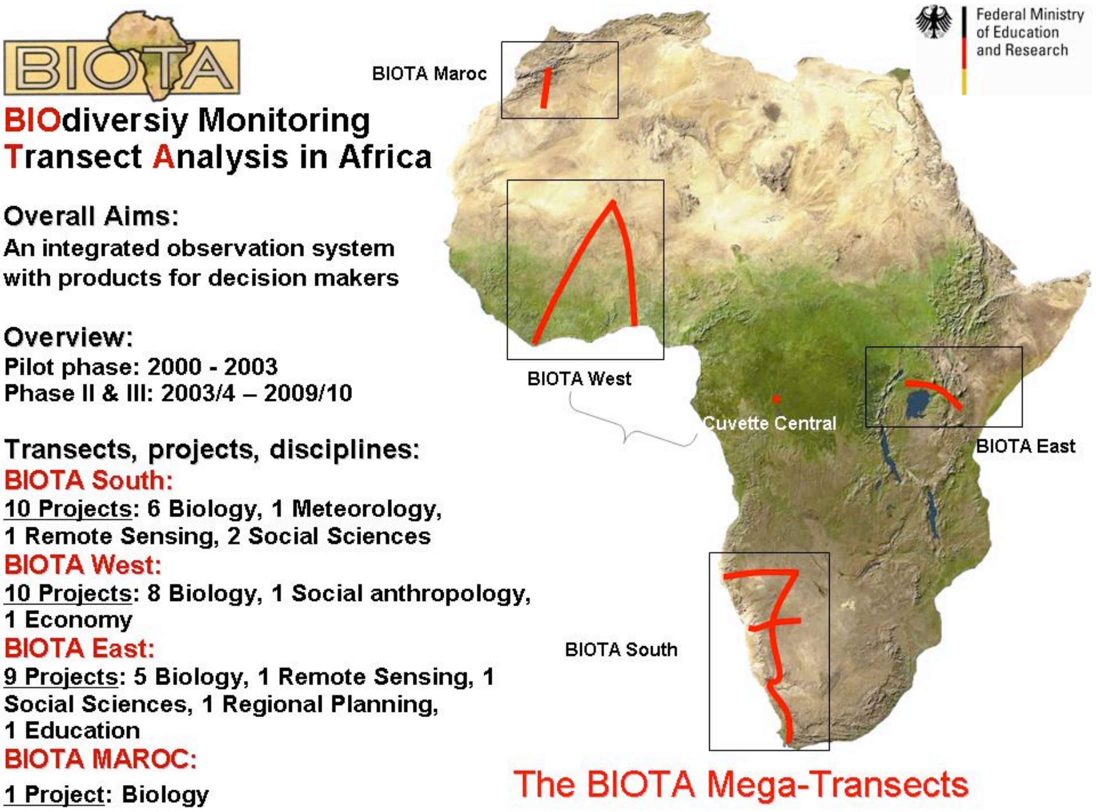
Table 2 Observatories and Exploratories, a comparison.

Common features	Multidisciplinary research Projects using the same research areas Uniform design of data collection Comparative approach Long-term projects Common database	
Differentials	**Observatories**	Mainly monitoring,
		Comparison of different types of land use
		Assessment of landuse on the basis of ecosystem parameters
		Mainly application directed research
	Exploratories	Monitoring plus ecological/landuse experiments
		Functional biodiversity research
		Mainly basic research with potential for application

BIOLOG AFRICA (BIOTA)

Observatories are the first and most widespread form of German ecosystem-related biodiversity collaborative research. They represent the core of the BIOLOG Africa programme ("BIOTA", www.biota-africa.org) which has been funded since 2000 by the Federal Ministry of Education and Research. BIOTA integrates multidisciplinary research on the various drivers of change in order to understand the bi-directional inter-dependence between climate change, change of land use and change of biodiversity. The results shall support adaptation to unavoidable climate change by stabilizing ecosystem functions. Forty-two observatories have been established along the **BIOTA** Transects in Southern, Western, Eastern Africa and in Morocco (Fig.1). They have, as far as the terrain allows, the same size (1 km^2) and structural design (subplots of 1 ha each) and a standardised mode of data collection (Fig. 2). In most of these exploratories the effects of different types of landuse on the sustainability of the biological diversity are directly compared. All observatories are cross-linked by data from remote sensing. From models that connect phytodiversity and climate, scenarios of phytodiversity have been calculated for the coming century, assuming a continuation of the present trends of climate change (Barthlott *et al.,* 2007, Sommer *et. al* in press 2008). Such scenarios clearly predict a pronounced decline of phytodiversity, especially in the West of the

African continent. In its present third phase of funding, the available time-series of about 8 years allows first validations of model predictions. As the degree of predictability increases with the time-period of monitoring and the frequency of simulation verifications, as well as with the number of observatories, a global observatory network has been proposed and DIVERSITAS and NASA have been appointed by GEO to lead the task of developing such an observation network (GEO •BON, www.bioobservation.net).



BIOdiversiy Monitoring Transect Analysis in Africa

Overall Aims:
An integrated observation system with products for decision makers

Overview:
Pilot phase: 2000 - 2003
Phase II & III: 2003/4 – 2009/10

Transects, projects, disciplines:

BIOTA South:
10 Projects: 6 Biology, 1 Meteorology, 1 Remote Sensing, 2 Social Sciences

BIOTA West:
10 Projects: 8 Biology, 1 Social anthropology, 1 Economy

BIOTA East:
9 Projects: 5 Biology, 1 Remote Sensing, 1 Social Sciences, 1 Regional Planning, 1 Education

BIOTA MAROC:
1 Project: Biology

The BIOTA Mega-Transects

Figure 1. Profile of BIOLOG Africa: The BIOTA megatransects and an overview of the 4 BIOTA Subprojects (Source: N. Juergens, Hamburg). As of May 2008, 1527 papers have been published from the projects (N. Juergens, personal communication).

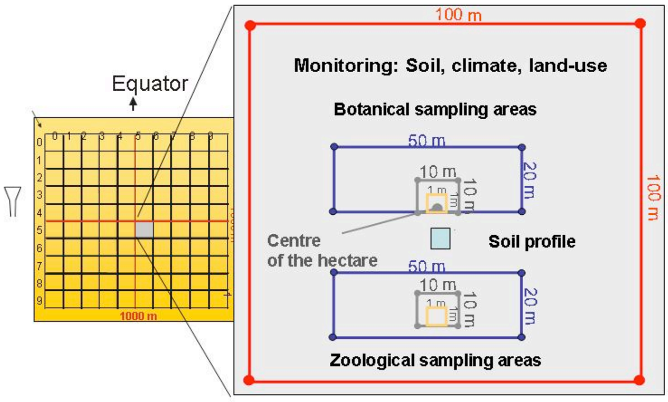


Figure 2. Standardised design of the observatories in the BIOTA-programme. All parameters are continuously monitored in regular intervals (Courtesy by Norbert Juergens, University of Hamburg)

The Biodiversity Exploratories

Exploratories, on the other hand combine both, monitoring of ecosystem and biodiversity parameters and examining hypotheses by experimentation. Three areas, all about 1000 km^2 and at least partly under environmental protection, have been selected in Germany (Fig. 3) and have been appointed as “Exploratories for large-scale and long-term functional biodiversity research” (**www.biodiversity-exploratories.de**), which are financed by the German Research Foundation as an “open-end” Priority programme since 2006 (Fischer *et al.,* in press). The exploratories represent a research platform operated by the Central Project, which was started in 2006 and provides basic data and organismic inventories (Fig. 4). The platform is open for peer-reviewed “Contributing projects” which shall examine biodiversity-related hypotheses preferentially by experiments. Twenty-seven contributing projects have been granted for the time-period of 2008-2011. The areas of the three exploratories comprise both forests and grassland and special plot designs have been developed for both types of vegetation. As in the case of the observatories in Africa, the exploratories represent real landscapes in Germany and research is conducted in cooperation with the land owners while the land is in use. The plots are selected to represent land use gradients from near-natural forests and extensively used grassland to intensively managed sites. Data are collected in a central database for long term data storage and intense mutual information. One of the key components of the programme is modelling of ecosystem traits in order to develop scenarios on the basis of proven hypotheses.

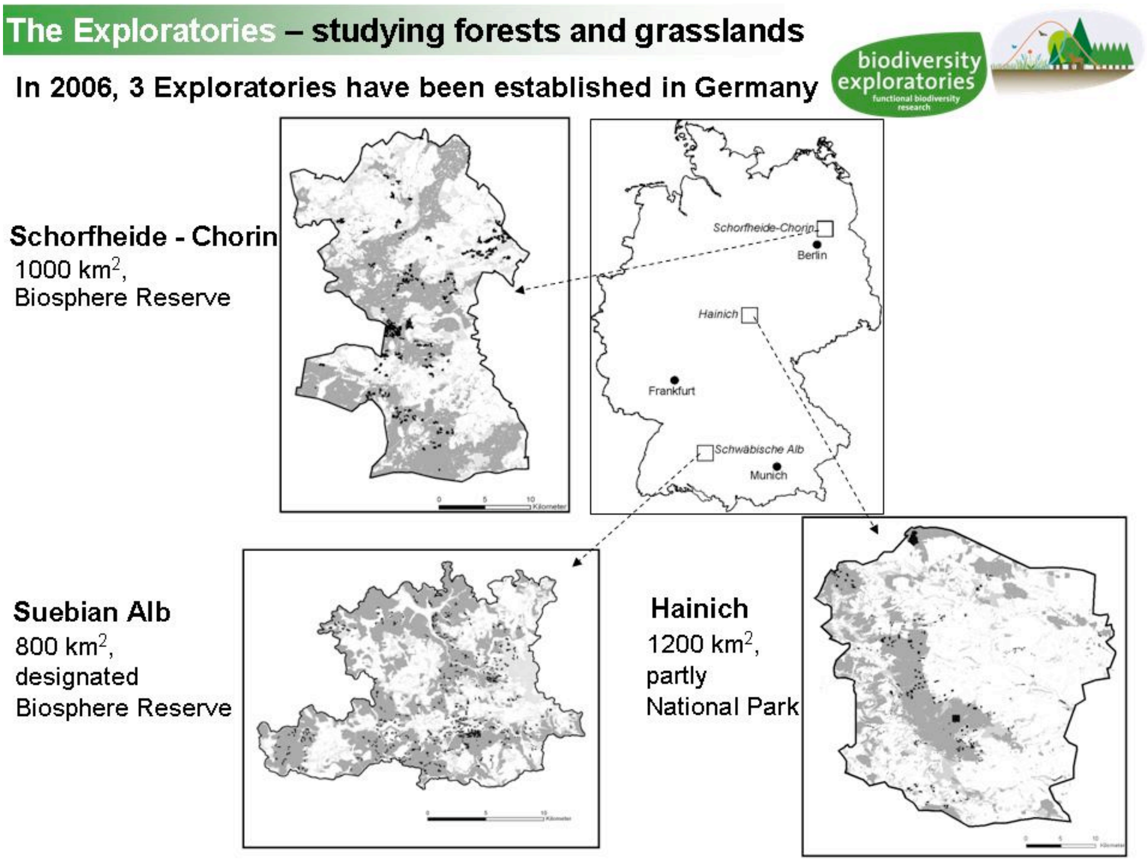
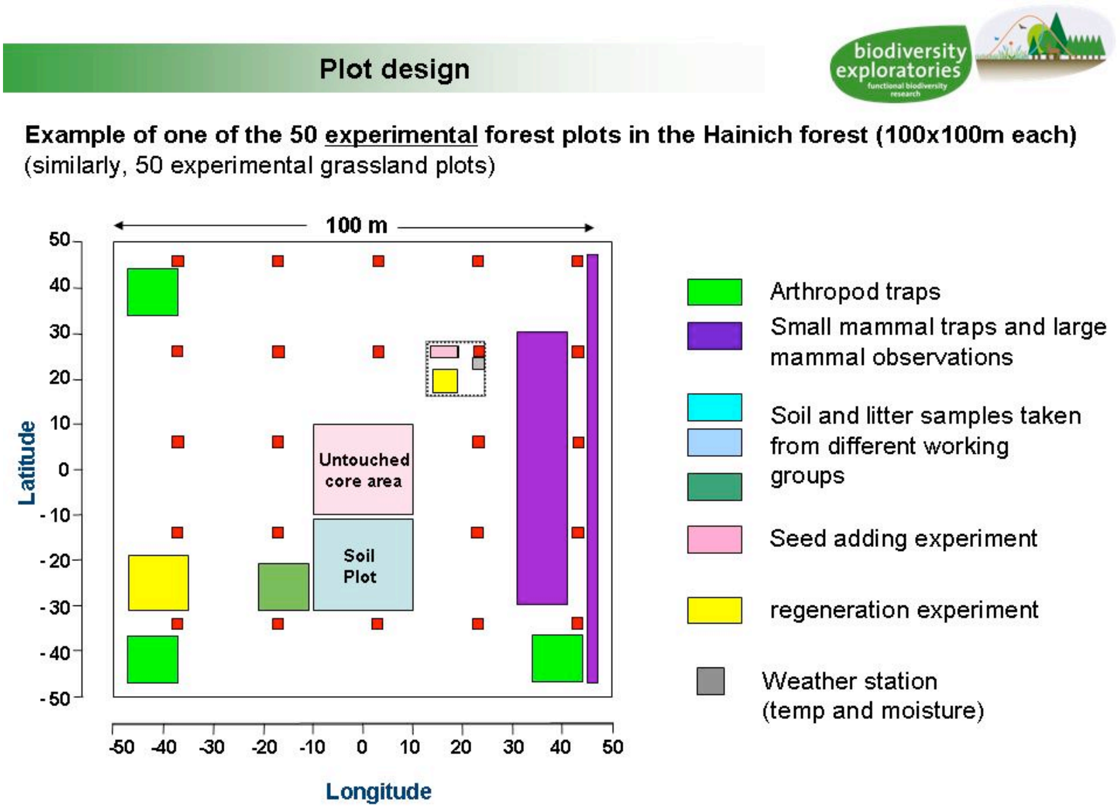


Figure 3. The 3 Biodiversity Exploratories in Germany: Position, size and vegetation composition. Signatures: grey: grassland, dark grey: forest, ■ selected grid plots (500 each in forest and grassland); Courtesy of Markus Fischer, Potsdam and Bern.

Cultivated landscapes of Germany, too, are the objects of 2 other collaborative projects related to biodiversity issues, the BIOLOG Europe projects which are financed by the Federal Ministry of Education and Research and the Göttingen International Training Group on the **“Role of Biodiversity for Biogeochemical Cycles and Biotic Interactions in Temperate Deciduous Forests”** (financed by the German Research Foundation for the time-period 2005-2009; prospected run of the project: 9 years; **www.forest-diversity.uni-goettingen.de**).



Plot design

Example of one of the 50 experimental forest plots in the Hainich forest (100x100m each)
(similarly, 50 experimental grassland plots)

Figure 4. Plot design of the Biodiversity Exploratories. The design of a forest plot is shown as an example; the indicated are run by the Central projects. This kind of platform is open to further specialised individual projects. Courtesy of M. Fischer, Potsdam and Bern.

BIOLOG Europe

BIOLOG Europe (www.biolog-europe.org/; funded by the German Ministry of Education and Research) investigates “Biodiversity and Global Change in a European context” and has been started, like BIOLOG Africa, in 2000. The current funding phase comprises 4 projects, all of which tackle important questions of both basic and applied research. The 4 projects are:

- “BIOPLEX: Biodiversity and spatial complexity in agricultural landscapes” in which the influence of landscape structure on biodiversity and ecosystem functions (basic research) is investigated, but also new market-based mechanisms are examined to improve the efficiency of agri-environmental schemes (applied research).
- “DIVA-Jena: Biodiversity and Ecosystem functioning in Grassland Ecosystems” where basic research focuses on food-web dynamics, biogeochemical cycling and indicators for biodiversity, while the evaluation on the agri-environmental schemes mentioned above contributes to applied research (www.uni-jena.de/ecology.html).
- “Invasion: Evolutionary, Ecological and Societal Consequences of Biological Invasions” is a multidisciplinary project about the effects of biological invasions at the genetic and the ecosystem levels on the one hand, whereas juridical options for dealing with GMO in agricultural systems are examined, a question of outstanding economic importance for Germany.
- “Subicon: Successional Change and Biodiversity Conservation” deals with the restoration of former mining areas, investigating the development of biodiversity on these areas, while in addition, probing citizen participation in managing and restoring such landscapes.

The outset of BIOLOG Europe is a wealth of data on the recent, but also the biodiversity of the past centuries, in combination with long-standing monitoring data of environmental factors e.g. of the climate, on which ecosystem-related biodiversity questions can be treated at a higher scientific level, while the implementation of measures meets a public whose life-style allows a higher degree of sensitivity for nature conservation.

The scientific output of BIOLOG Europe covers basic as well as applied aspects of biodiversity research. Results (more than 220 papers in scientific journals) *inter alia* include:

- New approaches for modeling biodiversity dynamics in cultivated landscapes

- New market-based instruments to conserve plant biodiversity in grasslands
- Novel indicators for food web integrity under different management regimes
- New approaches to stakeholder participation in ecological restoration planning (workshops, regular meetings)

In the following paragraph two long-standing projects will be touched on which are, like BIOTA Africa, pacemakers in other tropical countries; the STORMA-project in Indonesia and the “Biodiversity Hotspot Project in Ecuador”. Both collaborative projects are financed by the German Research Foundation. They have involved biodiversity research not only in an inventorial sense, but are aiming at a functional understanding of biodiversity for the respective ecosystems. Both projects have proceeded from a status of observation and monitoring to sophisticated ecological experiments. Only the biodiversity-related parts of the projects can be presented here.

STORMA

STORMA is the acronym for the project **“Stability of Rainforest Margins in Indonesia”** of the University of Goettingen (**www.uni-goettingen.de/de/sh/40515.html**) and the research is conducted in the Lore Lindu National Park in Central Sulawesi. It started in the year 2000 with a perspective of 12 years and comprises currently 17 subprojects (Fig. 5). It is based on the observation that destruction of natural tropical forest commonly starts at their margins, which in the case of Indonesia are used for agroforestry in coffee and cacao production. In the research area these margins are severely threatened by an intensification of agriculture and the expected increase of ENSO oscillation resulting in a reduction of the annual precipitation.

Stability of Rainforest Margins in Indonesia (STORMA)
Collaborative Research Center

Profile:

- Funding by the German Research Foundation (DFG): 2000 – 2009, with a perspective until 2012
- General aim: Identifying the processes that are helping to stabilize rainforest margins, both
  - economically
  - ecologically
- Study area: Lore Lindu National Park (LLNP), Central Sulawesi, Indonesia
- 17 subprojects
- Disciplines:
  Agricultural and forestry sciences, life sciences, ecoscience, computer science, law, economics;

The Sulawesi throughfall displacement experiment

Sulawesi

Forest clearing by slash and burn

Figure 5. Profile of the Collaborative Research Centre STORMA: Stability of Rainforest Margins in Indonesia. Courtesy of Dr. Melanie Grosse Goettingen.

Among the 17 subprojects, five are biodiversity- and global change-related:

- Distribution, diversity and composition of plant communities as depending on habitat, elevation and topography, soil and climate and land use
- Effects of fertilization, weed control and increasing ENSO dryness on the diversity of insects and associated ecosystem functioning (pollination, biological control)
- Fine roots of trees in undisturbed forests and agroforestry systems and their response to increasing dryness
- Significance of endophytic fungi living symptom-free in the leaves of cacao trees and their relation to agroforesty diversity and management
- Stability of rainforest margins in space and time: Holocene rainforest, climate, fire, human impact and land use dynamics

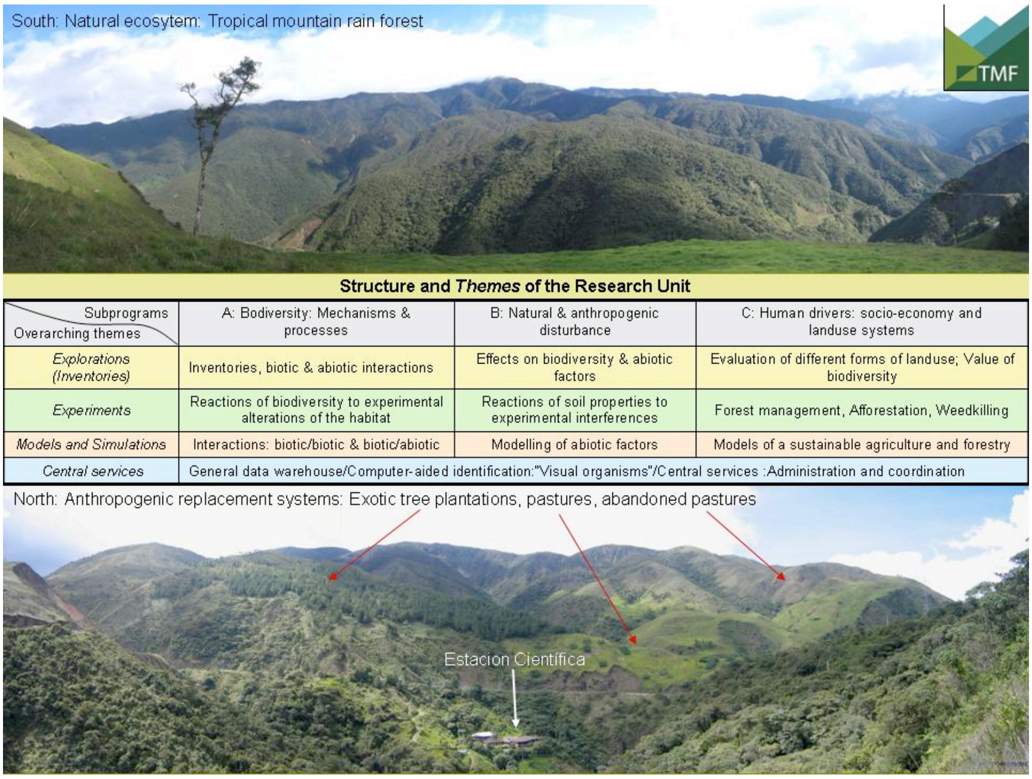
In the scope of the research into the effects of intensification of agriculture it could be shown that:

- Indonesian Coffee yields in LLNP were related to species richness in bees.
- Pollination limits cacao production
- There are trade-offs between increasing farmer‘s yields and the protection of the forest‘s biodiversity.

The effects of the expected El Niño droughts are investigated in the “Sulawesi throughfall displacement experiment” in which large transparent roofs have been installed in both the rain forest and the agroforestry plots.

The “Ecuador Project”

The Ecuador Project “**Biodiversity and Sustainable Management of a Megadiverse Mountain Ecosystem in South Ecuador”** (**www.tropicalmountainforest.org**) started in 1997 (with a perspective until 2013), when a research station was built in the Eastern Cordillera of South Ecuador, an area which borders, or is part of, the Podocarpus National Park, one of Ecuador’s’ biggest areas of protected rain forest. The number of subprojects increased from the initial 6 to now 27. Since its beginning it has turned out to be one of the hottest hotspots of biodiversity worldwide, which is a special challenge and triggers additional questions about the origin and persistence of such a hotspot. Nevertheless, Ecuador forests are severely threatened by the ongoing encroachment of agriculture. Agricultural and already abandoned agricultural areas immediately border the natural mountain rain forest (Fig. 6) and thus, a comparison of the natural ecosystem, with its anthropogenic replacement system, provides an excellent basis for identifying and quantifying ecosystem services and assessing ecosystem resilience to human impact. Emphasis is put on the “supporting ecosystem services” i.e. the role of the extremely high biological diversity for the functioning and stability of the ecosystem. After inventorying many groups of organisms of the research area, some parameters of the functioning of the ecosystem appeared; e.g. the lack of keystone species in the natural system (in contrast to the anthropogenic), which is due to resource limitations and the stability of the natural forest representing a dynamic equilibrium brought about by ongoing and frequent natural small-scale disturbances. On the other hand, the instability of the pastures is a result of heavy infestation by invaders, which are favoured by inappropriate land use techniques.



Structure and *Themes* of the Research Unit

Subprograms / Overarching themes	A: Bodiversity: Mechanisms & processes	B: Natural & anthropogenic disturbance	C: Human drivers: socio-economy and landuse systems
Explorations (Inventories)	Inventories, biotic & abiotic interactions	Effects on biodiversity & abiotic factors	Evaluation of different forms of landuse; Value of biodiversity
Experiments	Reactions of biodiversity to experimental alterations of the habitat	Reactions of soil properties to experimental interferences	Forest management, Afforestation, Weedkilling
Models and Simulations	Interactions: biotic/biotic & biotic/abiotic	Modelling of abiotic factors	Models of a sustainable agriculture and forestry
Central services	General data warehouse/Computer-aided identification:"Visual organisms"/Central services :Administration and coordination		

Figure 6. The research area of the GRF(DFG)-Research Unit 816 in the Valley of the Rio San Francisco in southern Ecuador. The natural mountain rain forest (extending between 1000 and 3000 m a.s.l. on the southern side is part of the biodiversity hotspot of the eastern range of the tropical Andes. Vis a vis, on the northern side of the valley pastures which have been abandoned to a great extent because of superior invaders, like the bracken fern. The natural ecosystem and its anthropogenic substitute can be directly compared. (Photo J. Bendix, Marburg)

Major hypotheses are now examined by experiments, e.g. a nutrient supply experiment in the forest and on the pastures to proof the idea of resource limitation for persistence of the biodiversity, or a controlled burning experiment of the abandoned pastures to model the invasive strength of the major weeds.

More than 140 papers in peer reviewed journals have been published, including a checklist of all identified organisms and a recent volume (198) of Springer's Ecological studies has been dedicated to the results of that project.

The "Jena Experiment"

The last project to be presented here in some detail is the "Jena Experiment" (funded since 2002 by the German Research Foundation, **www.the-jena-experiment.de**), which differs from all others as it uses experimental plant communities that were established from a pool of 60 species from Central European *Arrhenatherum* grasslands, divided into the four functional groups grasses, legumes, tall herbs and small herbs (Roscher *et al.,* 2004). In the main experiment, ninety-two synthetic model ecosystems, each 20 x 20 m in size, make up the main diversity gradients from 1 to 60 species. The number of species is varied independently.

This setup enables the separation of the influence of functional diversity of plants from the influence of the number of species. A series of well-planned accompanying investigations of biotic and abiotic parameters reveal species interaction networks and allows the quantification of the effects of diversity on ecosystem pools and fluxes, i.e. of water, carbon and nutrients. The special plot design is shown in Fig. 7.

Due to the selected composition of the plant species diversity and the fact that only herbs are used, several general conclusions on the functions of biodiversity in an ecosystem could be drawn already, after an experimental phase of 6 years.

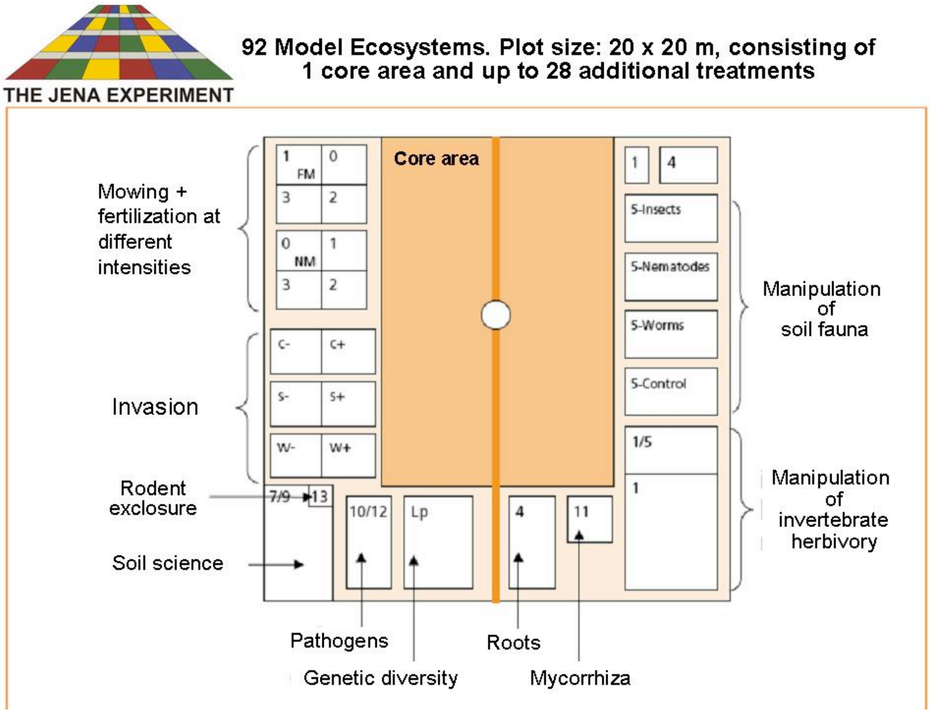


Figure 7. The Jena Experiment. Design of one of the 92 experimental plots demonstrating the setup of the additional investigations surrounding the core area. Each experimental plot belongs either to a species-diversity gradient or a functional group line. (Courtesy of W. Weisser, Jena).

For example, of the more than 520 ecosystem variables measured so far, about 25 percent are significantly affected by plant species richness *per se* (Weisser, personal communication 2008). The question whether biodiversity increases plant productivity found a differentiate answer: While above-ground biomass increases with biodiversity enrichment (Roscher *et al.,* 2005), the below-ground biomass does not (Bessler in press). However, carbon sequestration to the soil apparently compensates for the missing enhancement of below-ground biomass by high plant diversity (Steinbeiss *et al.,* 2008).

Further projects

Comparable experiments with tree and shrub species are burdened with much more technical and logistic problems. One such study, with a relatively species poor Central-European beech forest, is the already mentioned Göttingen International Training Group on the **“Role of Biodiversity for Biogeochemical Cycles and Biotic Interactions in Temperate Deciduous Forests”(www.forest-diversity.uni-goettingen.de),** which started to work in 2005. Another one that has just been implemented as a tri-national collaboration (China, Germany, Switzerland) in southern China, with the partial funding by the German Research Foundation, is the “China project **“The role of tree and shrub diversity for production, erosion control, element cycling and species conservation in Chinese subtropical forest ecosystems”** (**www.botanik.uni-halle.de/bef-china**). The first funding phase is 6 years. However, it is clear that this time-period is much too short for the achievement of reliable conclusions and perspectives for a long-term extension of the funding have to be worked out.

Conclusions

Which are possible perspectives of the German biodiversity research under the aspects of ecosystem functioning and global change? When the first projects were started at the end of the past century, long-term aspects were less favourable for getting a project granted. In the meantime, funding agencies have more and more accepted that particular requirement of ecological research. Nevertheless, long-term chances for funding must always be connected with special questions or general hypotheses. Also, simulations and models of the role of biodiversity in ecosystem functions and stability will gain increasing importance.

Acknowledgements

The author is grateful to the coordinators of the reported projects for providing the requested information. At the same time, he apologizes for mistakes and undue omissions which might have happened in his endeavour for a compact presentation.

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Specific articles

Instead of an endless list of references, the web-pages of the individual projects have been included in the text, where the actual overview of the publications can be found.

Conservation genetics: from species to habitats

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Conservation genetics - and indeed conservation in general - falls into the two broad areas of the identification and preservation of (1) endangered species and (2) habitats with high biodiversity. Most research has been towards the first aim, with hard-won findings on the importance of genetic variation in population management, but genetics promises to be at least as important in the second aim. To this end, molecular phylogenies have long been proposed as an important approach that can capture conservation worth and evolutionary distinctiveness better than simple species richness and avoid common problems in defining species identity and boundaries. Progressively faster and cheaper DNA sequencing and the rise of DNA barcoding are making the phylogenetic approach to habitat conservation widely applicable. Barcoding was seen initially solely as a means to species discovery and to species identification, but it now holds promise as a resource-efficient means of rapidly estimating the evolutionary history preserved by different sets of reserves. Initial indications are that biodiversity assessment, using the short *cox1* sequence standard for barcoding animals, reliably reflects the picture from longer sequences. The phylogenetic approach, assisted by barcoding, not only infers evolutionary history but also in synergy with morphology will speed species discovery and the subsequent expansion of general biological knowledge.

Keywords
Species preservation, phylogenetic biodiversity, DNA barcoding, mitochondrial DNA, Madagascar ants.

Two kinds of conservation genetics

The application of genetics to conservation has two broad aspects, the preservation of individual endangered species and the preservation of endangered communities. Of these, by far the most effort has gone into the first approach and indeed, the second is usually not mentioned in textbooks of conservation genetics. Given the diversity of life on earth (Odegaard 2000), the preservation of communities leading to the preservation of very large numbers of species, is the major aim of conservation biology, so that the second approach should come increasingly into its own.

Conservation genetics, as applied to relatively well known single species, has made great progress (Frankham *et al* 2002). The chief findings have been that, for a very great many species, the loss of genetic variation and a consequent occurrence of inbreeding depression not only weakens individuals (Brown and Brown 1998; Hedrick and Kalinowski 2000; Spottiswoode and Møller 2004), but also increases the risks of population extinction (Frankham 2005; Saccheri *et al* 1998). Immigration can reverse the decline of inbred populations (Madsen *et al* 1999; Saccheri and Brakefield 2002; Vila *et al* 2003; Vrijenhoek 1998). Not all species suffer from inbreeding depression, for example, inbreeding hymenopteran parasitoids do not (Hamilton 1967), but very many charismatic species with public appeal do, so that the hard-won findings from conservation population genetics are highly relevant, not only to policy for wild populations but for management of zoo stocks.

Conservation genetics - as applied to the selection of policies to best preserve mass biodiversity - is best embodied in the weighting of species by phylogenetic distinctiveness, rather than by counting them all equally in the traditional approach maximising species richness. Species richness has been recognized as inadequate as a conservation currency by some for a long time, for example Wilson (1992) argued against relying on rapid speciation to replace extinct species because the new species would be similar to each other and lack the depth of evolutionary history lost by extinction. A favorite example of differential weighting was given by May (1990), namely that the tuataras constitute the long-divergent sister group to all other lizards, so that losing them would entail a vastly greater loss of evolutionary history than a pair of, say, skink species.

Phylogenetic approaches to conservation weighting

The idea that evolutionary distinctiveness should be taken into account stems from the fact that longer periods of evolutionary divergence are expected to yield more new features of organisms than short ones (Crozier 1997; Wilson 1992). Initial approaches to differential weighting of species according to phylogenetic distinctiveness concentrated on node-counting on dendrograms (reviewed by Crozier (1997)), but attention to the degree of change along branches became the norm from 1990 (Crozier 1992; Faith 1992; May 1990; Pamilo 1990; Witting *et al* 1994) (see Crozier (1997)). Use of the branch lengths gives a better indication of the length of time evolution has had to produce differences than the number of perceived speciation events.

The distinction between using species richness as the sole criterion and using evolutionary history is shown in figure 1. Protecting habitat α would preserve most species (four), but while protecting habitat β would preserve only two species, the portion of the tree that joins them (shown in green) is 20 units long as against 14 for the species in habitat α (assuming a rooted-tree approach, see below). Given that more new features evolve if there is a longer evolutionary time for them to do so, more novel features, including ones currently unseen, would be preserved by protecting habitat β than habitat α. While habitat β would preserve as many species as habitat γ, it preserves more evolutionary history (20 as against 18 units) and so, other factors being equal, it would be the preferred choice. Similarly, if two sites can be protected, although sites including α always preserve more species, more tree length is preserved if the sites protected are β and γ.

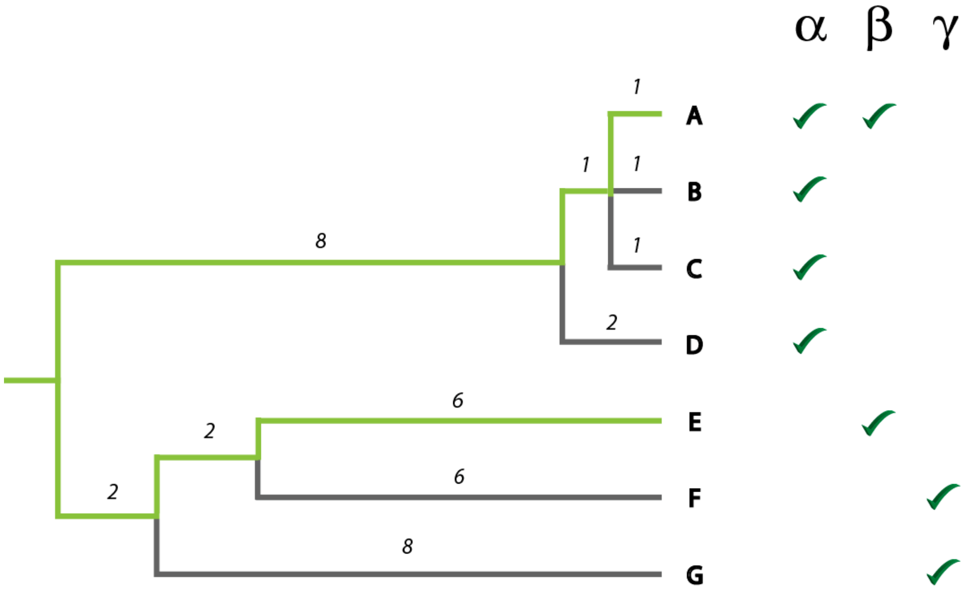

Figure 1. Optimal selection of sites α, β, or γ, according to the phylogeny of the included species A--G. While site α has the highest species richness it would preserve less of the evolutionary history of the group than either of the other two sites. Green lines trace the phylogenetic diversity (PD) of site β.

Distance measures specifically aimed at estimating the genetic variation preserved by different combinations of sites (Crozier 1992; Witting *et al* 1994) seem well suited to closely-related species, but Faith's (1992) simple measure of total tree length (phylogenetic diversity, PD) has become that most generally applied and underlies the approach in Figure 1. There is uncertainty about when this became the current consensus view (Crozier *et al* 2006; Crozier *et al* 2005; Faith and Baker 2006; May 1994), but is now generally agreed that the tree's root is best included when calculating the amount of evolutionary history preserved. Pardi and Goldman's (2007) notation suggestion of using rPD for rooted PD and uPD for unrooted PD should be followed if the measure used is not otherwise made clear. Strictly speaking, the branch connecting the species under consideration to the rest of life should also be included and should become increasingly easy to do.

As more species are added to a study, does phylogenetic diversity yield different answers to the use of species richness? Nee and May (1997) in a simulation study found that randomly removing 95% of species still preserved 80% of the tree, leading to the conclusion that when large enough assemblages are considered, there is no advantage to considering evolutionary distinctiveness in selecting sites for preservation. A similar conclusion was reached by Rodrigues et al. (2005). Various lines of evidence suggest that this conclusion is too optimistic. The assumption of random extinction is often violated, with phylogenetically divergent mammal and bird species tending to be at greatest risk (Johnson *et al* 2002; Purvis *et al* 2000). The assumption of random distribution of species to sites, implicit in the simulation models, did not hold for a study of the Cape flora (Forest *et al* 2007), because the degree of phylogenetic dispersion varies between one part of the region and another. Further, the very meaning of "species" seems to vary more between groups of animals than would [relatively] objectively inferred trees, especially molecular ones (Agapow 2005; Agapow *et al* 2004).

In the absence of a well-founded phylogeny, still now and for the near future the most likely situation, the systematics of a group can be used as a surrogate (Crozier *et al* 2005; Faith 1994; Strahan 1989; Warwick and Clarke 1995). Forest et al. (2007) found that such surrogacy led to results reflecting the more precise picture derivable from the molecular phylogeny.

The tree alone

Using species, even within a phylogenetic framework, still entails potential difficulties from the state of taxonomy differing between groups and such problems as unrecognised cryptic species. These problems have been clearly recognized for a long time in microbial studies, where many organisms were first discovered from their sequences and many remain only known in that form. A study using eubacterial rDNA sequences from the Oklo region of Gabon to estimate evolutionary history found significant differences in the phylogenetic dispersion of sequence diversification between sampling sites at different depths (Crozier *et al* 1999). Mace et al. (2003) suggested that for multicellular organisms, use of the tree of individuals could avoid problems of species boundaries. Others are now making the same point (Faith and Williams 2005; Faith and Williams 2006; Forest *et al* 2007).

Using a tree of individuals would provide a speedy estimate of biodiversity, but as a first estimate. Links to the rest of biology and possible refinements to the biodiversity estimate, would follow through more traditional processes, as argued below. Maximization of the preservation of evolutionary history as an aid to preserving functional communities has been suggested for some time (Cattin *et al* 2004; Warwick and Clarke 1995; Webb *et al* 2002) and draws experimental support (Maherali and Klironomos 2007).

Statistical sufficiency

We hope that very often the results of an analysis between different proposed preservation schemes will be very clear cut, but even in such cases it is desirable to be able to tell policy makers that the best choice not only appears clear but actually is statistically significantly better. Under this logic, the same level of statistical rigor should be applied to biodiversity estimates as to other scientific endeavours. As part of this process, the best methods of phylogenetic analysis should be used. We hope to no longer see the use of suboptimal methods justified by the 'size of the dataset'. Programming virtuosos have rushed to provide programs capable of estimating PD for hundreds of thousands of sequences 'in seconds' (Levy *et al* 2006; Minh *et al* 2006; Pardi and Goldman 2007; Steel 2005) and Bayesian methods able to provide estimates of uncertainty of phylogeny can also handle very large numbers of sequences in tolerable lengths of time (Hebsgaard *et al* 2007).

Two sources of variability in estimates can be identified – uncertainty in tree construction and incompleteness of sampling. Uncertainty in tree construction can be taken into account by using trees from bootstrap sampling of the character data (Crozier *et al* 1999), or those derived after stationarity following Bayesian procedures. Uncertainty stemming from incomplete sampling can be investigated using bootstrap samples from the complete array of sequences (Crozier *et al* 2005) and standard statistics such as from sample coverage theory (Chao and Lee 1992; Shen *et al* 2003). So far, programs taking uncertainty into account have looked at one source or the other, but not both, but a combined examination presents no serious methodological or conceptual obstacles.

Other external constraints, such as the budget available and the long-term preservation costs of sites under consideration (Hartmann and Steel 2006; Pardi and Goldman 2007; Weitzman 1993) and weights, such as those favouring the inclusion of adjacent sites, could be readily included.

For large numbers of sequences or potential reserve sites, we suggest that an optimization procedure, rather than an exact solution search strategy, be used. Simulated annealing has been used, in combination with weights favouring contiguous sites, for species richness maximization (McDonnell *et al* 2002).

DNA barcoding

DNA barcoding, the use of a short piece of DNA to characterize a specimen, has become extremely popular (Dasmahapatra and Mallet 2006; Hebert *et al* 2003; Herre 2006) as well as controversial (Hickerson *et al* 2006; Rubinoff 2006). We will not dwell on technical aspects, but will note that although a region of the *cox1* gene is the standard sequence for most animals, other sequences are required for plants (Taberlet *et al* 2007) and bacteria (which lack mitochondria) and the use of a particular sequence should be separated from the concept of rapid characterization. Thus, rDNA has also been used for DNA barcoding (Page *et al* 2005).

DNA barcoding has so far been seen in terms of specimen identification (the identification of an unknown specimen (Armstrong and Ball 2005), or part thereof, using the match to known sequences in a database (Ratnasingham and Hebert 2007)) and species discovery (finding that a new sequence falls sufficiently far from known ones as to indicate the likely existence of a new species, e.g., Hebert et al. (2004)).

Specimen identification and species discovery are vital contributions to biodiversity and general biological research; we now propose that DNA barcoding be used directly for the initial rapid estimate of biodiversity, using the sequences found from a set of sites. There is no practical alternative for assessing bacterial biodiversity and probably no real alternative for other microbes. For most other groups, we argue that DNA barcoding is now becoming the most practical means for rapid biodiversity assessment. Given current throughput rate at leading DNA barcoding centers of 2000 specimens per week, results of even quite extensive surveys should be obtained and analysed within months or weeks of return from the field. Indeed, given access to the molecular technology, May's (2004) remark that the field component is the rate-limiting step for surveys remains true.

Although DNA barcoding as the starting point for biodiversity surveys is demonstrably practical for many groups, further work is needed before truly general analyses involving large fractions of the biota can be routinely implemented. One question for example, pertains to differences in *cox1* evolutionary rate between groups – a bias in preserving species with more rapidly evolving mtDNA should be avoided! However, the question is not whether differences in rates occur, but to what extent would they compromise biodiversity assessment. A further question that should be explored is the extent to which tree-reconstruction errors using a short DNA barcoding sequence compromise phylogenetic biodiversity assessment. Trees built using the *cox1* sequence bear a surprisingly close resemblance to those constructed using much longer sequence, although they do show occasional marked differences (Hebert *et al* 2003; Smith *et al* 2005b). Such differences do not necessarily mean that phylogenetic biodiversity assessment using a short DNA barcoding sequence differ very much from assessment using longer sequences, but the extent to which this does should be examined. The finding that comparative analyses are quite robust to errors in phylogeny inference (Symonds 2002) gives grounds for optimism that the same will be so for biodiversity estimation using DNA barcoding.

Barcoding to taxonomy

A reliable taxonomy and systematic nomenclature give us the framework on which to organize biological knowledge of life on earth. DNA barcoding yields a rapid assessment of biodiversity, but does not reduce the need for well-trained specialists able to move knowledge from the initial survey to more refined stages of taxonomic knowledge (Figure 2). Thus, the second stage of the recognition of molecular operational taxonomic units (MOTUs) absolutely requires taxonomist participation to see whether the sequences grouped in the tree correspond to one or more already known species. The setting of the similarity level between sequences of the same MOTU (e.g., 2% or 3%) requires the collaboration of both taxonomist and molecular ecologist. Once MOTUs are established, a second estimate of biodiversity can be made in terms of the number of these and of course using the phylogeny relating them.

Finally, the use of other sources of information, such as from other loci (especially nuclear ones), behaviour, morphology and other sources of taxonomic knowledge, will lead to the firm discovery of new species or the inference that some species have deep phylogenetic splits inside them (step G above). Of course, such knowledge of the genetic structure of single species can assist in their individual management (Avise 2005; Moritz 1994) if desired, but in terms of conserving whole habitats, considerations of variation within single species are likely to be important for particularly charismatic or culturally important ones. This discovery of new species then allows further estimates of biodiversity and allows the regular pursuit of biological knowledge, enlightened by better understanding of what is there.

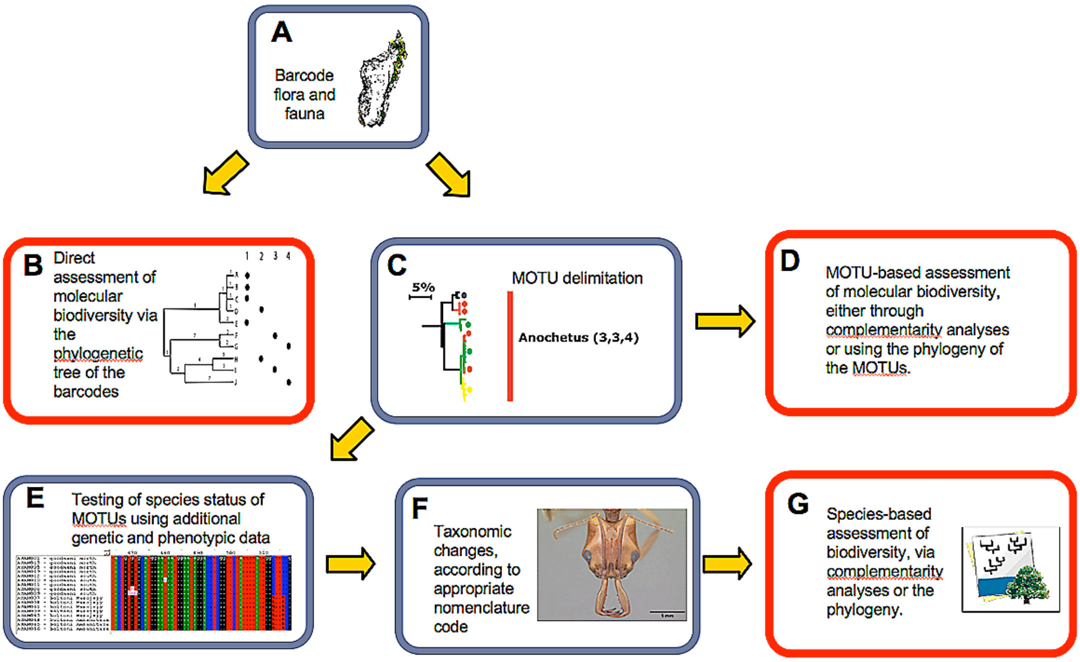

Figure 2. Stages in the uses of DNA barcoding for biodiversity assessment. Red-bordered boxes denote stages where biodiversity assessment can be made: step B rapid assessment using the tree alone, step D using molecular operational taxonomic units and step G using species defined and described using a wide range of data.

A test case of the method is provided by a survey of ants in Madagascar, involving a partnership between a barcoder and an ant taxonomist (Smith *et al* 2005a). Calculating the loss of biodiversity in terms of either morphospecies lost or PD lost if a site is not preserved, from the four northernmost studied, yields the same order of preference. Recording the Genetic Diversity (Crozier 1992) preserved by different combinations of 4, 3, 2, or 1 sites yields a clear priority order for preservation. Within this group the study of the related genera *Anochetus* and *Odontomachus* has yielded several new species, made new associations of sexuals with workers (by identity of *cox1* sequences), highlighted species whose deep phylogenetic splits may yet prove to be several species and yielded diagnostic *cox1* nucleotide positions for each (Fisher and Smith 2008).

Our suggestion is to cut the Gordian Knot linking biodiversity assessment to species counts, yielding a method of rapid biodiversity assessment. DNA barcoding does NOT replace traditional taxonomy and systematics, but rather hastens its progress in a time when conservation biology is a "discipline with a deadline" (Wilson 2000).

Acknowledgements

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Nature as a model for technical innovation

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I've long been suspicious about attempts to see energy as the overwhelmingly central item setting both options and criteria for design in nature. Indeed, when I tried to create a conceptual framework for teaching biology to college students, I ended up putting energy distinctly second to information. Where energy rules, one can find some analog of voltage – a potential, like the difference in height of water on two sides of a dam. But in nature, who eats whom boils down to the design and operation of one's particular teeth and other equipment. I once set up an electrical analog of an ecosystem, but it gave an unreasonable picture until I added ad hoc *diodes to keep the trees from eating the caterpillars at night and other such misbehaviour.* (Steve Vogel, Duke University, 2007)

Biology has solved many technical problems. Examples are the temporary attachment by hooks of a seed to the fur of a passing animal, thus obtaining ‘free’ transport for a seed that is too heavy to be spread by the wind; dry adhesion achieved by the conformable ‘hairs’ on the gecko’s foot that enable it to run up walls and across ceilings (Arzt et al., 2003); the superhydrophobic surfaces of many plant leaves that stops them being wetted and weighed down with water and enables the run-off to carry dirt with it (Barthlott and Neinhuis, 1997). Since these designs are very amenable to our current skills in materials processing, the immediate response is to take some of these solutions and incorporate them into our own technology. Then the seed hooks become Velcro (Velcro, 1955), the gecko’s trick is used to make robots that climb walls, the plant surface informs water-proof clothing and Lotusan for self-cleaning surfaces on buildings. These are all examples of successful biomimicry (=biomimetics, bionics, bio-inspired design . . .). These successes do not necessarily help our deeper understanding of biology, although many people believe that its a good way to innovate. The assumption is made that our way of processing and forming materials is proper.

However, biomimetics at this level is still largely adventitious. More often than not, the biomimetic abstraction is possible only because a biologist has pointed out an interesting or unusual phenomenon and has uncovered the general principles behind its functioning (e.g. the self-cleaning lotus effect). The transfer of a concept or mechanism from living to nonliving systems is not trivial. A simple and direct replica of the biological prototype is rarely successful, even if it is possible with current technology. This is because the biological prototype works within a context that has to be analysed and separated from the putative prototype before an effective transfer to technology is possible (fig. 1). The result may be unexpected (e.g. self-cleaning buildings) and the final product— in this instance, a paint containing particles— seldom resembles the biological prototype. However, even this may not be particularly useful, since it commonly happens that the workings of the biological principle are understood only in terms of extant engineering or physics so that the “biomimetic’ device illustrates ‘best practice’ of known technology but does not necessarily extend it.

It is possible to approach biomimetics at a more fundamental level and look at the way in which biological organisms solve problems to see how that compares with our own solution of the same or similar problems within a technical environment. In order to do this, we have used the Russian system *TRIZ* (theory of inventive problem solving) (Altshuller, 1999). Its originator, Genrich Altshuller, formulated a framework within which problems and their solutions (taken from the patent database) can be formalised and classified. His intention was that this should provide focused ideas for the solution of newly-recognised problems. Amongst his assumptions were that nearly all the manipulations of technology had been recognised (making allowance for the rare discovery of ‘new’ physical effects and principles) and that the way in which those manipulations are used constitutes a compendium of best practise. His first assumption is defensible; the second (we believe) is not. If the class of biological organisms is also regarded as a database of the solution of technical problems, then biology can also be analysed and described by TRIZ (Vincent et al., 2005b). Overall, at the systems level, we have found that the degree of similarity between problem-solving in biology and technology is small – about 12% (Vincent et al., 2006). Sometimes this is because biology starts from a different set of constraints; sometimes because biology simply works differently.

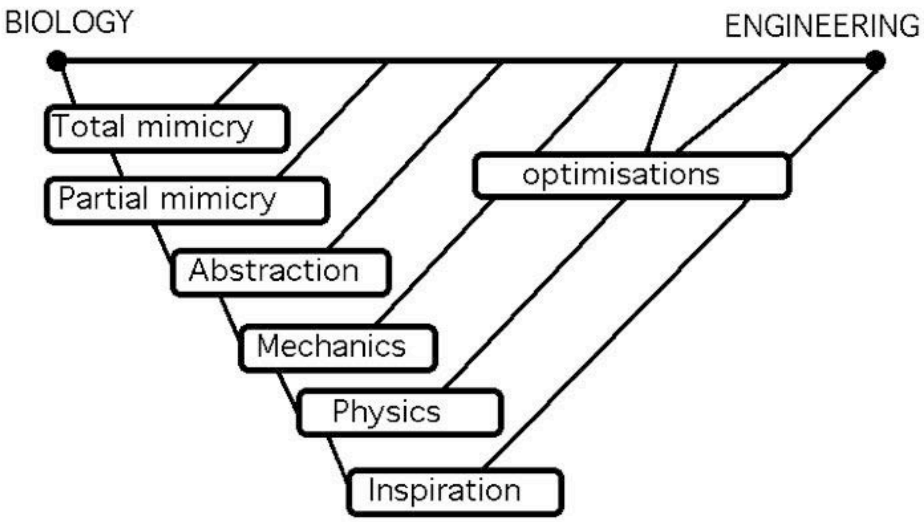

Figure 1. Levels at which ideas, functions or concepts can be moved from biology to engineering.

First we need to know whether biology can provide us with a credible replacement for our technology, which is largely based on materials and materials processing. Natural materials are composites based on polymers (proteins and polysaccharides) and some minerals (Ca, Si salts). Metals are but little used as structural materials, but can be significant (e.g. addition of 10% molecular Zn or Mn provide hardened surfaces to insect and spider mandibles (Hillerton and Vincent, 1982; Lichtenegger et al., 2003); molecular Fe hardens mollusc and fish teeth (Jones et al., 1935; Motta, 1987)). Silks can be stronger and stiffer than high tensile steels (Gosline et al., 1999). In their specific mechanical properties, biological materials can match most technical materials (fig. 2). Importantly, biological materials commonly have better resistance to fracture than technical ones (Bell and Gosline, 1996). This is particularly true of ceramics, such as bone and mother-of-pearl (Currey, 1999; Jackson et al., 1988; Mayer, 2006).

In order to be able to compare the ways in which biology and engineering solve problems, we identified six fields of operation in which all actions with any object can be executed: substance, structure, energy, information, space and time (Bogatyreva et al., 2004). In each of these categories some simple manipulation (e.g. changing speed, changing a structure, reducing or increasing the energy supply, or changing its source) provides a solution to the problem. In analysing a large number of technical and biological solutions, we assigned the solution to one of these fields and also arranged them according to the size at which they occur, ranging from molecular (nm) through to environmental (km – equivalent to a town or an ecosystem) (Vincent et al., 2005a). We can now comment quantitatively on the differences between biology and technology (fig. 3). Up to a size of about 1 mm we are mostly concerned with materials processing; from 1 mm to about 10 m we are more concerned with structures; above this level we have factors involved with communities. So far we have considered only materials.

Since TRIZ has allowed us to bring biology and engineering to the same level, biology can challenge engineering on its home ground. This challenge has some urgency about it since worldwide our consumption of energy far exceeds the instantaneous supply. Therefore we can't, at present, be 'sustainable', but could biomimetics help us? In addressing this problem I make a single assumption – that the biological system that we inherited on this planet is the paradigm for sustainability. This is disputable, but there is no evidence that any other system would provide us with the resources we need for survival, at least on Planet Earth. Can biomimetics point us towards a more sustainable future? We have been developing biomimetics at the level of systems rather than specific mechanisms and find that there are several levels at which biology can transform our approach to engineering.

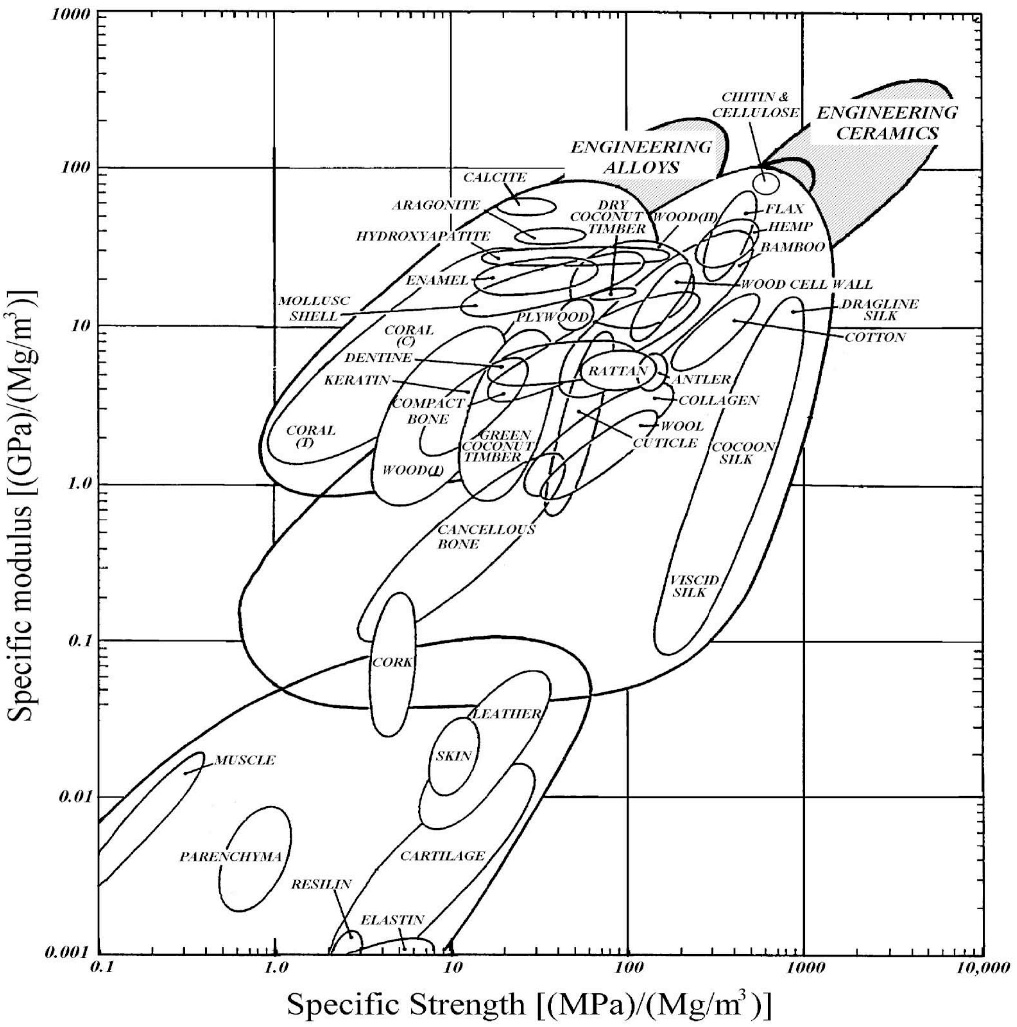

Figure 2. Comparison of specific properties of biological and engineering materials. Both groups of materials are plotted, showing that they cover nearly the same ranges except for high performance ceramics and alloys. (Constructed from data in papers by Wegst and Ashby)

Materials Processing

At size levels of up to 1 cm, where most technology is sited, the most important variable for the technical solution of a problem is manipulation of energy (up to 70% of the time), closely followed by use of material (fig. 3, top). Thus, faced with an engineering problem, our tendency is to achieve a solution by changing the amount or type of the material or changing (usually increasing) the energy requirement. However, while engineering commonly processes materials by fabrication (e.g. from the melt), biology uses rich embedded molecular information (composition, arrangement of components, molecular size and shape, hydrophobicity, charge) to direct net forming in growth and assembly processes, since in biology the most important variables for the solution of problems at these scales are information (derived mainly from DNA) and space (fig. 3, bottom). This can be illustrated by comparing the functionality of biological and man-made polymers, proteins and polysaccharides. Our technology has produced over 300 basic polymers, but none of them is as versatile or responsive as the two biological polymers, protein and polysaccharide. For example, at the primary level, proteins are remarkably similar in the energy required for their synthesis since the peptide bond is the pervasive motif. However, functionally there is a wide range of proteins varying from inert fibrous (such as collagen or silk) to responsive fibrous (such as muscle) and from inert globular (such as skeletal proteins in insects) to responsive globular (such as enzymes). The difference between these proteins is less to do with the initial energy required for their synthesis than the complement and order of the amino acids, which is a derivation of information stored in the DNA of the nucleus or elsewhere. Space is also relevant, since the shape of the protein is an essential part of its function and derives, by folding or association, again from the information (the order and type of amino acid) dictated by the DNA. The same story pertains when considering biological hard tissues. Calcium and to a lesser degree silicon, derivatives are most common whilst carbonates and phosphates are predominant. This limited range of chemicals (with the occasional addition of iron, zinc or manganese) suffices for nearly all biological hard materials.

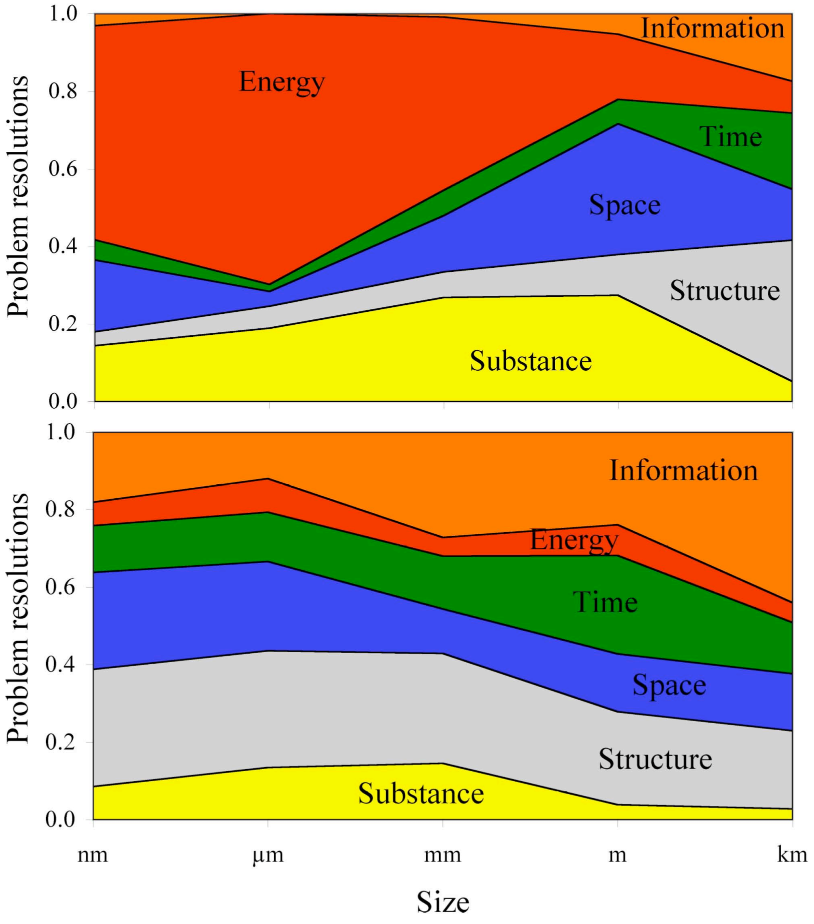

Figure 3. How problems are solved in technology (top) and in biology (bottom). While 70% of the technical solutions involve manipulation of energy (amount, source, type, etc.), the use and manipulation of information, from DNA to pheromones, is most important in biology (from Vincent et al. 2006).

Biological systems have developed relatively few synthetic processes; but the main variety of function is achieved by manipulations of shape and combinations of materials at larger sizes, achieved by many levels of hierarchy, where energy is not an issue. Instead of developing new materials each time, we want new functionality. We should be adapting and combining the materials we already have (Ashby and Brechet, 2003). Obviously, we are doing this to an extent, but it is unclear whether we recognize this as a significant route rather than a route of convenience.

Hierarchy and interfaces

Hierarchy is one of the basic attributes of biological materials. It arises partly because a biological organism is not made; it 'becomes'. At a small scale, intermolecular forces are sufficient to convert the amino acid sequence of a protein into a shape and these forces are probably sufficient to account for the structure of biological materials up to the µm scale. Above this size a major organizing principle is represented by liquid crystalline structure, which occurs in a very wide range of systems going from 1 to 500 µm or more (Neville, 1993). At larger sizes larger forces come into play: the initiation of a leaf primordium in a plant meristem is probably due to the interaction of the orientation of cellulose in the cell wall under the influence of the microfilament / microtubule system at the cell membrane and the more global effects of turgor pressure (Green et al., 1996). Broadly speaking, in biological structures there is a level of hierarchy at every order of magnitude in size. Thus a mammalian hair has 6 levels of hierarchy and a tropical forest has 20.

In technology, hierarchy occurs by accident and is rarely designed into a structure. In naïve terms it is easy to show that an aircraft has 7 or 8 levels of hierarchy, as does the airport building outside which it stands (Fig. 4). In engineering materials, hierarchy is related to heterogeneity that is deemed to militate against the perceived requirement of continuity and predictability within a material. The desire is to remove any original structure and to impose new structure as part of processing the material, thus destroying the inherent information and imposing information extrinsically. This requires energy both for the destruction and for the reinstatement. Thus the material is more or less homogeneous from the nanometer level up to the size of the component for which that material is used – at the cm or even the m level.

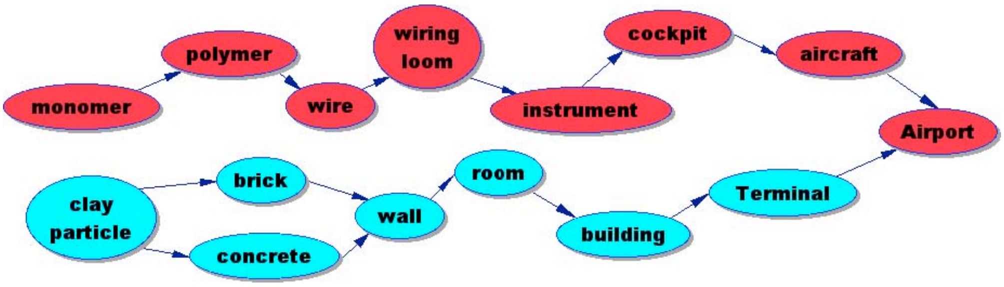

Figure 4. Levels of hierarchy in the wiring of an aircraft and the building outside which it stands.

Stiffness of materials is not influenced by hierarchy since the definition and measurement of stiffness does not include size or scale. But areas of local compliance, due to the hierarchical arrangements, can greatly affect the failure properties. For example, in wood the vessels that transmit water up the trunk of a broad-leaved tree are much larger (500 μm diameter) than the bulk of the wood cells (50 μm diameter). When the wood is compressed across the grain the large vessels collapse first and in doing so entrain the collapse of surrounding cells (Hepworth et al., 2002). Depending on the distribution of the vessels the wood can be relatively brittle (e.g. oak, where the vessels develop in a single layer in the wood – 'ring porous' – concentrating collapse into a small zone) or tough (e.g. hickory or beech, where the vessels are distributed evenly throughout the wood – 'diffuse porous' – and so spread the collapse amongst many more cells). The reverse can also occur. Rod Lakes reported making hierarchical honeycomb, used as the middle layer in lightweight structural composite plates, by stacking unexpanded small cell layers of honeycomb and using wide stripes of glue between them so that when he expanded them they became cells whose walls were made of larger cells; another method he used was by gluing together segments of first-order honeycomb to form a larger honeycomb. This structure looks very much like a piece of hardwood. He found that the specific out-of-plane compressive strength of the second-order hierarchical honeycomb was about 3.5 times greater than the first-order honeycomb. This was fairly close to his predicted value of 4.6 (Lakes, 1993).

The advantage of hierarchy is, therefore, as much in improving failure properties as improving structural efficiency. This is taken much further in biological materials. Simply put, since the size of a typical Griffith flaw (which will start catastrophic failure) in a ceramic or crystalline material is of the order of 10 – 30 nm (Griffith, 1921), it follows that if the reinforcing particles in a biological ceramic composite are smaller than that dimension, they will be free of flaws and will not fail in a brittle manner. In bone the crystallites of hydroxyapatite are less than 5 nm thick and about 25 nm wide, so they will not be able to accommodate such a flaw at normal operating stresses. This means that fracture will occur at a higher size level within the hierarchical structure, thus enabling the stiffening element to function with no danger of failure. Thus the particles that are large enough to accommodate a flaw are themselves hierarchical composites and the strain energy that the crack might cause to be released can be dissipated by plastic deformation between the subparticles, so that the interatomic interactions providing stiffness do not themselves have to show ductility, as has to happen in a tough metal. Essentially, therefore, hierarchy with its attendant interfaces, allows the origins of stiffness and toughness in a material to be separated in terms of size and therefore to be separately controlled. This is impossible in most technical materials, which therefore have to sacrifice stiffness for toughness and vice versa. Hence a single material –"bone"– can display a remarkable range of properties, depending on the volume fractions of the components and the control of the interfaces between the levels of hierarchy. For this reason bio-ceramic structures are much tougher (10 times or more) than technical ceramics (fig. 5); much the same goes for polymers. Therefore a direct consequence of hierarchy is increased adaptability. Functions can be modified or enriched by structuring at each level of hierarchy. Adaptability increases as a function of the number of levels of hierarchy. Also the hierarchy is a direct outcome of the self-assembly system in biology, itself driven by information from the molecular level.

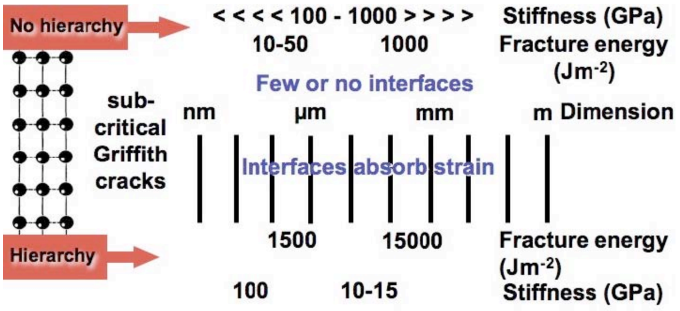

Figure 5. The effect of interfaces between level of hierarchy on stiffness (which may fall ten-fold) and fracture energy (which can increase one hundred-fold).

Resources and recycling

If biomimetics is to define a new way of doing engineering, then resources and recycling become part of the scheme. Biology has evolved a system that works very well. One wonders how many prebiotic polymer systems failed because they were unsuitable for recycling and consequently, how many types of living organism did not survive. The very paucity of material types used by living organisms has evolved such that recycling is simpler and the availability of resources to the next generation that much better. The whole topic of the temperature stability of biotic chemicals and structures underlies resource recycling. With only two polymers in use the central problem of separating the materials becomes trivial. It would be entirely possible to reduce the number of basic polymers which we use in our technology (we probably need only 6) and increase their range of properties by having a greater variety of functional groups. Can a tropical forest teach us about the dynamics of effective recycling, even when the mineral resources are scarce?

Actions

By comparison with the valuable pharmaceuticals that have been identified in plants and animals in rainforest and other partially explored environments, such as the sea, are there similar mechanical or structural or developmental systems that we haven't questioned yet? Currently biomimetics is taken up with investigating individual tricks or structures. Our analysis suggests that this might be interesting and useful, but only in the short term. Our economy is based on the development of new materials and we know full well that biological materials outperform technical materials in many important areas (Gordon, 1976). They are tougher, more adaptable, cheaper, lighter. Most important, they are hardly at all reliant on energy (Vincent, 2002). Biomimetics should be combining with nanotechnology to investigate the way in which biological materials are assembled. In some areas this is already bearing fruit, most notably in photonics (Vukusic and Sambles, 2003). But nanotechnology is obsessed with the small. I have shown here that it is the informed assembly, producing hierarchy and interfaces, which underlays the desirable properties of these materials.

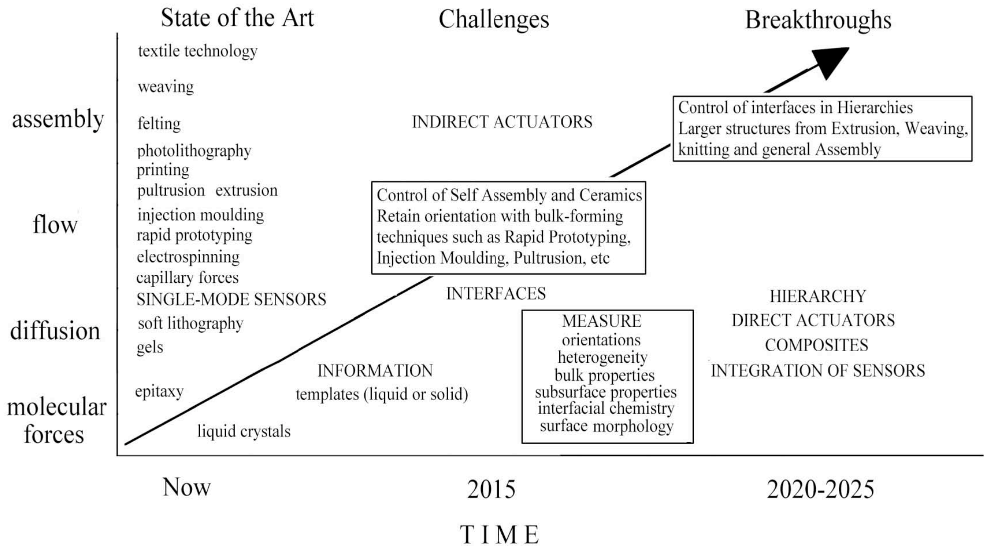

Figure 6: Biomimetic nanotechnology – The Roadmap.

Much of nanotechnology relies on self-assembly, yet self-assembly is really needed only at the very lowest size level. After that there are other assembly techniques available such as electrospinning, surface templating relying on shapes and chemical binding and a wide range of fibre-handling techniques developed in the paper making and textile industries. Such techniques of assisted self-assembly, 'State of the Art' on the roadmap (fig. 6), overcome a major criticism of the synthesis of biological materials – that it takes too long and is too small. With assistance provided by an external energy source this is no longer an issue.

Biology clearly has much to teach technology, but I think we are short-sightedly looking in the wrong places and need to understand better some of the fundamental processes in the natural world. How do bamboos and fungi grow so quickly to become stable structures? How are leaves supported? Why is wood the most efficient material? How do banyan trees grow? And there are all the organizational issues that I haven't touched upon, but which appear at the larger size levels in fig. 3. For instance, in Bath, Olga and Nikolay Bogatyrev are successfully developing applied management systems based on ant ethology. There have to be many more questions that haven't been asked, but if we haven't got the organisms to ask we'll never find the answers, let alone know how useful they might be.

Biomimetics/bionics can have a significant effect on our survival if we can use it to redesign a technology that it is not so reliant on energy. This is eminently possible and with the tools currently available we can produce a wide range of materials, structures and systems to replace the current ones. But we still need the biological versions of these materials, structures and systems to show us the best ways. We cannot afford to go on making mistakes.

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Appendices

Conference Program:
Biodiversity Research – Safeguarding the Future

Bonn, May 12-16, 2008

Monday May 12:

Time	Task/Theme	Location
16.00 – 22.00	Registration	Museum Koenig (ZFMK)
18.00 – 22.00	Ice breaker party	ZFMK

Tuesday May 13:

Symposium I: Acceleration of Biodiversity Assessment and Inventorying

Time	Speaker	Task/Theme	Location
8.00 – 18.00		Registration	University Main Building (UMB)
9.00 – 9.10	W. Barthlott, J.W. Wägele	Welcome, Introduction, Logistics, Announcements	UMB
9.10 – 9.30	W.R. Erdelen	Addressing Future Challenges in Biodiversity Science and Policy -A UNESCO Contribution	UMB
9.10 – 11.15	Chair: S. Tillier		
9.30 – 10.15	M. Walpole	A world where Biodiversity counts (Plenary lecture)	UMB
10.15 – 10.35	C.R. Brandao	Present situation of Brazilian biodiversity studies	UMB
10.35 – 10.55	R. Medellin	Biodiversity conservation and sustainable development: feasible solutions to real challenges, the case of Mexico	UMB
10.55 – 11.15	S. Knapp	Accelerating global taxonomy -the Solanum Planetary Biodiversity Inventory experience	UMB
11.15 – 11.45		COFFEE BREAK	UMB
11.45 – 12.45	Chair: K. Riede		
11.45 – 12.05	M. Willig	Networks by Design: Recommendations for a Global Diversity Monitoring Program	UMB
12.05 – 12.25	K. E. Jones	iBats: Global acoustic monitoring of bat biodiversity	UMB
12.25 – 12.45	P. Taberlet	DNA barcoding for biodiversity assessment	UMB
12.45 – 14.00		LUNCH	UMB
14.00 – 15.00	Chair: W. Barthlott		
14.00 - 14.20	C.-B. Kim	Activities on species conservation and DNA barcoding as one of ways on monitoring species in Korea	UMB
14.20 – 14.40	W. Laurance	Impacts of global climate change on tropical ecosystems: recent findings and debates	UMB
14.40 – 15.00	P. L. Nimis	KeyToNature: New tools for teaching and learning biodiversity	UMB
15.00 – 15.30		COFFEE BREAK	UMB

Tuesday May 13:			
Symposium I: Acceleration of Biodiversity Assessment and Inventorying			
Time	**Speaker**	**Task/Theme**	**Location**
15.00 – 15.30		COFFEE BREAK	UMB
15.30 - 17.00		Statements and Panel discussions	UMB
	Chair: E. Kalko	Introductory statements	UMB
17.00 – 18.00		BREAK Poster sessions	UMB
18.00 – 20.00		Write-up Committee	ZFMK

Wednesday May 14:

Symposium II: Biodiversity: Functions and uses

Time	Speaker	Task/Theme	Location
8.00 – 18.00		Registration	University Main Building (UMB)
9.00 – 11.00	Chair: B. Schmid	Ecosystem Services: Provision, Regulation & Support	UMB
9.00 – 9.30	H. Mooney	Ecosystem Services: Human use of biodiversity functions (Plenary lecture)	UMB
9.30 – 9.50	J. McGlade	Biodiversity & Marine Resources	UMB
9.50 – 10.10	T. Chakraborty	Biodiversity and Infectious diseases	UMB
10.10 – 10.30	D. Wall	Biodiversity, Carbon storage and Trace gas release	UMB
10.30 – 11.00		COFFEE BREAK	UMB
11.00 – 12.30	Chair: Th. Speck	Nature as a model for technical applications and innovations	UMB
11.00 – 11.30	J. Vincent	Biomimetic diversity (Plenary lecture)	UMB
11.30 – 11.50	R. Bonser	Biomimetics: Industrial innovation driven by nature	UMB
11.50 – 12.10	J. Casas	Nature inspired technology: tapping into biodiversity	UMB
12.10 – 12.30	W. Barthlott	Do we need the Sacred Lotus Flower? – A Case study in Biomimicry	UMB
12.30 - 14.00		LUNCH	UMB
	Chair: L. Salles		
14.00 – 15.30		Regulations of Access and Benefit Sharing	UMB
14.00 – 14.30	M. Footer	Access and Benefit Sharing: the current debate on regulation in perspective	UMB
14.30 – 14.50	K. Holm-Mueller	Transaction costs in the ABS procedures	UMB
14.50-15. 10	E.C. Kamau	Access to genetic resources and benefit sharing: Undoing or tightening the knot	UMB
15.10 – 15.30			
15.30 – 16.00		COFFEE BREAK	
16.00 - 17.30	H. Mooney	Statements and Panel discussions	UMB
		Introductory statements	UMB
17.30 – 18.03		BREAK Poster sessions	UMB
18.30 – 20.30		Write-up Committee	ZFMK

Thursday May 15

Symposium III: Biodiversity Change – The 2010 Target and Beyond

Time	Speaker	Task/Theme	Location
8.00 – 18.00		Registration	University Main Building (UMB)
	Chair: A. Larigauderie		
9.00 – 9.45	R.J. Scholes	Taking the pulse of biodiversity: a vision for a Global Biodiversity Observation Network (Plenary lecture)	UMB
9.45 – 10.45		The loss of biodiversity and approaches for a sustainable world: A state of the art assessment	UMB
9.45 – 10.05	G. Mace	Approaches to biodiversity planning in a changing world	UMB
10.05 – 10.25	J. Soberon	Challenges and approaches in (a/the) mega-diversity country(ies) of the south	UMB
10.25 – 10.45	J. Freyhof	The Hidden Freshwater Biodiversity Crisis	UMB
10.45 – 11.30		COFFEE BREAK	UMB
11.30 – 12.30	Chair: J. Heinze	Change of ecosystem functions and services	UMB
11.30 – 11.50	J. Ollerton	Pollinators as critical ecosystem service providers: the biodiversity of species interactions	UMB
11.50 – 12.10	R. Crozier	Conservation genetics: from species to habitats	UMB
12.10 – 12.30	P. Genovesi	Biological invasions: a major driver of ecosystems change	UMB
12.30 – 14.00		LUNCH	UMB
14.00 - 15.00	Chair: G. Mace	Towards an integrated biodiversity observation system	UMB
14.00 - 14.20	W. Turner	A Global Biodiversity Observation Network: What Do Satellites have to offer?	UMB
14.20 – 14.40	P. Leadley	Techniques & targets: The present potential and the future role of projections & predictions	UMB
14.40 – 15.00	E. Beck	Observatories and exploratories: German interdisciplinary approaches to realise biodiversity changes and understand their functional consequences	UMB
15.00 – 15.10	R. Kohsaka	Experiences from implementing CBD in the local context; Restoring Satoyama and urban biodiversity through citizens' participation in Higashiyama, Nagoya Aichi, Japan	UMB
15.10 – 15.30		COFFEE BREAK	UMB
15.30 – 17.00		Statements and Panel discussions	UMB
		Introductory statements	UMB
17.00 – 18.00		BREAK Poster sessions	UMB
18.00 – 20.00		Write-up Committee	ZFMK

Friday May 16:		
Time	**Task/Theme**	**Location**
9.00 – 12.00	Final Discussion, Resolutions and recommendations to the COP9	UMB
12.00 – 13.00	Press conference	UMB
12.00	Farewell Party	UMB

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