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BIOLOG

German Programme on Biodiversity and Global Change

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Status Report 2001

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Introduction to the Programme BIOLOG

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BIOLOG: The history BIOLOG is Germany's most outstanding scientific and also financial response to the UN-Convention on Biological Diversity, the so-called 1992 RIO-Convention. It is part of the Federal Government's programme for research into aspects of global change. In 1997 the German National Committee for Global Change recommended the launching of a research programme on "biodiversity in the scope of global change". In April 1999 the guidelines of the "BIOLOG" programme and a call for projects were published. From 251 proposals 93 projects were finally selected which started their work during the course of the last year. Affiliation with other programmes on biodiversity research, e.g. the ICSU and IUBS Diversitas programme is expected.

Biodiversity is severely threatened by man There is general agreement among scientists and politicians that biodiversity is severely threatened by the activities of the tremendously increasing human population. Estimates of the worldwide loss of biodiversity range between 2 and 130 species per day. Even if a number on the lower side of this range is assumed, the extinction rate by far exceeds that at the end of the Cretaceous when the Saurians died out.
Research into biodiversity is therefore not a luxury but a necessity. It is a major challenge, not only because of the great variety of related scientific aspects and the multitude of disciplines involved, but also with respect to the high expectations of the public as to practically applicable results and solutions of urgent environmental problems arising in the context of global change.

Only a small part of the kingdom of organisms is known at present A primary problem in biodiversity research is the lack of basic knowledge. Estimates of the total number of species on earth range between 5 and 100 million, of which less than 2 million are known at present. Therefore further inventories are indispensable, but it is clear that the progress in knowledge can hardly keep up with the rate of disappearance of species. This holds in particular for the realm of microorganisms where we are just beginning to develop methods for identifying organisms which can not be cultivated in the laboratory.

The value of biodiversity is inestimable, and proper use of it has not yet been accomplished If only a minor part of the estimated wealth of organisms is known, can we validate biodiversity and especially the losses of biodiversity? In an economic sense this is not possible and from the biological viewpoint we must admit that the value of biodiversity is in fact inestimable. With each extinct species a functioning genetic system is lost and with it genes and gene products which could have been of great importance for the needs of the rapidly growing human population. This holds for all kinds of organisms, but will be illustrated only by the example of crop plants: Of 270,000 species of higher plants about 3000 serve as food plants, and of these 3000 only 30 species are more or less domesticated crop plants of which only the 4 species maize, rice, wheat and potato produce more than 70 % of the food supply for 6.4 billion people. There is no doubt that even in the food sector man is making not yet proper use of the resource biodiversity.

Biodiversity and the stability of ecosystems Biodiversity is understood as a major factor involved in the stability of ecosystems. However, the investigation of the functional roles of all species of an ecosystem is not feasible because of our incomplete knowledge of the respective biological inventory. Therefore so-called key species must be identified which may be essential for the ecosystem under consideration, and their specific functions in that ecosystem must be elucidated. This kind of research is not only necessary for the understanding of functionality in an ecosystem, but also for the recognition of environmental changes which may destabilize or even cardinally change the ecosystem.

Biodiversity and sustainable use of an ecosystem Stability of an ecosystem is the primary prerequisite for its sustainable use by man. Sustainable use means an almost indefinite number of possibilities of exploitation, which depend on the ecosystem itself and the people living in it. Important examples with special regard to global change are the worldwide endangered tropical mountain forests which gather the rain for the benefit of the lowlands and the semiarid ecosystems which are threatened by desertification. Even in these ecosystems knowledge of functionality of individual organisms, such as presumptive key species is still missing.

The Pilot Phase: Research into biodiversity requires capacity building It is conceivable that research into the already mentioned and additional topics of biodiversity, especially with respect to global change, will require special scientific and logistic capacity and in particular sufficient time.

The scientific advisory committee which has been in charge of the arrangements of BIOLOG has therefore given priority to R&D projects which are based on a fair degree of international integration and capacity building. Especially with respect to these requirements and to a strong and effective cooperation of the disciplines involved, the committee's policy was - and still is - to concentrate the projects to regions expressing different levels of biodiversity, regions of different levels of relevant knowledge and expertise, and of differently endangered biodiversity.

BIOLOG Africa and BIOLOG Europe Projects operating in several regions of subsaharian Africa (the so-called BIOTA-projects: 3 individual projects and 3 clusters of projects with a financial volume of 30.1 million DM) and, as an antipole, projects in Central Europe ("BIOLOG EUROPE", comprising 13 projects, awarded grants of 14.2 million DM) were selected to start BIOLOG. A pilot phase of 3 years should be used to develop scientific as well as logistic capacity, and to examine the methodologies. A geographical information system (GIS) will be established in order to model scenarios when sufficient data become available.

In the BIOTA projects special emphasis is given to biodiversity inventories at different scales, combined with long-term monitoring in so-called "observatories" which are standardized plots of usually 1 km^2 left untreated or subjected to selected kinds and varying intensities of utilization. In the BIOLOG EUROPE projects, the effects of fragmentation of the landscape, of intentional and accidental invasion of exotic species and other impacts on biodiversity are being studied, as well as the diversity, dynamics and function of microorganisms in terrestrial ecosystems. In both BIOLOG EUROPE and BIOLOG AFRICA special attention is given to history and tradition, policy implications and socio-economic dimensions of the loss and preservation of biodiversity.

BIOLOG: Biodiversity Informatics In addition to the projects investigating aspects of terrestrial biodiversity, a subprogramme "Biodiversity Informatics" was advertised. An immense amount of organismic data are deposited at the big Natural History Museums, e.g. at Frankfurt ,Berlin, Stuttgart, Braunschweig and Munich and also at smaller specialized collections of biological materials. A substantial part of these data is not yet readily accessible or is incomplete; in particular molecular genetic data is still missing for the majority of the collected specimens. The aims of "Biodiversity Informatics" are to improve the methods of biodiversity data capture and maintenance, to digitalize and network the wealth of the already available data collections, and to interlink biodiversity-related infrastructures nationally and worldwide. Out of 56 drafted proposals 31 were selected and have been organised within 7 projects with a financial volume of 14.6 million DM. Three of these projects represent major clusters comprising e.g. insects, pathogenic fungi and special families of higher plants.

The BIOLOG Status Symposia Status Symposia will report on the achieved scientific progress of the projects, on their difficulties, their future plans and on their collaborative integration. The first symposium of this series in December 2001 will be of special interest with respect to the announcement of the main phase of BIOLOG.

BIOLOG EUROPE
A MULTIDISCIPLINARY APPROACH TO EUROPEAN BIODIVERSITY

Volkmar Wolters & Barbara Reinhold-Hurek

As a continent, Europe is unique in the extent to which its natural and cultural landscape is fragmented into a patchwork pattern. Humans have deliberately changed Europe's environment for hundreds of years (1). Today there is no place in Europe below 2000 m that has not been affected by anthropogenic impacts in one-way or the other. The resulting mosaic of natural, semi-natural and cultural landscape fragments is a major factor supporting European biodiversity by creating a complex spatio-temporal pattern of ecosystems and habitats (2). There is growing concern, however, about potentially detrimental consequences of large-scale changes on biodiversity, because recent alterations induced by human beings occur at unprecedented rates and scales (3, 4).

Biodiversity is the variety of life at all levels of biological organization (5). The 13 projects of BIOLOG-Europe that are currently funded study the impact of environmental change on Europe's biodiversity by focusing on a diversity of ecosystems such as floodplains, grasslands, coastal areas, forests and arable fields (Tab. 1). The following topics are covered:

- Evolution, maintenance and alterations of biodiversity as a result of natural and anthropogenic changes in global environmental conditions;
- Links between biodiversity and both ecosystem stability and functioning;
- Development of indicator systems for rapid survey and evaluation of biodiversity change;
- Policy dimensions of biodiversity.

Ecological processes observed and quantified in experimental approaches include secondary succession, invasion of non-native species, changes in landscape complexity, modifications in water availability, manipulation of diversity, and management. The various taxa considered include woody and herbaceous plants, grasses, different guilds of insects, soil biota, basidiomycetes, and terrestrial microorganisms. In addition, past biodiversity is reconstructed from historical sources, policy dimensions of biodiversity are studied, socio-economic aspects of preserving biodiversity are explored, evolutionary consequences of hybridisation are evaluated, and strategies for the conservation of genetic resources are developed.

A particular focus is on the development and adaptation of methods for analysing diversity, dynamics and function of prokaryotic microorganisms in terrestrial ecosystems. Prokaryotes exclusively or predominantly catalyse key transformations within the global N, S and C cycles, and significantly contribute to the mineralization of xenobiotics. According to recent estimates more than half of the earth's biomass is stored in prokaryotes. Conservative estimates suggest that only 0.4 % of the naturally occurring species of the *Archaea* and *Bacteria* have yet been described, making prokaryotes by far the most unexplored group of organisms. This apparent lack of knowledge reflects the limitations of traditional techniques for studying complex microbial communities. Only a minority of the naturally occurring prokaryotes can be obtained by classical enrichment and cultivation methods. Recently developed DNA- or RNA-based techniques allow studying the diversity, *in situ* population structure and activity of complex microbial consortia. Special attention will be given to those terrestrial prokaryotes, which are essential to global nitrogen and sulphur cycling and/or to the production of greenhouse gases.

Table 1: Overview over the 13 BIOLOG-Europe projects that are currently funded.

Monitoring and Complexity Analysis

- Biodiversity and spatial complexity in agricultural landscapes under global change.
- Biodiversity change in salt meadows.
- Ecology and biodiversity of fungi in Central Europe (with emphasis on Homobasidiomycetidae).

Experimental Approaches and Process Analysis

- Biodiversity and ecosystem function in grasslands – the effects of insect herbivory and draught stress.
- Biodiversity and Ecosystem Function: Grassland as a Model System.
- Biodiversity of terrestrial microbiota.
- Evolutionary consequences of biological invasions – Hybridisation between invasive and native Brassicaceae taxa.
- Global change-dependent spread of neophytes: relationship to ecosystems change (case study: floodplains of the river Rhine).

Temporal Dimensions and Socio-economic Perspectives

- Mechanisms of biodiversity changes of selected functional groups in Red oak ecosystems.
- Management concepts based on biodiversity change during a 20-years succession.
- Reconstruction of historic biodiversity from archival sources.
- Conditions of a biodiversity-oriented policy for Germany as a part of the EU.
- Use and conservation of genetic resources: A strategy for preserving biological diversity?

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BIOLOG AFRICA

BIODIVERSITY MONITORING TRANSECT ANALYSIS IN AFRICA

BIOTA AFRICA (Biodiversity Monitoring Transect Analysis in Africa) is the joint frame for the three BIOLOG projects, *BIOTA West Africa*, *BIOTA East Africa* and *BIOTA Southern Africa*, and altogether includes 34 sub-projects.

BIOTA AFRICA is the synonym for the corporate identity of these BIOLOG projects and sub-projects, aiming at coherent research concepts and monitoring activities in various regions of Africa. During the planning phase, a number of basic paradigms were defined which finally resulted in a large number of research proposals:

- The programme puts a major focus on the assessment, understanding and prediction of the change of biodiversity on the African continent, in the context of global environmental change and impacts of human land use. In the main phase, approaches towards a scientifically based management and monitoring of biodiversity will gain higher importance. The programme will not be restricted to one in-depth case study, but will aim at comparable results derived from various scales and different regions.

- In order to record the driving factors controlling biodiversity, research sites were selected along the predominant environmental gradients, allowing better comparability by standardised scales and measurement techniques.

- The programme will strengthen the impulse towards the initiation of a global network of standardised biodiversity observation sites.

- Biodiversity in various land use systems is being analysed, monitored and compared with natural systems.

- Continental scale and ecosystem scale will be linked by suitable research structures that allow an up- and down-scaling.

- The major biomes of the continent will be represented.

- Special emphasis is placed on research close to the boundaries or transition zones between major biomes, as these regions might show more rapid changes of biodiversity.

- The possibility of the extrapolation of results will be optimised by putting a clear focus on zonal ecosystems of a larger spatial representation.

- The strong interdisciplinary structure of the project aims at the development of integrative, applied management and monitoring concepts.

Based on these goals and paradigms, as well as on the already existing disciplinary and regional competence and co-operation, a regional concentration along two large continental transects in Southern and Western Africa was combined with regional investigations into altitudinal gradients, aridity as well as land use intensities in Eastern Africa and Southern Arabia.

The research areas are shown in the figure below, and cover the following vegetation zones in Southern and Western Africa:

- Mediterranean Fynbos (South Africa)
- Arid mediterranean Succulent Karoo (South Africa)
- Arid tropical Nama Karoo (South Africa and Namibia)
- Arid and semi-arid Savanna types (South Africa, Namibia, Burkina Faso)
- Dry Forest (Namibia, Burkina Faso, Benin, Ivory Coast)
- Forest (Burkina Faso, Benin, Ivory Coast)
- Rain Forest (Ivory Coast)

In Eastern Africa and Southern Arabia, the following larger ecological units are covered by the sub-projects of BIOTA Eastern Africa:

- Humid Highland Forest (Kenya, Uganda)
- Montane Rain Forest (Kenya)
- Coastal Rain Forest (Kenya, Tanzania)
- Semi-humid Savanna Types (Kenya)
- Wetlands (Kenya, Tanzania, Uganda)
- Xerotropical deciduous and semideciduous woodlands (Yemen, Socotra)

The realisation of the above mentioned research goals will be linked with capacity building in all countries involved, with the participation of stakeholders wherever possible, and with an innovative data sharing protocol. The project has been accepted as an IBOY (International Biodiversity Observation Year) core project, and aims at providing scientific data to the Convention on Biodiversity (CBD) and the Convention to Combat Desertification (CCD).

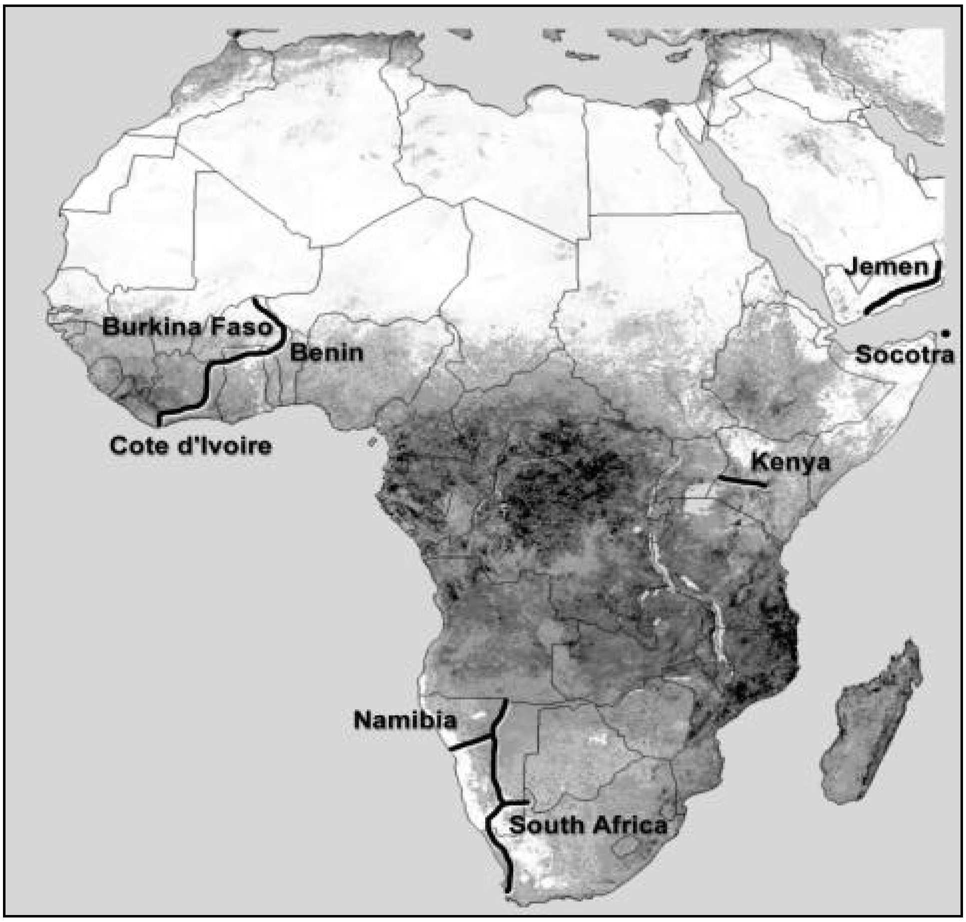

Fig. 1: Research areas of BIOTA AFRICA

BIODIVERSITY INFORMATICS IN THE BIOLOG PROGRAMME

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Key words: biodiversity informatics, BIOLOG programme

Abstract:

This article briefly introduces the field of Biodiversity Informatics in general and details the role of this discipline within the BIOLOG programme.

Introduction

"Biodiversity Informatics" circumscribes the application of IT tools and technology to biodiversity information, principally at the organismic level. It thus deals with information capture, storage, provision, retrieval, and analysis, focusing on individual organisms, populations, and taxa, and their interaction. It covers the information generated by the fields of systematics (including molecular systematics), evolutionary biology, population biology, behavioural sciences, and synecological fields such as pollination biology, parasitism, and phytosociology. Biodiversity Informatics is considered a part of biological informatics sandwiched between - and strongly overlapping with - environmental informatics and molecular bioinformatics. [1]

BIOLOG and Biodiversity Informatics

The choice to include a section titled Biodiversity Informatics in the BIOLOG Programme [2] was undoubtedly influenced by the German government's decision to become a founding member of the Global Biodiversity Information Facility (GBIF). The rationale for the GBIF [3] also applies to BIOLOG: vast information resources have to be accessed, and are produced, by a biodiversity research programme of BIOLOG's scale. An effective electronic information infrastructure is the prerequisite for an efficient dissemination of results and a sustained effect of the invested research funds. Effective access to past research results and to data resources like collections is essential because it will provide the necessary background for knowledge gain from the new results. The information provided has to be of high quality, it must be accessible, relevant, accurate, complete, referenced, and affordable. [4]

BIOLOG's sub-programme on biodiversity informatics is to explore and develop the very substance of information processing present in the German biodiversity research infrastructure. It is a showcase for the biodiversity research community's ability to co-operate, both within the community and with related fields such as geography and climatology. With its explicit funding focus on biodiversity informatics, BIOLOG treads new ground. The US, Australia, Mexico and the UK, among others, have started funding such research much earlier than the German government, but on a project-by-project basis. However, the results are so convincing that, for example, the Australian government is now providing Au$ 10 million to digitise all Australian herbarium specimens over the next 5 years in the Australian Virtual Herbarium [5].

The novelty of the topic in Germany is perhaps also the reason for the explicit limitation of the sub-programme to 3 years, while the rest of BIOLOG is seen as a potential a long-term programme. The stated intention is to integrate biodiversity informatics research into the general terrestrial biodiversity research programme. In some cases this has already happened: there are several projects within BIOTA and BIOLOG-Europe with a distinct focus on biodiversity informatics. Further build-up of the infrastructure and the provision of base data is to be covered by other programmes such as GBIF-

Germany, and eventually the biodiversity informatics infrastructure is to be institutionalised to ensure long term sustainability.

For the planned creation of a system of German GBIF nodes [6], we can already draw on the results of several projects in the sub-programme. The following EU-funded projects are also directly supported by collection-oriented activities in the BIOLOG programme: ENHSIN (The European Natural History Specimen Information Network [7]), BioCASE (A Biological Collection Access Service for Europe [8]), and the forthcoming ENBI (European Network of Biodiversity Information) [9].

Presentation of projects

The sub-programme on biodiversity informatics consists of 7 main projects, 4 of which are more or less closely-knit assemblages of sub-projects; in total 24 individual projects are funded. Most of the investigators participating in the ongoing projects were brought together in 3 workshops to discuss options for collaboration and for the presentation of the sub-programme in the Statusseminar. For the 3 time slots available within the conference's programme, workshop participants generally preferred a coordinated thematic focus to a sequence of individual project presentations. The three subject areas selected cover (i) the discovery and identification of organisms with various computer-aided methods, (ii) the documentation and data mining of the enormous information resources represented by biological collections in Germany, and (iii) a summary of efforts directed at the interoperability and networking of the project results as well as their inclusion and interrelation with international projects such as the aforementioned European initiatives and GBIF. This selection of activities is to be supported by a range of horizontal subjects, such as software development, georeferencing, IPR, and data quality aspects.

After little more than a decade of development, the field of Biodiversity Informatics is still in its infancy. Presently the overriding objective – also within BIOLOG - is to provide a sound and effective information management infrastructure for biodiversity and Global Change research. The BIOLOG sub-programme is already making an impact in that respect. Although many methodological, operational, and research questions remain to be solved, BIOLOG represents an important step towards the realization of a vision: mobilizing existing biodiversity information resources and the application of new methods of analysis to that information will stimulate new insight into the evolution, functioning and role of ecosystems and their components.

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BIOLOG EUROPE

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GLOBAL CHANGE-DEPENDENT SPREAD OF NEOPHYTES: RELATIONSHIP TO ECOSYSTEM CHANGE (CASE STUDY: FLOODPLAINS OF THE RIVER RHINE)

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Key words: neophytes, floodplains, Lower Rhine, C4 plants, increase of vegetation period, *Amaranthus*, *Solanum*, *Impatiens*, plant productivity, competition, river flood regimes

Abstract:

Biodiversity changes due to increased neophyte colonization of river banks and floodplains in the Lower Rhine area are described and their impact upon ecosystem peculiarities assessed.Generally, these habitats show high short-term changes of α*-diversity from disturbances by the river activity and diaspore inputs* via *the waterway. Under the global change effects of extended vegetation periods due to increased average temperatures and of changed flood regimes, the spread of neophytes in these habitats is intensified. The impact of these processes on the floodplain vegetation can be indicative for future trends and for perspectives of stability of this ecosystem complex. .*

Since few decennia the percentage of C4 centrospermic taxa and of other neophytes of subtropical origin on the river banks has considerably increased. In other floodplain vegetation units high growing neophytes are spreading. This is mapped, and the competition dynamics of autochthonous taxa and of already established resp. of recently spreading neophytes is analyzed both by detailed biomass harvests in the floodplain vegetation units and by pairwise cultivation of relevant species pairs under controlled conditions (oblique-window rhizotrons, moisture gradient beds). Nutrient relations both of the soils and the plants are quantified, the impact of submergence, waterlogging or drought upon the neophytic species is measured by ecophysiological methods, and the environmental requirements for growth of these taxa are determined (germination studies, productivity measurements, biometric measures). First results after half a year duration of the project are presented as examples for the approaches of this study.

Results:

Mapping of the Rhine river bank vegetation of the Lower Rhine area with emphasis on neophyte colonization is underway. A locality-point map of Amaranthaceae and Chenopodiaceae on the Rhine river banks between Dormagen and Duisburg is given in Fig. 1. If relevées from the second half of the 20th century are compared (Tab. 1), the increase of neophytes of these families is obvious. Only *Amaranthus retroflexus* from temperate North America is naturalized in the area since the 19th century. The other taxa, with meridional/subtropical origins started spreading only two decennia ago. Another nine *Amaranthus* spp. of tropical origin have not yet left the bridgeheads of harbors. A similar situation is given with various *Solanum* species. The floodplain forest understory is, among other neophyte facies, dominated by four *Impatiens* species. Only *I. noli-tangere* is indigeneous, and in one location (Knebel 1998) it meets since

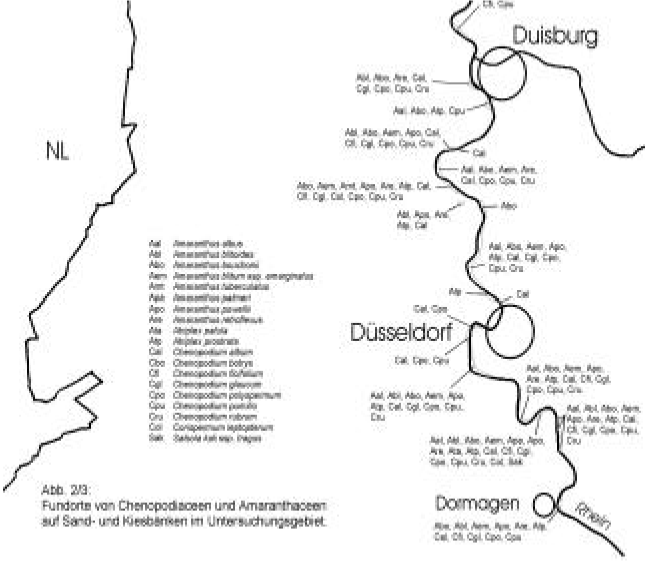

Fig. 1: Centrospermic taxa on Lower Rhine river banks

few years *I. capensis*, the vicariant taxon from temperate North America: It would be a unique case of documentation if we could follow in the next years a hybridogenic introgression among this trans-atlantic species pair from the very beginning onwards.

Tab. 1: Number of neophytic Amaranthaceae and Chenopodiaceae in Polygono-Chenopodietum relevées alongside the Middle and Lower Rhine river between 1964 and 2001.

Year	Source	Number of species	
1964	LOHMEYER & SUKOPP 1992	**2**	A.blitum A.retroflex
1983	MAY 1988	**2**	A.blitum A.retroflex.
1986 - 89	WISSKIRCHEN 1995	**6**	A. albus A.blitoides A.blit:2 ssp A.buchonii A.powellii
1989	LOHMEYER & SUKOPP 1992	**6**	**A. albus** **A.blitoides** **A.blitum** A.buchonii A.powellii A. retrofl.
1998-2001	SCHMITZ, unpubl.	**10**	**A. albus** **A.blitoides** **A.blitum** A.buchonii A.powellii A.retroflex. A.tubercul. Ch. botrys Ch. pumilio Corisp. lept.

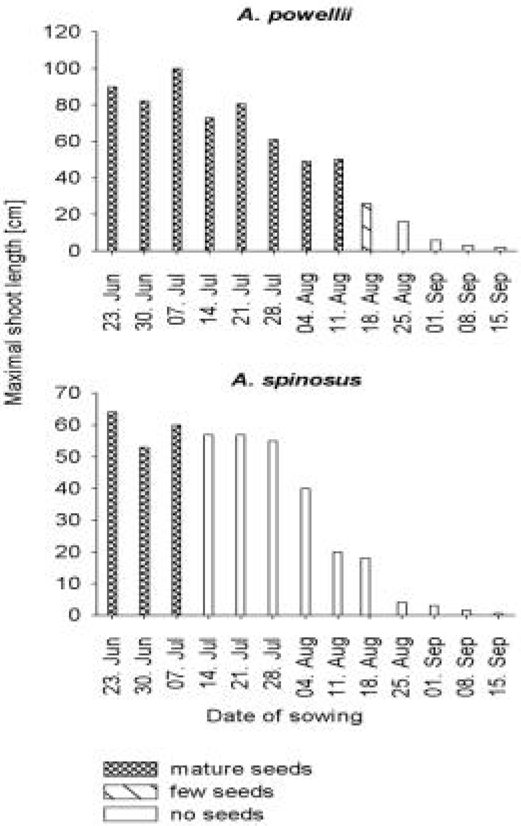

Fig. 2:Maximal shoot lengths and seed maturation depending on sowing date of an already spread (*A. powellii*) and a still ephemeral (*A. spinosus*) sub-tropical amaranth.

The rhizotrone and moisture gradient cultivation of related indigenous and neophytic plants demonstrated a partly differentiated, partly competing exploitation of the growing substrate due to taxon-specific root systems and different preferences with respect to waterlogging. Biometric data are just under evaluation; ample samples for mineral nutrient determinations are stored for the analysis. Measurements of the photosynthetic gas exchange will be done in the following year, anatomical studies of the Centrospermic taxa concerning Kranz-type leaf structures are already completed.

In the floodplain forest understory and in spring-inundated wet grasslands 30 permanent observation plots have been installed, in part with individuum-level mapping of the species. Biomass harvest occurred from equally-sized nearby plots so that finally biomass data of the neophyte-free herb layer can be compared with the stand biomass of neophyte facies.

Germination experiments rendered first approaches to causal interpretations of the colonization success of established or still ephemeral neophytes (Fig. 2): If, for temperature or river flood reasons, the germination of the latter does not occur in late spring they cannot produce ripe seeds. However, such suitable conditions do not occur each year, as the inter-annual variability of the flood regime of the river indicates (Fig. 3).

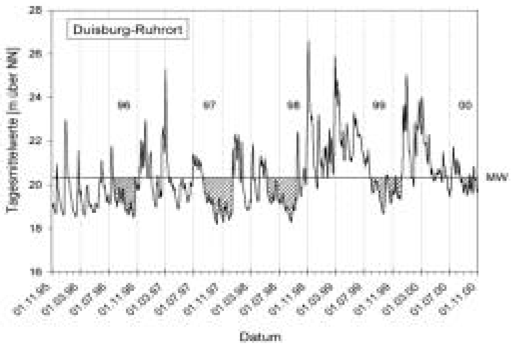

Fig. 3 : Rhine water level 1996-2000: Hatched areas indicate periods of water-free river bank conditions suitable for amaranth germination.

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RECONSTRUCTING HISTORICAL BIODIVERSITY FROM ARCHIVAL SOURCES

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Key words: biodiversity, nature conservation, environmental history, Brandenburg (Germany)

Abstract:

The research project aims at developing a tool for nature restoration to make more reliable judgements on the diversity of ecosystems by considering historical biological information. For that, proxy-data are made available out of archival sources and, standards are set according to which historical species stocks can be compiled from archival sources, be checked and be used as references for changes of biodiversity in the past. By taking a landscape drained in the 18th century (Oderbruch, Brandenburg) as an example, we are developing a method which guarantees a systematic approach to the relevant archival sources and which allows their efficient analysis.

Results:

So far, the stocks of archives have not been consulted for measuring historical biodiversity. In comparison with exclusively temporary data collections on biodiversity, they represent, however, an irreplaceable source of information for reconstructing the conditions of nature in the past. The project’s aim is to trace back the functional changes certain elements of biodiversity fulfilled for human needs by looking at historical examples at different stages in the past. Apart from that, it is the project’s aim to determine parameters for assessing shifts of biodiversity. By following both aims the project addresses a deficiency of relevant research. At the same time, we will gain some information on how reliable historical data are for the reconstruction of the fauna and flora of the past.

In our research, the land reclamation measures in 18th century Prussia and their impacts on the existence of plants and animals serve as an example. Land reclamation mainly served the goal to raise agricultural production and to create new land for foreign colonists to settle on. The process of land transformation lasted many years and transformed our sample region, the Oder marshlands – situated east of Berlin and in the state of Brandenburg – which were formerly mainly used by fisheries, into fertile grass and arable land. This resulted in considerable alterations of the respective ecosystems. After more than two hundred years, we still do not know which elements of fauna and flora actually disappeared.

Our investigations focus mainly on the stocks of the former Prussian State Archives in Potsdam and Berlin-Dahlem. The significance of archival records relating to certain questions on matters of historical species diversity varies considerably and thus, the records need to be classified to guarantee that they can be used in an efficient way. For the adequate processing of archival sources we are developing a catalogue of features which should allow to distinguish between types of sources which contain a lot of information relevant to us and types of sources which are irrelevant.

In general, there are no proper historical lists of species which will give us an immediate idea of the fauna and flora of the "Oderbruch" at the time of its melioration. Therefore, it is necessary to put the main emphasis on Indicator Species which point to the existence of other species with similar necessaries of life. The concept of Keystone Species allows to concentrate the search specifically on those species the existence of which determines significantly the structures and functions of an ecosystem.

The reconstruction of fish stocks of the Oder river in the marshland area at six different times compiled so far from printed sources serves as an example of possible results of our research approach (Fig. 1). Compared to the oldest data given by Jobst (1571), Bekmann (1700) and von Borgstede (1788), the fish stocks of the Oder river today consist of less species. The early sources give an additional account of the existence of those fish species which are of no economic use today but were nevertheless significant in the 18th century as, for instance, they were used for pig and poultry mast. Incidentally, the differences of species numbers in the sources concern mainly species with low frequency. We assume that their decline was principally caused by the effects of the growing trade and industry along the Oder river since the middle of the 18th century, rather than by the drainage measures.

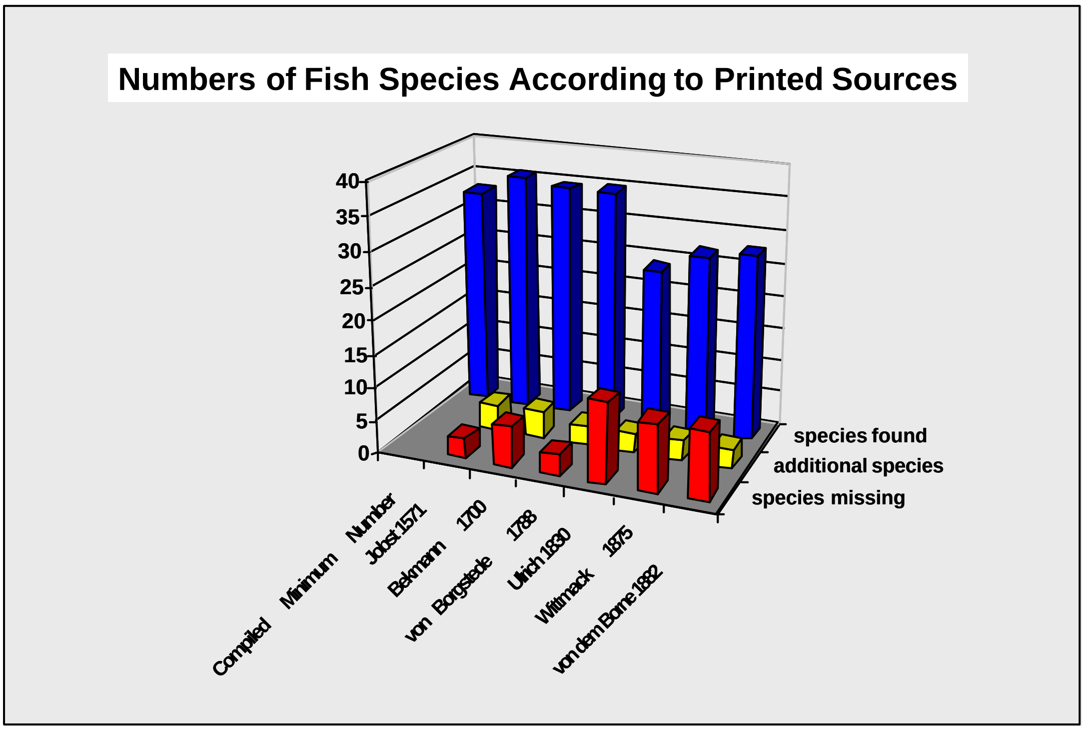

Fig. 1: The reconstruction of the Oder fish stocks in the area under investigation represents a successful example of consulting historical data for the assessment of species diversity.

Knowledge gained by research in archives may be utilized not only in a regional context, such as the "Oderbruch", but over an above that, for those developing countries which came under European influence at a rather early stage in history. As far as land reclamation happened by colonial powers and files have been stored according to European tradition attempts to reconstruct ecosystems might be based on the experience of our pilot study.

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01.10.2000 – 30.09.2002

BIODIVERSITY CHANGE DURING 20 YEARS OF SUCCESSION: IMPLICATIONS FOR MANAGEMENT OF RESTORATION

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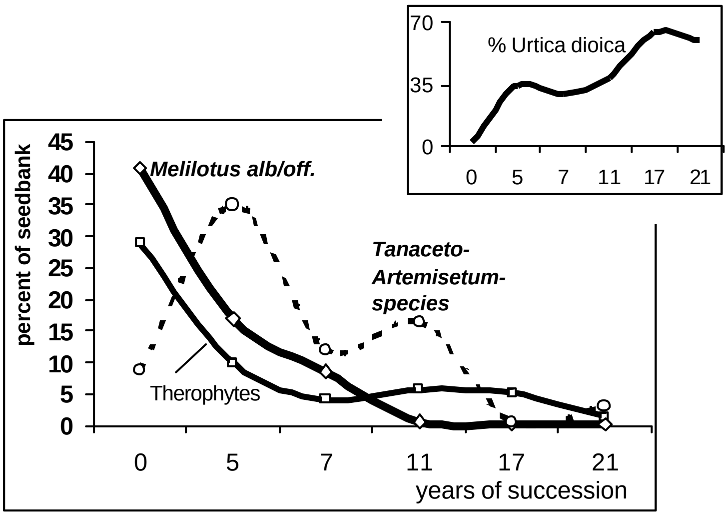
Key words: succession, long-term monitoring, biodiversity, vegetation, seed bank, soil fauna, Gamasina, restoration, management

Abstract:
The succession of soil mesofauna and vegetation has been studied since 1980 on two experimental plots, one left for undisturbed succession, the other managed as a lawn until 1987 (thereafter ruderalization). The results document very different patterns for soil mesofauna and vegetation, both at group and species levels. Within the first three years, recultivation leads to a transitory pioneer-maximum, followed by a steady increase over more than 10 years. The development of vegetation depends on historical conditioning of the seed bank, whereas survivors of fauna are of minor importance. Although above- and below-ground plant structure influence the development of soil mesofauna, their dynamics are not synchronised. Diversity of predatory mites (Acari, Mesostigmata: Gamasina) is increasing over long periods of time, whereas the seed bank is impoverished. Restoration management with focus on biodiversity should consider processes in the soil, and allow or introduce patchiness diversified in space and time.

Results:
The former rubble-and-debris dump in the vicinity of Bremen (Northern Germany) was covered in the late 1970ies with loamy sand (C= 1.6 – 3-5; N= 0.1 – 0.3). In 1980, the plateau was graded and two plots were prepared, one with standard recultivation measures (REC), the other was left for natural succession (SUC) (Weidemann 1985).

Vegetation

The development of the vegetation was studied on permanent plots and with germination experiments synchronously to succession, in the greenhouse and also in the field.

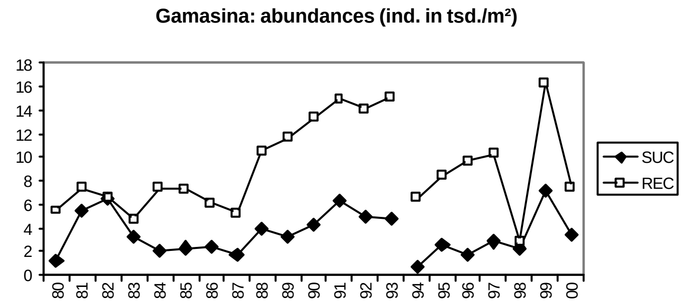


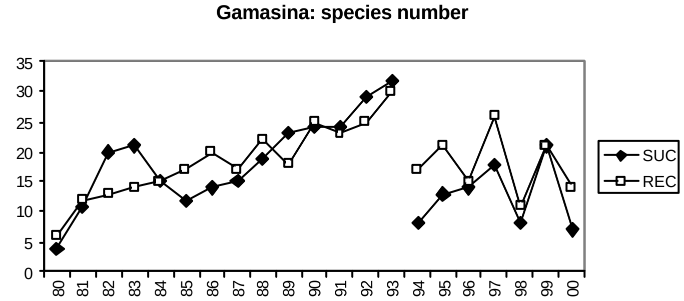
According to the model of initial floristic composition (Egler 1954), the seedbank is the controlling driving force of secondary ruderal succession of vegetation. Our results document for the first time seed bank dynamics in a true time-series and reveal substantial „dispersal in time“, even of species with persistent seeds (seedbank-types after Thompson et al. 1997). After 15-20 years, the seedbank is almost derelict concerning the former pioneer species (*Sinapis arvensis, Melilotus spp.*). Consequently, succession would restart after a disturbance without adapted pioneer species, tolerant to limiting factors during initial succession and hence important facilitators of vegetation dynamics.

On the other hand, diversity in structure and pattern in later successional stages is determined by dispersal strategies, landscape context (*Rubus*-invasion) and biotic interactions. Experimental disturbance (turfing) of late successional stages lead to accelerated development of species with high vegetatitive regrowth (e.g., *Agropyron repens, Solidago gigantea*). Germation from available seedbank, especially of species of proceeding succession (e.g., dominant *Urtica dioica*, see inlet fig above), was greatly suppressed.

Mesofauna

Soil mesofauna has been investigated on group and species level (Acari: Gamasina) over the depth of 12 cm. For routine reasons, sampling design was changed in 1994 from campaigns every three months to one in October with two-fold sample size. The effect is drastic at first sight, both on species numbers and on abundances; however, it must be evaluated in further detail, which is possible because of a three years period with both sampling regimes in parallel. The results are of great importance for monitoring in general.


Gamasina: abundances (ind. in tsd./m²)


Gamasina: species number

For all investigated mesofauna groups pioneer maxima are documented which have been described before for early stages of zootic successions (e.g. by Meijer, 1989; Pionieroptimum, Dunger, 1991; Ettema & Bongers, 1993). These may be explained by a timely limited easy availability of nutrients. In the initial phase with sparse vegetation cover, high amplitudes of climatic factors break-up organic material and minerals (Vitousek & Walker, 1987).

In contrast to the decrease of underground floristic diversity, species numbers of soil dwelling predatory mites increase over 14 years. In total, 82 spp. have been found (68 on SUC, 64 on REC) with 50 common to both sites. Early, intermediate and late species complexes were identified. Over the first decade, the similarity between SUC and REC does not increase. Preliminary evaluations with correspondence analysis even suggest a diversification with time.

Implications for management

With increasing human pressure on the landscape, successional sites with their specific biodiversity become more and more restricted. Disturbance management could combine demands from the society and protection of biodiversity. The results, which will be evaluated in much more detail in the remaining period of the project highlight the consideration of underground floristics and soil fauna to complement above-ground developments. Based on results from our integrated long-term study, biotic processes as well as various temporal and spatial scales can be included in management models, which may be extrapolated to other systems than ours.

Outlook

The expertise gained in this project will be incorporated in suggestions for restoration management. Future research and application is intended in the development of restoration approaches for undeveloped or degraded soil (ReviTec®; Kesel et al. 1999), such as open-cast mining, intensive agriculture, urban green, Mediterranean landscapes and savannah. Additionally to synergistics within BIOLOG-Europe, links to BIOLOG-Africa are aspired.

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1.4.2001 – 31.12.2003

ECOLOGY AND BIODIVERSITY OF HIGHER FUNGI IN CENTRAL EUROPE (GERMANY)

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Key words: database, PILZOEK, fungi, Basidiomycetes, Hymenomycetes, Germany, Rhön, biosphere reservation, biodiversity, ecological parameters, chorology, mycoflora

Abstract: *Studies on fungal diversity in regard to ecological and chorological parameters are carried out in the biosphere reservation Rhön and by the aid of the database PILZOEK in general.*

Results:

The database PILZOEK has been developed in order to collect and to compute data connected with fungi. It is possible to establish lists of fungi in association with various other data like different nutritional behaviour, substrates, habitats, soil characters, geology, microclimate, chorological features, grid square frequency, red list status, occurrence in different areas defined by their geological and geomorphological background ("Naturraum"; landscape natural unit) and presence or absence in the different federal states of Germany. Information from the database can be drawn in whatever combination. The database PILZOEK has been checked for its capability to store and to recall data from literature and the field as well. Nearly 1000 different sets of data have been established so far. The reference list of the database is available via
www.biologie.uni-regensburg.de/Botanik/Bresinsky/Pilzoek_homepage.html

According to present calculation the 4185 species within Basidiomycetes occurring in Germany contribute to the different trophic groups as follows: parasites (19%), saprotrophes (48%) and symbionts (33%). Among the latter most of the species are involved in ectomycorrhizal interrelationships between various trees and fungi. In case of the Ascomycetes - the other main group within the Mycobionta - lack of knowledge about the presence of species in Central Europe does not allow to present even tentative calculations about species diversity in different trophic groups. Even in our country which is thought to be explored intensively, there is a considerable lack of knowledge regarding species diversity. This is an obstacle since fungi are important members of the different ecosystems for instance as decomposers of wood and litter, as parasites on trees, herbals, mosses, other fungi and animals and last but not least as symbionts interacting with higher plants, microorganisms and animals.

The project being here in focus aims to contribute data to a "Mycoflora Germaniae Program (MGP)" with special emphasis on ecological and chorological data linked with Basidiomycetes (Hymenomycetes s. l.). The genus Hygrocybe will be treated in a pilot study in the context of MGP and of the here discussed project. The expected approach in case of Hygrocybe and other fungi is based on the evaluation of widespread publications in various journals (partly also in books) and on a field work project in the biosphere reservation Rhön as well. Amazingly enough, the Rhön has been neglected by mycologists to a considerable extent so far.

Regarding field work in the Rhön, carried out by L. Krieglsteiner, 69 daily excursions have been undertaken with a total crop of 1881 observed fungal species, being collected, determined and in case of interest dried as herbarium specimens: Basidiomycetes (1128 species; i.e. Boletales 49, Agaricales 662, Russulales 101, "Aphyllophorales" 284, Heterobasidiomycetes 109, "Gasteromycetes" 23), Ascomycetes (336; i.e. Pezizales 79, Leotiales and other groups 257), mitosporic and lower fungi (53), Myxomycetes (81). Quite a number of those species are to be regarded as the first records for the Rhön, others for one of the three federal states (Bayern, Hessen, Thüringen) covered partially by the Rhön. Each of the fungal species has been recorded together with ecological data at the place of fructification, i.e. substrate (including host species), vegetation (if possible identified as plant associations) and other habitat characters, soil type, including acidity and nitrification.

Fungi could be observed in about 70 different types of vegetation, 45 of them being identified as plant associations. Some of the latter apparently never have been examined for the presence of fungi so far, like for example in case of Betuletum carpaticae, Caricetum appropinquatae, Caricetum paniculatae, Caricetum rostratae, Chaerophylletum temuli, Epilobietum angustifolii, Geranio-Trisetetum and others. The fungal components of the different habitats will be evaluated in respect to various parameters, for example share of endangered species in different trophic groups etc.

The observations in the Rhön will also be evaluated comparatively to the adjacent landscape natural unit "Mainfränkische Platten", treated in the doctoral thesis of L. Krieglsteiner.

More then 16% of the species (i.e. rare species, species with concentration in montaneous regions, on acid soils, or sensitive to fungicides) observed in the Rhön have not been found in Mainfränkische Platten with a total of 2600 observed fungal species. An example for fungi being sensitive to fungicides, occurring in the Rhön, however missing in Mainfränkische Platten, are some of the smut fungi (6 of a total number of 13 species) like *Microbotryum marginale* and *M. pustulatum*, both on *Polygonum bistorta* as their host.

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Project ID: 01LC0010
1.1.2001-31.12.2003

CONDITIONS OF A RATIONAL BIODIVERSITY POLICY FOR GERMANY, AS A PART OF THE EUROPEAN UNION

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Key words: biodiversity policy, cost-benefit analysis, conservation, opportunity costs

Abstract:

The aim of the project is to determine the requirements of a rational biodiversity policy for Germany and its institutional framework within the European Union (EU). Methods for the evaluation of cost and benefits associated with biodiversity conservation activities will be analysed. Furthermore, instruments for an implementation of a biodiversity policy based on rationality and efficiency will be developed.

Results:

The global biodiversity loss is mainly an outcome of the human use of the biosphere. Exploitation of natural resources results in social welfare benefits. However, costs associated with biodiversity loss are widely ignored in cost-benefit analysis evaluating human activities.

From an economic perspective, biodiversity is characterized by attributes (lacking property rights, public good) constituting a market failure. Therefore, decentralised decisions by autonomous agents, which are typical for markets, will not provide a solution to the biodiversity decline, instead governmental intervention is required. The aim of our project is to determine the requirements of such a rational biodiversity policy and its institutional framework. It is crucial to identify the aims of such policies in order to use rationality as a criterion for evaluating alternative policies. Therefore, the determination of biodiversity functions influencing human well-being is a prerequisite.

In a first step, we are trying to identify biodiversity measures, which could be used as a basis for the evaluation of cost and benefits associated with biodiversity conservation activities.

Therefore a preceding task is to explore latest theoretical approaches on measuring diversity in general (1,2,3). After having outlined aspects about its essential theoretical characters we will be able to examine critically if some properties might be helpful in delimiting appropriate measures of biodiversity. In this context an important and interesting objective is to find out how far biodiversity can be a matter of calculus and where subjective valuations become inevitable. To a certain point biodiversity policy is always based on normative decisions. The question is to define the limits of such a normative approach in order to establish the starting point for rational decisions in the context of real word policies. Another topic of interest is the spatial distribution of biodiversity (regional, national) and its potential for specialization and allocation of conservation efforts between regions and nations within the borders of the European Union. After the identification of relationships between social welfare and biodiversity and establishing the relevant policy goals, the appropriate instruments to achieve these goals in an economically efficient way have to be chosen. Standard methods in economic theory will be used to assess the applicability of the chosen instruments.

Based on the characterisation of a rational national biodiversity policy, also international aspects have to be considered. The European Union assumed already many tasks related to biodiversity conservation. However, we have to examine if this centralisation is in accordance with our proposed rational biodiversity policy. Another area of research will be the eastern extension of the EU. This extension provides a variety of perspectives and opportunities for a pan-European biodiversity strategy. The efficient use of these opportunities and the required institutional condition are of major importance. In addition, there is still the necessity to negotiate biodiversity conservation issues with non-EU countries. Analysing the available instruments to create self-enforcing treaties will be another point of interest.

Preliminary analyses of strategies for the identification of priority areas for the conservation of biodiversity revealed the "complementarity approach" (4,5) as the most promising. In this process areas are ranked according their complementarity value, that is the degree to which a single area or subset of areas represents the total number off biodiversity attributes found in the evaluated system, or adds unrepresented attributes to already selected areas. Comparisons between the implementation of the Habitat Directive of the EU and the complementarity approach in identifying the most efficient network of areas for protection and specific management are in progress. The analysis will focus on social-economic factors and their incorporation as opportunity costs in conservation planning methods.

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Project ID: 01LC0012 (Subproject 1)
01.10.2000 – 30.09.2003

EVOLUTIONARY CONSEQUENCES OF BIOLOGICAL INVASIONS – INTROGRESSIVE HYBRIDIZATION BETWEEN INVASIVE AND NATIVE *RORIPPA* SPECIES (BRASSICACEAE).

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Key words: AFLP, chloroplast DNA, evolution, introgression, invasive species

Abstract:

The aim of the project is to assess the evolutionary consequences of interspecific gene flow between invasive and native plant species using the Brassicaceae as a model system. First results of molecular analyses (cp DNA, AFLP) provide evidence for the spread of molecular markers of an invasive species (Rorippa austriaca) via native species (R. sylvestris) and the evolution of a new invasive taxon (R. ×armoracioides) via hybridization. Such ongoing processes may even be reinforced in the future when global warming and further habitat destruction favour the invasion of R. austriaca and other invasive species into northern parts of Central Europe.

Results:

Since several decades *Rorippa austriaca* is extending its range from southeastern Europe into Central Europe. Clonal growth provides the capacity to compete with indigenous *Rorippa* species. Hybridization is common in *Rorippa* (Bleeker & Hurka 2001) and can be expected along the invasive and native species contact zones since several hybrids between *R. austriaca*, *R. sylvestris*, and *R. amphibia* have been reported. One of these hybrids, *R. ×armoracioides* (putative hybrid *R. austriaca* × *R. sylvestris*) is itself invasive in man-made habitats in northern Germany and adjacent regions (Bleeker, in press). The aims of the project are to study invasion dynamics of *R. austriaca*, to localize contact zones between *R. austriaca* and native *Rorippa* species, to analyse interspecific gene flow using molecular markers, and to assess the evolutionary consequences

Several native *R. austriaca* populations in the Tchech Republic, Hungary, and eastern Austria and invasive *R. austriaca* populations in Germany have been visited in 2001. In southeastern Europe *R. austriaca* occurs in flood-plain meadows and at ruderal sites. Invasive *R. austriaca* populations in Germany were predominantly found along disturbed river banks and in urban and industrial sites. Contact zones between the invasive *R. austriaca* and the native *R. sylvestris* were detected along disturbed river banks of the rivers Ruhr and Main. The morphologically intermediate *R. ×armoracioides* was found at several locations either with or without its putative parent species, *R. austriaca* and *R. sylvestris*.

Maternally inherited chloroplast DNA (*trn*L intron) and biparentally inhereted AFLP markers (amplified fragment length polymorphism) were used to analyse interspecific gene flow between the invasive *R. austriaca* and native *Rorippa* species. First results provide substantial evidence for hybridization and introgression between *R. austriaca* and *R. sylvestris.* Analyses of noncoding chloroplast DNA (*trn*L intron, *trn*L/F spacer) showed that the *trn*L intron of *R.austriaca* is characterized by a deletion of 169 bp in length. (Bleeker et al., accepted). *R.austriaca* shows a *trn*L intron length variant of approximately 420 bp, the native species *R. amphibia*, *R. sylvestris*, and *R. palustris* are characterized by a *trn*L intron length variant of

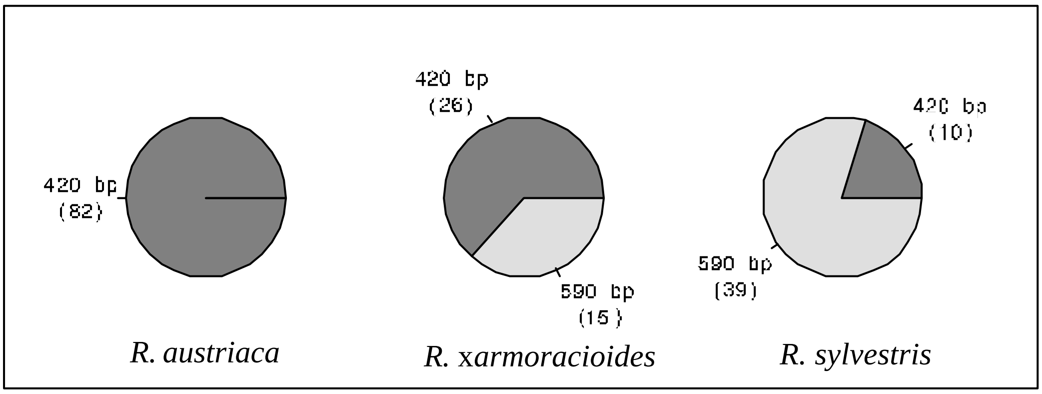

Fig. 1: Distribution of two *trn*L intron length variants in the invasive *R. austriaca*, *R.* ×*armoracioides*, and *R. sylvestris* from contact zones with *R. austriaca* (from Hurka et al, in press).

590 bp. The 420 bp length variant typical for *R. austriaca* was found in ten indivíduals of *R. sylvestris* which were collected in contact zones between both species indicating hybridization and introgression of the *R. austriaca* chloroplast into *R. sylvestris* (Fig. 1). The morphologically intermediate *R.* ×*armoracioides* showed either the chloroplast character of *R. austriaca* (26 individuals) or the character of the native species (16 individuals, Fig. 1).

AFLP analysis provided further evidence for introgressive hybridization between the invasive *R. austriaca* and the native *R. sylvestris* and the spread of *R. austriaca* characters via the hybrid *R.* ×*armoracioides*. Hybrid zones were localized at the river Ruhr near Mülheim and at the river Main near Würzburg. 102 individuals were analysed so far. We were able to identify several species specific AFLP markers of *R. austriaca* and *R. sylvestris*. In an invasive *R. austriaca* population at the river Ruhr, three hybrids could be detected showing an additive banding pattern of diagnostic *R. austriaca* and *R. sylvestris* markers (Tab. 1).

Tab. 1: Distribution of selected diagnostic *R. austriaca* and *R. sylvestris* AFLP markers in three hybrids collected in an invasive *R. austriaca* population near Mülheim.

Primer combination / Fragment length	***R. austriaca*** invasive	hybrid 1	hybrid 2	hybrid 3	***R. sylvestris*** native
Mse I-CTA / Eco RI-AAC					
52 bp	-	+	+	+	+
54 bp	-	+	+	+	+
56 bp	+	+	+	+	-
99 bp	-	+	+	+	+
103 bp	+	+	+	+	-
110 bp	-	+	+	+	+
112 bp	+	-	-	-	-
117 bp	-	+	+	+	+
137 bp	-	+	+	+	+
194 bp	-	+	+	+	+
236 bp	-	+	+	+	+
269 bp	+	+	+	+	-

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Project ID: 01LC0012 (Subproject 2)
01.10.2000 – 30.09.2003

EVOLUTIONARY CONSEQUENCES OF BIOLOGICAL INVASIONS – ONGOING HYBRIDIZATION PROCESSES BETWEEN CARDAMINE TAXA AT THE URNERBODEN, CENTRAL SWITZERLAND

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Key words: AFLP fingerprinting, evolution, introgression, invasive species, vegetational records

Abstract:

The aim of the project is to assess the evolutionary consequences of interspecific geneflow between invasive and native species using the Brassicaceae as a model system.
Natural hybrids between Cardamine rivularis *auct. non Schur ($2n = 2x = 16$; genome RR)* and C. amara *L. ($2n = 2x = 16$; genome AA) were discovered in 1971 at the Urnerboden in Switzerland (Urbanska et al. 1997). The triploid hybrid* C.x insueta *Urbanska forms vigorous populations in man-made, fertilised hay meadows which were created early in the 20th century. This hybrid species by polyploidisation gave rise to the the hexaploid* C. schulzii *Urbanska (genome constitution RRRRAA) which also occupies only man-made habitats (drainage ditches), and its origin may not be older than 50 - 70 years when farmers began to drain land. Molecular studies carried out in our group (cp- and nrDNA, isozymes, RAPD) confirmed the hybridisation event and established the precise parentage of* C.x insueta *(Neuffer & Jahncke 1997, Urbanska et al. 1997, Franzke & Mummenhoff 1999). We have evidence for multiple origin, introgressive hybridisation and recurrent formation. In 1994, the lowland species* C. pratensis *L. s .str. ($2n = 4x = 30$) was first observed at the Urnerboden and since then began to spread. The invasion of* C. pratensis *into the Urnerboden has already led to the formation of contact zones with the native species. This might have direct or indirect evolutionary consequences. A new natural experiment in evolution has started at the Urnerboden and offers the rare opportunity for long term monitoring of the evolutionary impact of an invading species along altitudinal belts.*

Results:

Distribution of *Cardamine pratensis* and contact zones between *C. pratensis* and the indigenous *Cardamine* taxa have been carefully mapped, and permanent plots for long term monitoring have been established. The plots enclose different species compositons with regard to the *Cardamine* species (Tab. 1). In each plot, the actual vegetation has been

Tab. 1: Field observations and sample numbers at Urnerboden, Central Switzerland, during the vegetation period 2001. Ca = *Cardamine amara,* Cr = *C. rivularis*, Cp = *C. pratensis*, Cs = *C. schulzii*, Ci = *C.* x *insueta*; n = number of individuals; veg. survey = vegetational survey following Braun-Blanquet.

permanent plots	1a	1b	1c	1d	1e	2a	2b	2c	3a
species	Ca/Cp	Ca/Cp	Ca/Cp	Ca/Cr	Ca/Cr/Cs	Ci/Cr	Cr/Ci/Cs	Ca/Ci	Cp
n (silica gel)	15/15	17/17	16/17	17/16	39/2/28	17/17	11/11/11	16/16	10
n (cytology)	5/5	5/5	5/5	5/5	5/5/5	5/5	5/5/5	5/5	5
n (seeds)	3/1	0/0	1/11	2/2	1/2/5	8/8	1/5/2	5/8	3
n (living plants)	2/2	2/0	0/0	0/0	2/0/2	3/0/0	0/3/3	0/0	2
veg. survey	yes	yes	yes	yes	yes	yes	yes	yes	yes

analysed by the method of Braun-Blanquet.

Samples from individual *Cardamine* plants within -and in addition also outside - the plots have been collected for several purposes: for cytological studies, for AFLP fingerprinting and DNA sequencing, and seeds for fitness studies.

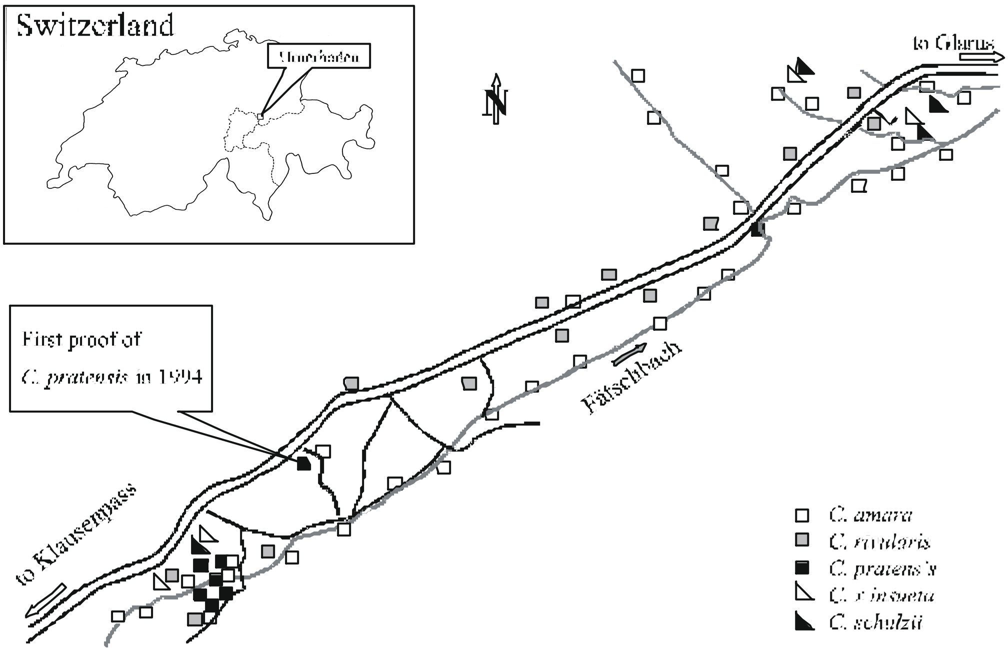

Fig. 1: Distribution of the invasive *Cardamine pratensis* and the „indigenous“ *Cardamine* species at Urnerboden in 2001.

AFLP technique has been optimised for *Cardamine*. In a first experiment, we compared the AFLP banding patterns of living material, silica dried material, and herbarium material. It turned out that silica dried leaves revealed high quality banding patterns comparable with the results of fresh material. This is an important result which makes sampling a lot easier.

In another set of experiments we searched for intra- and interspecific variation in the AFLP patterns. Knowledge of the genetic variation is a prerequisite for analysing the evolutionary processes at the Urnerboden. Summarising the results, we now know (1) that all species involved in the evolutionary scenario at the Urnerboden display species-specific AFLP bands, (2) that hybridisation and introgression can be detected, (3) that geographic variation within species is obvious allowing to analyse colonisation events. Hybrid nature of *C.*x *insueta* and *C. schulzii* was verified by AFLP as with other molecular markers before, and analyses of *C. pratensis* contact zones are in progress.

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Project ID: 01LC0013
1.1.2000 – 31.12.2003

BIODIVERSITY AND ECOSYSTEM FUNCTION IN GRASSLANDS - THE EFFECTS OF INSECT HERBIVORY AND DROUGHT STRESS

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Key words: Biodiversity, Ecosystem function, Nutrient cycling, Grassland, Experiment

Abstract:

This project is a collaborative research effort of the Friedrich-Schiller-University and the Max-Planck-Institute for Biogeochemistry, both in Jena, and the Bureau for Ecological Studies in Bayreuth/Erfurt. Using grasslands in Thuringia, Germany, as model ecosystems, the project is designed to investigate the relationship between genetic/phenotypic diversity and ecosystem processes such as carbon and nitrogen fluxes. Seven research groups in the areas of plant physiology, biogeochemistry, entomology, mathematical modelling, plant taxonomy, mycorrhizal biology, and landscape modelling will use empirical and theoretical approaches to investigate the importance of biodiversity for the stability and functioning of ecosystems. Characteristic for this research network will be a close cooperation between the various research groups for example by using the same sites for empirical investigations.

Results:

In the past decades, it has been increasingly realised that species are disappering from our planet at an unprecedented rate. This extinction crisis has raised the question how the loss in biological diversity affects the functioning of ecosystems. First experimental studies in the past years have shown that a loss in biodiversity will have negative consequences for ecosystem function. For example, a number of studies have shown that decreasing the number of plant species in a grassland will decrease biomass production and will adversely affect other processes in the ecosystem. These studies have also made clear, however, that a general understanding of the relationship between biodiversity and ecosystem processes can only be gained if research programs include both various groups of organisms (e.g. animals, plants, microbes) and different levels of organisation (e.g. leaf, ecosystem, landscape) (Fig. 1, left). The present research network with its six subprojects therefore uses an interdisciplinary approach to address current scientific questions. Grasslands in Thuringia, Germany, will serve as model ecosystems and all research groups will focus their activities on the same set of natural and manipulated grasslands.

In an experimental approach (simulation of a disturbance) the project aims to unravel causal relationships between the genetic and phenotypic diversity and ecological processes in grasslands (Fig 1, middle). The project will be the first to investigate the importance of insect herbivory for ecosystem processes in stressed vs. unstressed ecosystems. In an exemplary manner, various biological disciplines will work together to quantify both various aspects of biological diversity (subprojects MYKO, ENTO, GENMOD, STOFF) and important ecological processes (subprojects PHOTO, GENMOD, STOFF), using modern technology. In addition, the results obtained will be implemented in a spatial model that will find application in landscape planning procedures (subproject RAUM, Fig. 1, right).

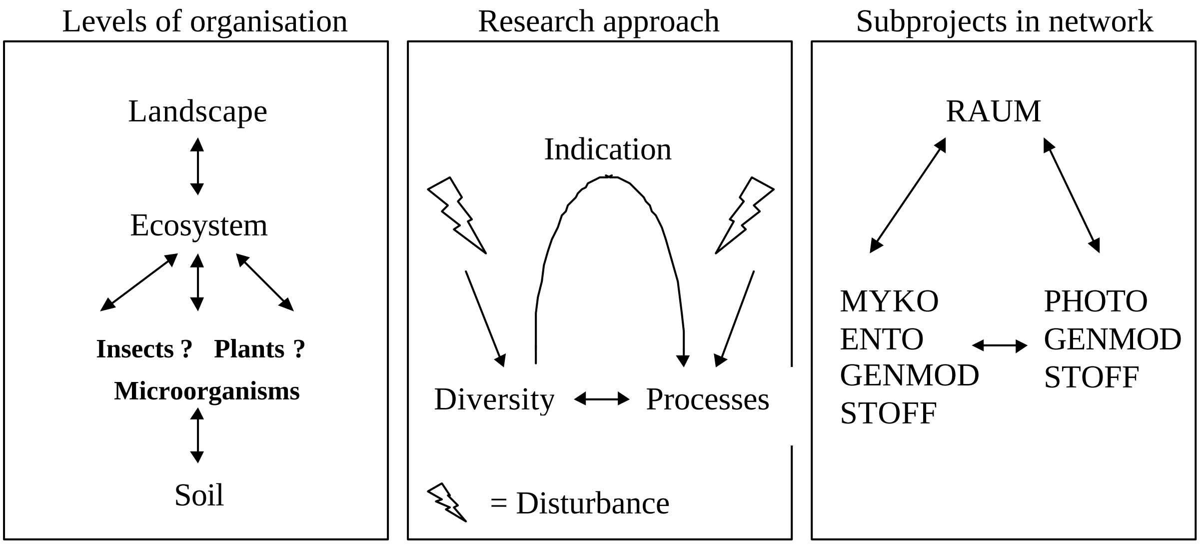
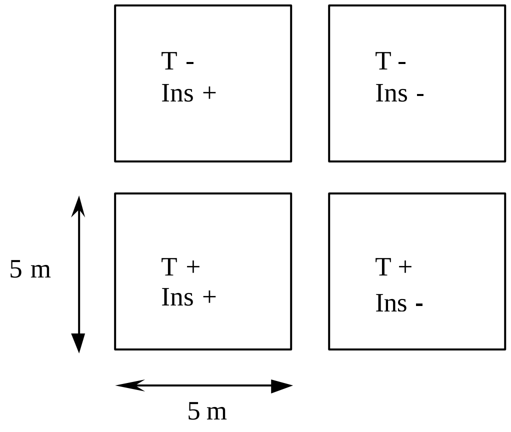


Fig. 1: Schematic view of research approach and links between subprojects in network

In the first year (2001) of the study, ca. 80 different grasslands in Thuringia at a range of plant species diversity will be visited in a collaborative effort of subprojects ENTO, GENMOD, STOFF and RAUM. The biodiversity of these grasslands will be charakterised, in particular plant species richness and abundance, vegetation structure and insect diversity. In addition, a number of parameters that characterise ecosystem processes both above- and below ground (C- and N-cycling, temperature, humidity), the ecophysiology of dominant plant species (e.g. N- and C-use, leaf water potential) and the field sites (exposition, land use etc.) will be measured. The results of the study will reveal first insights into the relationship between biodiversity and ecosystem function. The results will be implemented in a spatial model (RAUM). Further activities in the first year are the development of suitable methodology to investigate the genetic diversity of selected plant species in grasslands, and the development of a first mathematical model on the relationship between biodiversity and ecosystem function (GENMOD).

In the second and third year (2002 and 2003), results from the first year will be used to select grasslands at different levels of diversity in which experimental manipulations will be carried out. In each of 20 blocks, the following manipulation will be carried out:

T-	Water regime unchanged
T+	Simulated drought
Ins+	Insect herbivory unchanged
Ins-	Insect herbivory reduced



In plots with where drought stress is applied, mobile roofs will be placed over the grassland for a short while in spring. In plots with reduced insect herbivory, insecticides will be applied repeatedly. All subprojects will collaborate in measuring ecosystem processes in all experimental plots.

Project ID: 01LC0013 (Subproject STOFF)
1.1.2001 – 31.12.2003

THE CARBON AND NITROGEN CYCLES IN GRASSLAND ECOSYSTEMS OF DIFFERENT DIVERSITIES

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Key Words: biodiversity, ecosystem function, pools, fluxes, C, N, nutrients

Abstract:

The subproject STOFF investigates the influence of biodiversity on bio-geochemical ecosystem functions in well-established, managed grasslands, with particular emphasis on the effect of plant and insect diversity on carbon and nitrogen pools and fluxes. In the first part of the project, relevant site and ecosystem parameters have been measured at 80 sites in the Thuringian Schiefergebirge to evaluate the relationship between plant diversity and productivity at the regional scale. These data will also serve as criteria for the selection of experimental sites in the second part of the project, when the influence of biodiversity on ecosystem resistance and resiliance will be tested at the local scale. First results show that plant diversity is lowest in grasslands with high and low productivities, whereas grasslands with highest levels of plant diversity show only average productivity.

Results:

Research within the subproject STOFF is conducted at two different spatial scales. During the 1st year, investigations are covering the entire region of the Thuringian Schiefergebirge (regional scale). During the 2nd and 3rd year, app. 20 sites will be selected for an experimental approach (local scale). During the first part of the project (2001), a well defined dataset has been collected, to determine the relationship of biodiversity and ecosystem functioning at the regional scale. Thus, data collection in summer 2001 at all 80 sites focused on the determination of taxonomic and structural plant diversity (e.g., species composition, life forms, LAI, height, etc.) and ecosystem parameters (e.g., carbon and nitrogen pools in the soil and the vegetation, soil pH, soil moisture, nutrient availability in the soil as well as nutrient concentrations of plant tissues of different species). In addition, this large dataset will be used to select the 20 experimental sites for the second part of the project (2002-2003).

In the 2nd and 3rd year, causal relationships between biodiversity and ecosystem function will be determined at our app. 20 sites, focussing on resistance and resiliance of grassland ecosystems with respect to experimental disturbances. By manipulating the water regime and the abundance of insects and invertebrates, we will determine if well-established, managed grasslands with low levels of biodiversity are less resistant and resiliant to disturbances than comparable systems with higher diversity levels.

Since several decades, ecologists have tried to reveal the relationship of biodiversity and ecosystem productivity in order to understand fundamental determinants of biodiversity (Mittelbach, et al., 2001). Species richness is often hypothesized to produce a hump-shaped or uni-modal relationship with productivity (Grime, 1973). Our results from the first part of this sub-project support this hypothesis for managed grasslands. Grasslands with low as well as very high productivities showed low plant diversities, whereas grasslands with intermediate productivity support the highest levels of plant diversity (Fig. 1).

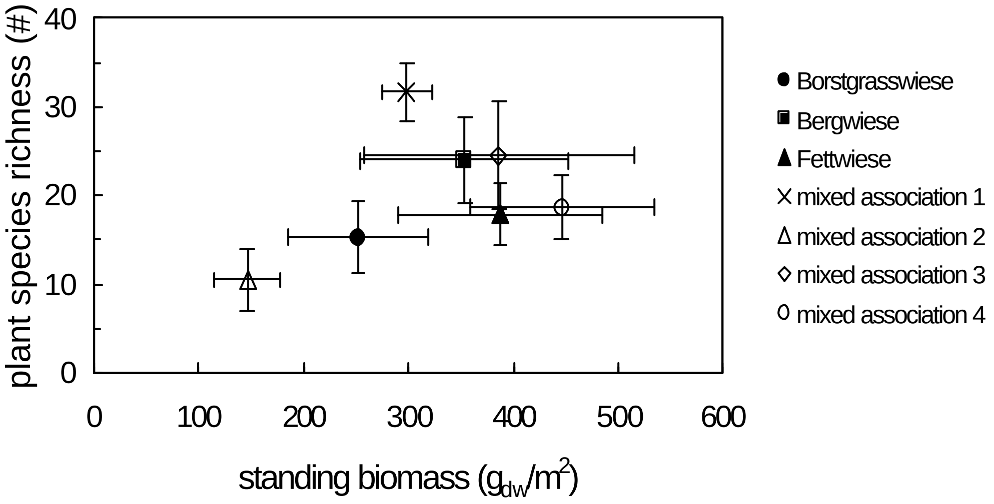

Fig. 1. The relationship of productivity (standing biomass until June) and plant diversity (species richness) shows highest diversity at intermediate productivity. The investigated grasslands were classified in three distinct vegetation types and a number of mixed associations.

Revealing the functional mechanisms of this relationship is the main goal of the on-going data analysis. Our interest focuses on the following questions:

1) Why is there a relationship between diversity and productivity?
2) Why do we observe highest diversity at intermediate productivity?

We expect these analyses to give relevant information on resource use and competition among different plant species present in managed grasslands under natural conditions. If functional groups or individual species identity will dominate this pattern, will be one of the anticipated outcomes.

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Project ID: 01LC0013 (Subproject RAUM)
1.1.2000 – 31.12.2003

A SPATIAL MODEL FOR INDICATING ECOSYSTEM FUNCTIONS

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Key words: Biodiversity, grasslands, indicator system, modelling, geographic information system (GIS)

Abstract:

Based on measurements of the relationship between biotic and abiotic variables and ecosystem function, the subproject RAUM aims at developing a predictive indicator system during 2001 and 2002. By using few and easily measurable variables, the indicator system will allow to predict certain ecosystem processes within grasslands with the help of a Geographical Information Systems (GIS). This model will be validated in the field in cooperation with the other subprojects in 2003. In addition, the subproject RAUM will spatially visualisize the results obtained in the entire research network using (GIS) and analyze vegetation data obtained in 2001. In the first year, 80 sites were studied in close cooperation with the subprojects STOFF, ENTO and GENMOD. First results show that the investigated grasslands can be differenciated into three distinct plant associations. In order to obtain additional information on managemetn history, a questionnaire for the landowners is currently developed.

Results:

Subproject RAUM will utilize the dataset that was collected in first project phase in 2001 for the development of an indicator system (2002), in which taxonomic and structural parameters of plant diversity are used to draw conclusions on ecosystem function in well-established managed grasslands in montane regions of central Germany. This indicator system will allow to predict certain ecosystem processes within these grasslands based on the measurement of easily measurable variables. This model will be validated in the field with the help of GIS by testing its spatial prediction in the second phase of the project (2003). After further development, the model will be made available for applications in landscape modelling and landscape planning. Thus, the subproject RAUM explicitly aims at a knowledge-transfer from science to the applied sector.

In cooperation with the other subprojects a broad dataset was collected in the year 2001 as a basis for the described model. The data collected include taxonomic and structural plant diversity such as the Ellenberg Indicator Values, life forms and plant functional groups, species cover, LAI, height and species composition as well as core ecosystem parameters such as carbon and nitrogen stocks in the soil and vegetation, soil moisture, available nutrients (N, P, Ca, K, Mg, S) and soil acidity. Also, the plant associations of the investigated grasslands were characterized by using species composition and abundance.

First results of the first project phase show that three distinct grassland associations (Borstgraswiese, Bergwiese und Fettwiese) with different ecosystem properties such as standing biomass and species diversity (see subproject STOFF) can be distinguished. Using GIS, we spacially visualized these results in order to obtain an overview of the research area (Fig. 1).

An additional goal of the first project phase is to inquire detailed information on the management history of the 80 investigated sites. For this reason, we have developed an explicite questionnaire for the responsible management agencies and farmers. From this questionnaire, we will obtain information on harvest method and intensity, fertilizer applications, age of the ecosystem and participation in special management and conservation programms. These data will not only be essential for the indicator model, but are also of fundamental interest for the cooperating subprojects and the selection of the 20 core sites for the further experimental manipulations.

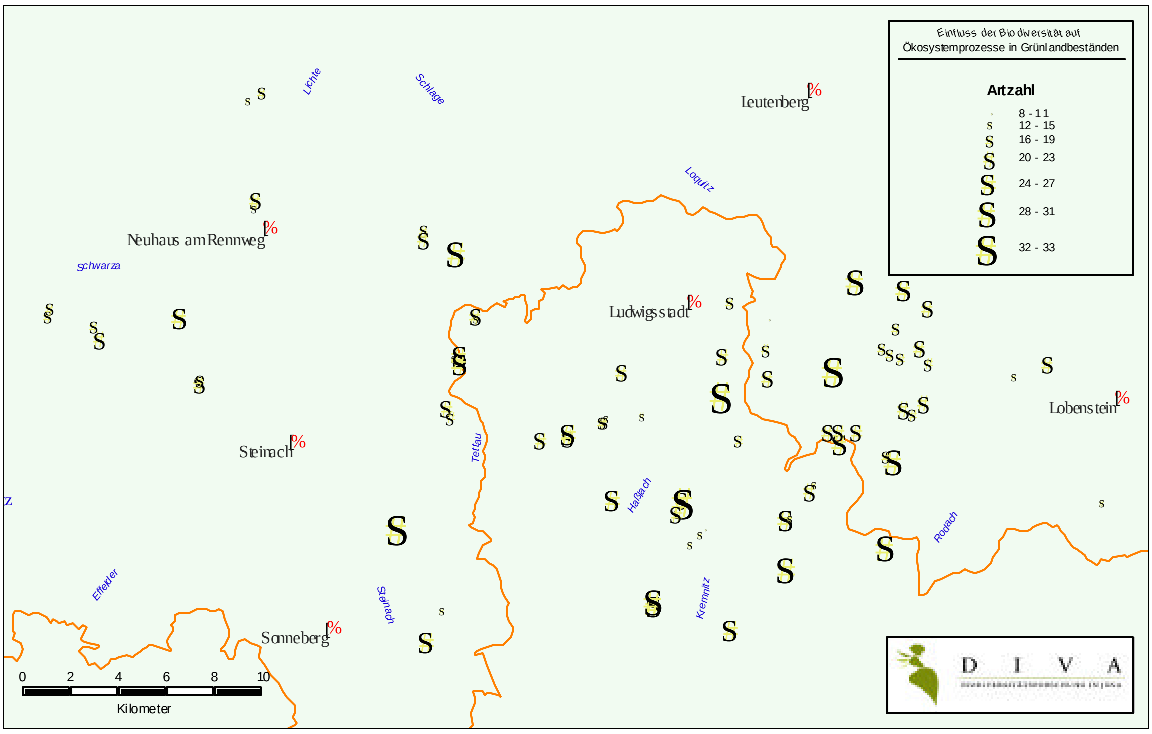

Fig. 1: Location and species richness in the grassland communities visited in 2001 (2 x 2 m-Plots).

Project ID: 01LC0013 (Subproject ENTO)
1.1.2000 – 31.12.2003

THE RELATIONSHIP BETWEEN INSECT HERBIVORIE, PLANT DIVERSITY, INSECT DIVERSITY AND ECOSYSTEM PROCESSES

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Key words: Herbivory, Insects, Ecosystem Function, Insecticide, Experiment, Grassland

Abstract:

Only recently has the significance of insect herbivores for the structure and dynamics of plant communities been recognized. There is some evidence that manipulating plant communities has an effect on insect herbivores, but little research has been performed to demonstrate the effects of insect herbivory on ecosystem processes. The purpose of the ENTO subproject is elucidate the role of above-ground insect herbivory for the structure and dynamics of the plant community. We will investigate the relationships between insect herbivory, plant diversity and ecosystem functioning and stability. Insect herbivore pressure will be removed using insecticides and the effects on natural grassland ecosystems determined. The manipulation of insect herbivory will also help us to determine the role of insects in ecosystem responses to stress (drought). In addition, the dependence of insect diversity on plant diversity will be determined for grasslands of different diversities.

Results:

It is generally accepted that large, plant-eating (herbivorous) vertebrates exert a great influence on vegetation dynamics. The importance of herbivorous insects for the structure and dynamics of natural plant communities has, however, only recently been recognized and investigated. Manipulative studies where insects were removed using biocides have shown that herbivory may not only change the diversity and composition of plant communities but also affect the direction of succession. In addition to trophic effects that arise directly or indirectly from removal of biomass by herbivores, herbivorous insects may also affect ecosystem processes through a number of non-trophic effects. Surprisingly, there have been very few studies on the effects of insect herbivores on ecosystem processes. The most convincing evidence that herbivores affect ecosystem processes comes from direct manipulations of herbivore populations. For terrestrial systems, such experiments have provided some clear demonstrations of significant effects of herbivores on ecosystem processes such as primary productivity and nutrient cycling, but so far they have only been performed with a focus on large mammalian herbivores. In almost all of the recent biodiversity-ecosystem function field experiments, the emphasis was on the manipulation of plant diversity only. Because insect herbivory will depend on plant species diversity, it can be hypothesized that insect herbivory will modify the relationship between plant diversity and ecosystem processes.

While insects affect plant communities, the plant community itself exerts a strong influence on the diversity of the insects associated with the plant community. Virtually all ecological models predict that an increase in resource diversity supports a more diverse array of consumers. Similarly, increased herbivore density is predicted to result in an increased diversity of parasites and predators but there may also be direct effects of plant diversity on parasite and predator diversity as well as changes in the interactions between herbivores and their natural enemies. Thus, it is likely that increasing plant diversity affects the diversity of the whole insect complex, but the relationship can be complicated.

The subproject ENTO has the following goals:

1. To manipulate the presence of herbivorous insects in grassland plots to study the relationships between plant diversity, insect herbivory and ecosystem processes. The manipulation of insect herbivory will also help us to determine the role of insects in ecosystem responses to stress (drought).

2. To assess insect diversity in the experimental plots to investigate the relationship between the compositional structure of the insect complex, plant diversity and plant productivity.

In the first year (2001) of the study, ca. 80 different grasslands in Thuringia at a range of plant species diversity were visited in a collaborative effort of subprojects ENTO, GENMOD, STOFF and RAUM. The task of this subproject is to quantify insect diversity in these plots. Suction samplers in connection with 'biocenometers' were used to obtain standardized samples of the insect fauna. The specimens in the samples will be separated into taxonomic groups. For certain taxa, all individuals will be determined to species level (*Heteroptera*, *Auchenorrhyncha*, certain groups of *Diptera* and *Coleoptera* etc.). The data will allow us to determine the relationship between plant diversity, plant productivity and insect diversity in these grasslands.

In the second and third year (2002 and 2003), results from the first year will be used to select grasslands at different levels of diversity in which experimental manipulations will be carried out. In the herbivore removal plots (see abstract of main project), insecticides will be applied repeatedly. Biomass production and other ecosystem processes will be measured in manipulated and control plots to determine the importance of insect herbivores for ecosystem function. The manipulation of insect herbivory in drought-stressed grasslands will also allow us to determine the role of insect herbivores in the stress response of grasslands. In addition, the insect diversity in the (unsprayed) experimental plots will be assessed to investigate the importance of plant diversity, plant productivity and stress for the insect complex.

Project ID: 01LC0013 (Subproject GENMOD)
1.1.2000 – 31.12.2003

GENETIC AND PHENOTYPIC DIVERSITY AND RESPONSE TO DISTURBANCES IN GRASSLAND SYSTEMS: MODELLING AND EMPIRICAL RESEARCH

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Key words: genetic diversity, phenotypic diversity, grasslands, ecosystem functions, modelling, RAPD-PCR, reproductive success,

Abstract:

The aim of the project is a two-fold one: the development of a mathematical model to cover the relationship between both phenotypic and genetic biodiversity and ecosystem functions and the quantification of genetic diversity of selected species in the field. The model will include multiple trophic levels and different functional types and shall give a conceptual answer how productivity and nutrient cycling are related to the diversity of species. Representative species of our grasslands will be selected to quantify genetic diversity within and between populations by RAPD-PCR.

The modelling part covers the development of an appropriate mathematical model which shall especially include the genetic diversity of the community and the response of the ecosystem to external disturbances, like drought stress or removal of herbivores. The results of the model investigations will give a more general answer how the response of the system depends on its diversity (with respect to functional types) and on the number of trophic levels. A special emphasis is given to the question how the degree of genetic diversity will influence the functioning of the community under disturbances and environmental changes.

The empirical part of the project is focussed on the quantification of the genetic diversity in the field. Typical species, like annual or perennial herbs and grasses of different growth form, will be selected to quantify the genetic diversity by means of a RAPD-PCR. These investigations will be performed over two years to detect possible changes after an experimental manipulation. Moreover, the genetic diversity will also be measured by using quantitative traits of reproductive success, as pollen and seed production and vitality and differences in germination success.

Results:

A basic model structure has been developed to include several functional types of primary producers plus an additional trophic level of herbivores with different food preferences. The model is explicitly based on the uptake of a resource (e.g. nitrogen), different ways of utilisation by the plants and cycling through local and regional pools. It can be shown that the indirect interactions through local resource use can support the coexistence of a certain number of species and, therefore, maintain diversity. Some other results obtained until now show that herbivores may essentially influence the performance of the community (net primary productivity) by their feeding behaviour and spatial mobility.

First attempts have been made to include the genetic structure and its change between generations. Growth throughout the year is modelled in continuous time, but reproduction (and genetic mixing) is a discrete event based on random mating, seed production and creation of vegetation gaps by mortality. Also a spatially explicit model structure has been tested to serve as a starting point for an individual-based modelling approach.

About 14 species have been sampled from the potential sites to check which of them are most suitable to be used for the genetic investigations. The genetic analysis by PCR is just being performed and first results will be available by the end of the year. Based on these preliminary screening and on the species list of the sites selected for our experiments, about five characteristic species will be selected for the detailed genetic analysis in the next two years.

Projekt ID: 01LC0014
1.4.2001 – 31.3.2004

BIODIVERSITY AND ECOSYSTEM FUNCTIONS IN GRASSLAND

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Grassland is an important type of agroecosystem covering about 60 million ha of land in middle Europe. The number of plant species in grassland communities may strongly vary depending on climate and soil conditions. In agricultural grasslands, plant diversity is strongly affected by agricultural measures such as frequency and date of harvest, and fertilization. Recent studies have shown that reduction of plant diversity may decrease the productivity of grassland (Hector et al., 1999). However, up to now there is strong debate on the general validity of diversity effects, and the mechanisms involved in the positive diversity effects found in some experimental studies (Grime, 1997; Kaiser, 2000).

It is the aim of this project to assess biodiversity effects on ecosystem functions in grassland. Biodiversity may be defined as taxonomical diversity, i.e. number of plant species, or functional diversity, i.e. number of functional types. Ecosystem functions include net primary production, accumulation of minerals and carbon in plants and soil, and filtering of water for ground water formation. The importance of taxonomical and functional diversity on these ecosystem functions is investigated in experimental grassland communities established in the field, in large lysimeters, or in small root boxes.

In the field, biodiversity effects are measured in grassland communities that were established in 1996 on 2 x 2 m plots („BIODEPTH" project). On 64 Plots, communities with 1, 2, 4, 8 and 16 species were established. Species were selected from 30 grassland species typical for the area. The plots were weeded from 1996 to 1998 to sustain composition and species number. In 1999, the weeding was stopped to allow succession to occur within the plots. The plots were under harvested twice a year (June and September) and were not fertilized. Emphasis of the investigation within the BIOLOG-Bayreuth project is put on the plots with communities showing similar taxonomical and functional diversity as that in the lysimeters (see below).

In the lysimeters with a surface area of 1.3 x 1.3 m and a depth of 1 m and in the root boxes (0.2 m diameter, 1 m depth) biodiversity effects are measured in grassland communities that were established in 2001. The plant communities are composed of either 2, 4, or 8 different plant species that may be attributed to 4 functional groups: grasses with low growth habitus, grasses with high growth habitus, herbs with low growth habitus and rosettes, herbs with high growth habitus. Legumes were not included. All communities are grown in 5 replicates. In the root boxes, in addition to the plant communities in the lysimeters, also monocultures of all species grown in the lysimeters are cultured.

The effects of biodiversity on ecosystem functions are studied in a research group including the disciplines botany, ecology, and soil science. The project is divided into three subprojects that investigate biodiversity effects on (1) above-ground and (2) below-ground plant characteristics and (3) soil characteristics and water and nutrient fluxes.

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Projekt ID: 01LC0014 (Subproject Vegetation)
1.4.2001 – 31.3.2004

TAXONOMIC, FUNCTIONAL AND STRUCTURAL CHARACTERISTICS OF ABOVE-GROUND PLANT FEATURES AND THEIR INFLUENCE ON ECOSYSTEM FUNCTIONS

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Key words: biodiversity, grassland, productivity, functional diversity, structural diversity, functional attributes

Abstract:

Biodiversity can be examined from different viewpoints. Besides the taxonomical view, structural and functional aspects of biodiversity get more in focus, especially when regarding the relationship between diversity and ecosystem functions.

These different aspects of diversity are the main objective of the subproject. Earlier studies in experimental grasslands have shown, that there is a relationship between the existence of specific functional groups of plants for example for productivity and nitrate leaching in grassland communities. These functional relationships shall be further investigated by dividing plant species into funtional groups and observing their performance within the communities.

Experimental questions and approaches:

How are productivity and biodiversity in grasslands related to each other? Several studies have shown a positive correlation (e.g. Hector et al. 1999). But the debate about this relationship remains controversial (e.g. Huston et al. 2000). For example, there is evidence that the diversity of functional types of plants is more important than taxonomic diversity (Spehn et al. 2001). Most studies have focused on this functional viewpoint only marginally, for functional classifications entail several problems (Beierkuhnlein & Schulte 2000). Within the vegetation-subproject of BIOLOG-Bayreuth, the functional classification of species and individuals and their role shall be examined in depth, using existing data on the species and biometric measurements of individuals in the experiments. The species composition of the lysimeter-experiment was designed according to this aim.

Besides the taxonomic and functional aspect of diversity, also a structural aspect will be addressed. Continuous LAI-measurements in different heights are carried out to look at the structural development of different plant mixtures on the lysimeters and the experimental field plots. Relating these data to biomass production, the role of a higher light use efficiency due to more diverse temporal and spatial development of above-ground plant-organs for productivity will be examined.

Adressing these different aspects of biodiversity it is aimed to evaluate the varying information contents implied with premise to a prediction on ecosystem functions. As perspective, the results of BIOLOG-Bayreuth shall be applied to the landscape scale by identifying the main traits of grassland diversity in central Europe.

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Projekt ID: 01LC0014 (Subproject Roots)
1.4.2001 – 31.3.2004

THE ROLE OF BIODIVERSITY FOR STORAGE OF CARBON AND MINERALS IN ROOTS, AND ACQUISITION OF SOIL RESSOURCES IN GRASSLAND

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Key words: nutrient uptake ability, root diameter, rooting depth, root growth, rhizodeposition

Abstract:

In this subproject the role of roots for biodiversity effects on productivity and cycling of carbon and mineral nutrients in grassland is investigated. The effects of plant diversity on root characteristics that are related to (a) net primary production and mineral accumulation of roots, (b) acquisition of soil resources by living roots, and (c) release of organic carbon and nutrients into the soil by decaying roots are assessed in grassland communities that were experimentally established in the field, or in lysimeters, or in root boxes. It is expected that the results will improve our knowledge about the processes involved in diversity effects on ecosystem functions, and finally may help to develop recommendations of agricultural measures for sustainable grassland management.

Experimental questions and methods:

Is below-ground productivity and mineral nutrient accumulation in roots affected by plant diversity ?

Below-ground productivity is assessed by measuring root growth in a well defined period of time using the ingrowth-core method (Oliveira et al., 2000). The soil cores are sampled twice per year to a depth of 1 m for measurement of biomass and nutrient content of roots.

Is acquisition of soil ressources affected by plant diversity ?

To examine this question morphological root characteristics related to nutrient and water acquisition such as root length and surface area are measured in the roots sampled from ingrowth-cores (see above). Physiological root characteristics related to nutrient and water acquisition are measured in these root samples using ^{15}N (Buljovcic and Engels, 2001), or are indirectly assessed from accumulation of tracers in the shoot. For the assessment of root characteristics related to nutrient acquisition, special emphasis is put on „critical“ time periods where root growth and activity are expected to be low (e.g. after cutting, in spring and autumn), and soil layers where root length density is expected to be suboptimal for complete capture of soil resources (i.e. below the main rooting zone). In the communities growing in root boxes, root growth along a transparent interface with the soil can continuously be measured, allowing assessment of root growth with the high resolution in time that is necessary for the critical periods.

Is carbon and nutrient release from roots to soil affected by plant diversity ?

It is to be expected that in agriculturally used grassland roots are the most important source for carbon and mineral input into the soil. The rate of rhizodeposition is dependent on root longevity that is affected in a species-specific manner by shoot pruning. Root longevity and root turnover are estimated by repeated observations of the same section of the root boxes allowing to estimate the time interval between appearance and disappearance of specific roots from the interface (Smit et al., 2000).

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Projekt ID: 01LC0014 (Subproject Soil)
1.4.2001 – 31.3.2004

THE IMPACT OF PLANT DIVERSITY OF GRASSLANDS ON WATER- AND NUTRIENT-FLUXES IN SOILS AND SOIL ORGANIC MATTER

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Key words: soil water- and nutrient-fluxes, leaching of NO_3 and DOM, characteristics of physical fractions of SOM

Abstract:

Main aims of this subproject are to investigate changes in soil parameters and to measure water- and nutrient-fluxes in BIODEPTH-plots and lysimeters. The soil inventories cover CEC, N_{min}, P_{CAL} and physical soil fractionation with subsequent analysis of the fractions. Soil solution and leachates are collected to evaluate changes in the solution phase and to calculate seepage fluxes of mineral elements and dissolved organic carbon.

Approach:

Does plant diversity affect water- and nutrient-fluxes in soils and soil organic matter characteristics?
It is postulated that increased diversity causes a higher use of soil-born resources which leads to detectable lower concentrations of nutrients in soil solution. Higher use of nutrients results in a decrease of NO_3-leaching to the groundwater (also HECTOR et al, 1999). Furthermore, the higher diversity is supposed to result in an increasing carbon-sequestration of the soil.
Soil parameters such as CEC, N_{min}, P_{CAL}, etc. will be investigated in an initial (autumn 2001) and a final soil inventory in autumn 2003 on BIODEPTH-plots and lysimeters. Special emphasis is given to physical fractionation of SOM (CHRISTENSEN, 2001) and subsequent analysis of the fractions.
The experimental grassland communities (BIODEPTH-plots) will be used to investigate the impacts of plant diversity on soil moisture, potential leaching of NO_3 and dissolved organic matter (DOM). Soil matrix potentials are continuously measured by tensiometers (30 and 50 cm soil depth) and soil solution is collected periodically by ceramic suction cups at 40 cm soil depth.
The main aim of the lysimeter studies is to balance water- and nutrient-fluxes in response to plant diversity. This task is achieved by acquisition of soil solution from 15 cm and 30 cm depth (using suction-cups) and leachates from 100 cm depth.
Solutions are analysed on a monthly basis for mineral elements (K, Mg, Ca, Mn, Fe, Al, Na, NO_3, NH_4, Cl, SO_4, HPO_4, HCO_3) and DOM. The study started in May 2001, the installations were recently finished, thus, results are not available yet.

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Project ID: 01LC0015 (Subproject VEGETATION ECOLOGY)
1.3.2001 – 29.02.2004

DEVELOPMENT OF BIOLOGICAL DIVERSITY IN SALT MEADOWS OF THE 'VORPOMMERSCHE BODDENLANDSCHAFT' – SPATIO-TEMPORAL DYNAMICS AND ECOSYSTEM FUNCTION OF BIODIVERSITY IN BRACKISH GRASSLANDS

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Key words: salt meadows, biodiversity dynamics, ecosystem function, multi-temporal analysis, ecological modelling

Abstract:

The project is part of the interdisciplinary research program "Development of biodiversity of salt meadows in the Vorpommersche Boddenlandschaft", which is carried out by several research groups of the University of Greifswald, the University of Bremen and the Technical University of Berlin. Biodiversity of salt meadows on the German coast of the Baltic Sea is investigated with regard to temporal and spatial dynamics as well as ecosystem function in order to explore quantitative and qualitative dimensions of biodiversity dynamics.

By means of vegetation and phytomass analyses and soil samplings on different study sites abiotic and biotic site factors and biodiversity will be correlated. Local and regional distribution patterns of phytodiversity are assessed and human impact is evaluated. Multi-temporal analyses are applied to detect previous biodiversity dynamics. GIS-integrated modelling is developed to enable predictions of future changes of biodiversity in the salt meadows. Studies of ecosystem function with regard to stability and productivity are based on experiments imitating changes of environmental conditions. Experiments include simulations of sea level change and nutrient decrease. 30 permanent plots comprising the whole variety of salt meadows were established to assess future biodiversity changes.

Results:

1. Spatial Aspects

In the beginning of this project vegetation ecologists and animal ecologists jointly selected nineteen study sites in order to analyse relationships between phytodiversity, zoodiversity and environmental conditions.

In summer 2001, vegetation was analysed at each of the 360 pitfall traps, which were set by the animal ecologists involved. Shannon-index and the Evenness-index were calculated for the vegetation data to characterize α-diversity. Concurrently with the vegetation records, phytomass was harvested within an area of 25 x 25 cm nearby the traps. The dry weight of the phytomass will be used as a measure of productivity of the different study sites. Furthermore, total C, N, P, and degree of salinity will be analysed in order to assess nutrient conditions.

Soil samples were taken at the end of the vegetation period. Examined soil samples will include soil moisture, mineral nitrogen, available phosphorus, C/N-ratio, organic matter, and soil-pH.

According to first results there is a negative correlation between productivity and salinity. Further evaluations are carried out to find relations between site conditions and phytodiversity.

2. Temporal aspects

Temporal changes in species and ecosystem diversity were investigated with multi-temporal analyses using a geographic information system. Research data were acquired from maps of the 17th, 19th and 20th century. The evaluation of a floristic database, which is available at the Department of Botany, shows a distinct decline for the most of the typical salt meadow species after the intensification of land use since 1964. Further data source materials (e.g. aerial and satellite images) were collected for the ongoing analyses.

The design of a model, which enables the development of different kinds of scenarios regarding future biodiversity dynamics (e.g. assuming a sea-level rise), is under development stage.

To ensure and improve data exchange between the different sub-projects of the research program, a database was designed and implementation has started. Furthermore this database serves as the basis for the projected database "Biodiversity Vorpommersche Boddenlandschaft", which is going to put results of the research program at public's disposal.

To assess diversity changes over a longer period, 30 permanent plots were established. Study sites comprise a salinity range from $2\ ^{0}/_{00}$ to $10\ ^{0}/_{00}$ and include natural types as well as embanked sites. Vegetation cover and above-ground phytomass were recorded and soil samples were taken to assess the abiotic / biotic site conditions as a reference for a regular monitoring program.

3. Functional Aspects

In 2001, two of three experiments on the ecosystem function of phytodiversity with regard to stability and productivity have been launched. Both of them focus on the functional role diversity under changing environmental conditions (i.e. sea level change and nutrient decrease).

For the experiments, three different types of species composition growing under comparable site conditions were selected in a 1 ha field-exclosure of a salt meadow 10 km north of Greifswald. Type 1: poor (4 grasses and herbs), type 2: rich (7 grasses and herbs), and type 3: rich with legumes (7 grasses, herbs, and legumes) serve for a comparison of different richness in species as well as in plant functional types.

To simulate rising sea level conditions 20 sods of each type were transplanted 15 cm beneath from their original level, 10 remained as a control and 10 were dug out and re-implanted to assess the mechanical impact of transplantation. Previously, species cover and above-ground phytomass were recorded for each sod.

Moreover, phytomass was measured for 20 sods and 10 controls of each type to detect the influence of nutrient decrease due to reduced N and P import by inundation. A N/P/K-solution will be added in next year´s early summer as a period of three years is to short to achieve a sufficient reduction in nitrogen as the limiting factor of salt meadows by mowing. Thus, the opposite trend will be simulated in order to draw respective conclusions for a nutrient reduction.

By the end of the vegetation period in 2001 the following site parameters are to be recorded for both experiments: soil moisture and bulk density, mineral nitrogen, available phosphorus, soil pH, cation exchange capacity (CEC), base saturation, C/N-ratio, and organic matter. Phytomass will be analysed with regard to the content of water, total N, P, C, and Cl.

The data base of 2001 will serve as a reference for the experimental effects to be recorded over the following two years.

PROJECT ID: 01LC0015 (Subproject LANDSCAPE ECONOMY)
1.3.2001 – 29.2.2004

DEVELOPMENT OF BIOLOGICAL DIVERSITY IN SALT MEADOWS OF THE 'VORPOMMERSCHE BODDENLANDSCHAFT' – ECONOMICAL VALUATION OF BIODIVERSITY

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Key words: Contingent Valuation, Use of salt meadowland, Costs and Benefits of Dyke building

Abstract:

The decline in biodiversity is also a great problem from an economic viewpoint. Therefore economists search for possibilities to preserve biological diversity with economic arguments. Within in the project there will be a calculation of a cost-benefit-analysis for a dyke-removing project at the German Baltic Sea coast. This includes a contingent valuation for the existence value of rare species and the costs of different use systems of salt meadowland were developed.

Results:

The decline in biodiversity is also a great problem from an economic viewpoint. It is clear that in the future we will depend even more on stable ecosystems with a high biodiversity if todays processes of biodiversity loss continue. Therefore economists search for possibilities to preserve biological diversity also with economic arguments. Economic valuation of costs and benefits of dyke building as an example must introduce not only benefits from use values of an ecosystem changed by a different water regime, also existence values and option values are important. In addition the costs of dyke building and the repair work must be introduced. This is the reason why for most cost-benefit analysis only estimations of the total economic value are possible. Over the last three decades economists developed a lot of different methods of economic valuation of individual preferences for rare species, ecosystems or historic landscapes (for an overview about economic valuation Gronemann und Hampicke 1997).

Within the project as part of the research on salt meadowland we calculate costs and benefits of dyke-removing and combine the results in a cost-benefit-analysis. To compare different situations three study areas were chosen. The Sundische Wiese, as an area where the dyke-removing is planned, the Karrendorfer Wiesen where the removing has been realized a few years ago and the Kooser Wiesen as a typical salt meadowland. The main use system on the meadowland is extensive pasturing with cattle and we estimate that after a dyke-removing 50% of the Sundische Wiese is not usable that way anymore. Also the provender quality will change after the ecosystem will come under the water regime of the Baltic Sea again (Kowatsch et al. 1997). What this means for the user was part of the work in the first year. In addition an overview about the literature with respect to the history of the use systems should give us informations about the possible use alternatives in the future and what might happen after the dyke-removing. All these parts were introduced in a scenario for the Sundische Wiese and will be part of the cost-benefit-analysis at the end.

During the next year we'll prepare the questionnaires for two examinations: On one side we want to know what people around the area think about the dyke-removing (acceptance of this) and on the other side we want to ask tourists about their preferences for rare species after the natural habitats will be restored. Not many contingend valuations deal with existence values and we hope that we can get some useful results here. Most of the species on natural salt meadowlands are not very common and not well known by the people (like orchids). In addition costs of dyke-removing, dyke-building and repair will be analysed over the next two years. After the first project phase (bejond 2004) the economic part will be oriented close to the research program of the other working groups within the project.

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Project ID: 01LC0015 (Subproject ANIMAL ECOLOGY)
1.3.2001 – 29.2.2004

DEVELOPMENT OF BIOLOGICAL DIVERSITY IN SALT MEADOWS OF THE 'VORPOMMERSCHE BODDENLANDSCHAFT' - DYNAMICS IN DIVERSITY OF ANIMAL SPECIES AND COMMUNITIES IN A CHANGING ENVIRONMENT WITH SPECIAL REGARD TO DISPERSAL PROCESSES

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Key words: salt meadows, salt marshes, Vorpommersche Boddenlandschaft, Baltic Sea, pitfall trap, lifestock taking, Carabidae, Saldidae, distribution patterns, area value rating, dispersal, population genetics

Abstract:

Ecological analysis is used to show the significance of the distinctiveness and dynamics of environmental factors which essentially determinate the diversity of animal species, communities and landscape sectors. The focus will be on the impact of human activities, with special regard to climatic changes and the dispersal abilities of animal species.

In close co-operation with the other project partners, recent developments and their influencing factors will be analyzed by molecular techniques, field ecological (and, if necessary, laboratory) methods, as well as a Geographical Information System (GIS).

Based on these results, prognoses (e.g. scenarios) to be used for the recommendation of measures for the maintainance and development of biodiversity with respect to economical relations can be statet. The following questions will be investigated:

- *Which regional dispersion patterns characterize the diversity of species, coenoses and landscape sectors? Are there areas with a high concentration of species that show a high spatial significance?*
- *Are there small-scaled and regional differences in the genetical equipment of populations that might give a hint for the genetical pauperisation due to isolation, or that reflect the range and intensity of dispersal processes?*
- *Which are the abiotic/biotic factors to determine diversity (distinctiveness, dynamics)? How do extreme events, such as inundations due to heavy storms, influence diversity? How important are area size, age and isolation?*
- *Which are the historical and recent impacts of land-use type and intensity (especially agriculture, coastal protection and tourism)?*
- *How does the dispersal ability of animals influence the distinction of biodiversity? Do the hydrodynamics of the Baltic Sea cause a 'hydrochoric network' of populations or coenoses? How far do human activities influence such a network (increasing isolation)?*
- *Which impacts can be expected of the predicted climatic changes? (direct: temperature, precipitation, wind; indirect impacts: sea level rise, rising frequency of inundations due to heavy storms, change of landuse type and intensity).*

- *Are there areas for the emigration of arthropods, which live exclusively in salt- and coastal habitats? Can biodiversity be regenerated/re-established by a retraction of the dike position towards inland (expansion of foreshore areas)?*
- *How can the results be used effectively within an Integrated Coastal Zone Management (databases, GIS, expert or indicator systems, monitoring concepts)?*

In cooperation with the project partners, along the "Vorpommersche Boddenküste" (investigation region) 20 investigation areas were selected with special regard to geographical location, geological development, hemerobiotic degree, soil type and recent agricultural use.

In the first year of study (2001), epigeic arthropods (especially Carabidae and Saldidae) were caught at 65 investigation sites (1 to 9 investigation sites per area) with pitfall traps from the end of March until the beginning of November. The pitfall traps were changed 16 times in 14-days-intervalls and remained outside for at most 224 days. The time consuming sorting of the animals is still in progress. Additionally in 2001, vegetation, biomass, inundation frequency (based on a nivellement; measuring in 14-days-intervalls) as well as several soil parameters are investigated in cooperation with the working group of Prof. Schickhoff.

Parallel, lifestock taking of Carabids in the entire investigation region was started: Nearly 25% of the 800 km coastline have been under survey so far. Much effort had to be done to get fresh material for DNA extraction because of the complex spatial situation. In order to make use of material already fixed, we tested specimens collected in ethylene glycol, the medium used in pitfall traps in order to get species which are rare or not easily to collect.

In Carabid beetles living north of the Alps, species are known without variability in their distribution area, others display variability from population to population. Therefore, we screened core and mitochondrial genes of those species which were collected first from most sites: Carabus clatratus, a species flightless and living on peat ground like coastal salt marshes and meadows with a high content of organic matter.

Results:

First results show partly considerable quantitative and qualitative differences in the Carabid communities between the investigation sites of the saltmarshes. Intensity and frequency of inundation (often regulated by coastal defense management), water salinity and landuse intensity (e.g. vegetation structure and soil compaction) seem to be the key factors for the development of diversity in Carabid coenoses.

In general, isolated populations of *Carabus clatratus* show sequence differences; the highest rate of substitutions was found in ND1 and ND5 (0.2 – 0.5 %), the lowest in the control region, ITS1 and ITS2 (about 0.1 %). Additional data exist for 12S rRNA, CO1, CO2, CO3. The most interesting result is a relatively high genetical difference in two populations (islands Grosser Werder and Hiddensee (Gellen)) that are about 7 km apart.

Although at this stage we are unable to interpret the pattern of variability, this flightless species display a high degree of within species diversity.

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Project ID: 01LC0015 (Subproject SOIL SCIENCE)
1.3.2001-29.2.2004

DEVELOPMENT OF BIOLOGICAL DIVERSITY IN SALT MEADOWS OF THE 'VORPOMMERSCHE BODDENLANDSCHAFT' - WATER AND SALT DYNAMICS OF SALTY MEADOW AND MARSH SOILS

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Key words: biodiversity, global climate change, salt marshes, salt meadows, physical and chemical soil parameters, modelling

Abstract:

Climate scenarios predict a global temperature increase within the next decades. Aim of the project is to gain insight in the future development of the salt meadows of the Vorpommersche Boddenlandschaft, a region of outstanding ecological relevance. Analyses of new collected data on chemical, physical and hydrological soil parameters in this region will supply the basis for a prediction of the soil lifetime dynamics associated with climate, groundwater and land use changes in this region.

The specific study plan of the project includes:

- *Exemplary soil ecological mapping of typical salt meadow areas.*
- *Determination of relevant soil parameters for typical soil profiles.*
- *Characterisation of the water and salt dynamics for two selected sites by means of soil hydrological measurements and numerical model calculations.*
- *Derivation of parameters concerning to soil water and soil salt balance as determined by temperature, humidity, rainfall patterns, sea level height and land use due to predicted climatic shifts.*

Project description and first results:

Targets of the investigations in the first project phase have been the selection of the appropriate study sites and of the suitable measuring probes.

For the purpose of a prolonged surveillance during the project, a transect with 10 experimental plots was set up at the “Kooser Wiesen”. Measurements of soil water contents and soil water quality are performed every 14 days in two soil depths. The soil pore water is subsequently analysed for pH-values, electric conductivity, concentrations of anionic and cationic salts and nutrients. The set-up of an intensive measurement field on the “Kooser Wiesen” is planned for next year. It is designed for measurements with higher analysis resolution in time and space (automatic probes measurements over soil profiles).

The selection of the appropriate water content measuring devices is up to now challenging, since most of the commercially available TDR-probes (time domain reflectometry) do not deliver reliable values at pore water salt contents above 20 mS/cm.

A first attempt to gauge probes coated with epoxy resin seemed promising up to water contents around 40% v/v, but since the peaty soils typical for the investigational sites may reach values of 70% v/v, probably the use of the coated probes will not always be possible.

Next to the set-up of the measuring plots for the continuous data collection, soils of two transects on the “Kooser” and “Karrendorfer” salt meadows have been investigated for important chemical and physical soil parameters. The results of the analyses will supply, along with water tension curves, the bulk densities, water contents, C/N ratio, organic matter contents, salt concentrations, and pH-values of the investigated soils.

Future investigations will focus additionally on soil mapping of typical vegetation units of the salt meadows and a subsequently soil ecological state assessment.

Modelling of the dynamic development of the soil water parameters under changing site conditions (salt contents, climate constraints, groundwater supply and land use pressure) shall help to answer the following questions:

1) Which consequences will arise from the current climate change scenarios in respect to the site parameters of the ecologically relevant salt meadows?
2) How will the so-called ecological soil moisture parameter develop and how will the length of the current dry and moist periods change in future, taking the different site characteristics into account?
3) How will the salt meadows develop, considering particularly the scenarios predicting recurrent situations of climate extremes (e.g., frequencies of flooding, dry periods)?

Project ID: 01LC0018 (SUBICON Subproject 1)
1.3.2001 – 29.02.2004

SUBICON - SUCCESSIONAL CHANGE AND BIODIVERSITY CONSERVATION IN A RED OAK CHRONOSEQUENCE –
SUCCESSION OF DIVERSITY AND FUNCTION OF ECTOMYCORRHIZAL TYPES IN RED OAK FOREST ECOSYSTEMS

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Key words: Dispersion of ectomycorrhizal types, Primary succession, Competition, Neophytes, Quercus rubra, Mining, Reclamation

Abstract:

The region of Lower Lusatia (Eastern Germany) is characterized by many active and reclaimed lignite mining sites. Of these, 15 % have been reafforested with red oak (Quercus rubra L.). Thus, this introduced tree species is nowadays widespread on the former mining sites. As a pioneer species, red oak is well adapted to extrem soil conditions. Like other oak species, red oak forms ectomycorrhizae with higher fungi (Ascomycetes and Basidiomycetes). In forest stands these mycorrhizae hold a key position for the water and nutrient cycle. The mycobionts are able to mobilize, accumulate and transport water as well as nutrients from different soil substrates and translocate them to the phytobiont.

The mycorrhizae and the extramatrical mycelium are part of the detritus food chain. The litter is intensively colonised by saprophytic and mycorrhizal fungi, bacteria and soil animals like earthworms, enchytraeid worms, nematodes, collemboles, mites and others which deminute and decompose organic components of the soil. Thus, the nutrients are being fixed in organic components which can be taken up very fast by the growing mycelium. The huge diversity of fungal species is based on the fungi`s different functions in mycorrhizal symbiosis. In consequence of the high variety of functional groups the determination of fungal species will be the first part of the investigation. After characterization of the autecological importance of single species, their interactions with other heterotrophic organisms will be estimated.

Questions:

The project will highlight some topics related to function, temporal and spatial dispersion of ectomycorrhizal types. The investigations will answer aspects of the following questions:

- How does primary succession of ectomycorrhizal types work?
- Which changes in successional stages can be observed along the chronosequence?
- Are there differences in the ectomycorrhizal species composition associated to native and neophytic oak species?
- Are there differences in the ectomycorrhizal species composition of mining substrate and undisturbed soils?
- Which ectomycorrhizal fungi are key species for the development of forest ecosystems on mining substrate, and how do these fungi disperse on different scales?
- How important is the role of ectomycorrhizal fungi within the detritus food chain?

Methods:

Our plots are located in former lignite mining sites reclaimed for forestry and planted with red oak. The chosen Quercus rubra stands are forming a chronosequence. To show the differences in mycorrhization between the meliorized mining substrate and naturally grown soils we prepared also a control plot in the neighbourhood of the mining area. To interprete the role of the tree species in community stucture of mycorrhizae, we compare our results from the *Quercus rubra* stands with stands of native Quercus and Pinus species formerly investigated in the same region.

For an analysis of the ectomycorrhizal community we identify the mycorrhizal fungi on three ways. First, we conduct a morphological and anatomical characterization of the mycorrhizae. This makes possible a quantitative analysis of the community composition. In a second step, we use molecular genetic techniques like PCR, RFLP and sequencing of ITS regions.

In using a capillar electrophoresis we try to analyse the content of different nutrient elements in the mycorrhizae. These results, together with the morphological and anatomical features and the autecological data, will give us hints to the function of a specific fungal species in this ecosystem.

First results:

After a preliminary sampling of our investigation sites we could differentiate 14 ectomycorrhizal types by means of anatomical and morphological characterization. Till now, we were able to determine four of these types to species level. Cenococcum geophilum is a well known fungus establishing mycorrhizae with a very broad range of phytobiots. In comparison to other mycorrhizal fungi, this species shows a wider ecological valency. Piloderma croceum and Scleroderma citrinum are also known as euryoecious species. Former investigations in reclaimed mining sites in the same region detected mycorrhizae of these three species as dominant in Scots pine stands. A fourth species was determined as Paxillus involutus which is the dominant species in our samples. All of these four fungi are typical early stage fungi. Thus, they were expected to occur in this sites of primary succession.

Other mycorrhizal fungi which we identified by their fruitbodies were Amanita muscaria, A. citrina, Boletus edulis, B. luridus and several species out of the Russulales.

In comparing natural forst stands with reclaimed mining sites our first samples indicate that root morphology can differ between these different habitats. Nevertheless, these findings have to be confirmed by further samples.

The first place we presented our project was the congress of the German Society of Mycology and Lichenology (GML 20. – 23. 09.01) in Halle, Germany.

Outlook:

First we want to create a sampling design which allows an up/down scaling of the dispersion of ectomycorrhizal types to different scales.

In experiments we want to investigate the influence of mycophagous insects on the establishment of mycorrhizas and the development of mycorrhizal communities under grazing pressure.

Information on ongoing studies is available at www.tu-cottbus.de/roteichen/teilprojekte/tp1/index.htm.

Project ID: 01LC0018 (SUBICON Subproject 2)
1.3.2001 – 29.02.2004

BIODIVERSITY OF PLANT COMMUNITIES AND SELECTED PHYTOPHAGES IN RED OAK DOMINATED ECOSYSTEMS

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Key words: Biodiversity, Brown coal mining areas, Disturbance, Community Function, Heteroptera, Succession, Quercus rubra

Abstract:

The temporal and spatial variation of biodiversity of plant communities and selected phytophagous arthropod communities in red oak dominated ecosystems is described. Species diversity of producers (higher plants and mosses) and first order consumers (phytophagous heteropteran species) are analysed in relation to influences of habitat diversity, disturbance regime, biotic interactions, and genetic diversity. Aim of the project is to give explanations for the generation, establishment, maintenance, and development of biodiversity, which should be confirmed by experimental analyses.

Questions:

In the restoration management of post mining landscapes widespread afforestation with non native red oak (Quercus rubra) took place. The main questions to be answered in the framework of the SUBICON research project are:
What factors determinate the species diversity of red oak dominated ecosystems and adjacent open landscapes?
Which of the various explications of biodiversity (e.g. number of species, Shannon-Wiener-Index, Preston´s gamma in species-abundance relations) are useful to describe biodiversity adequately in order to generate models to explain the maintenance and development of biodiversity?
What about the relations among the biodiversity of different compartments of the communities (producers, first and second order consumers, different sets of species with special ecological functions)?
What about the temporal variation of biodiversity at different spatial scales and which of the general theories on the development of biodiversity in ecosystems can be confirmed as to explanatory and predictive power?

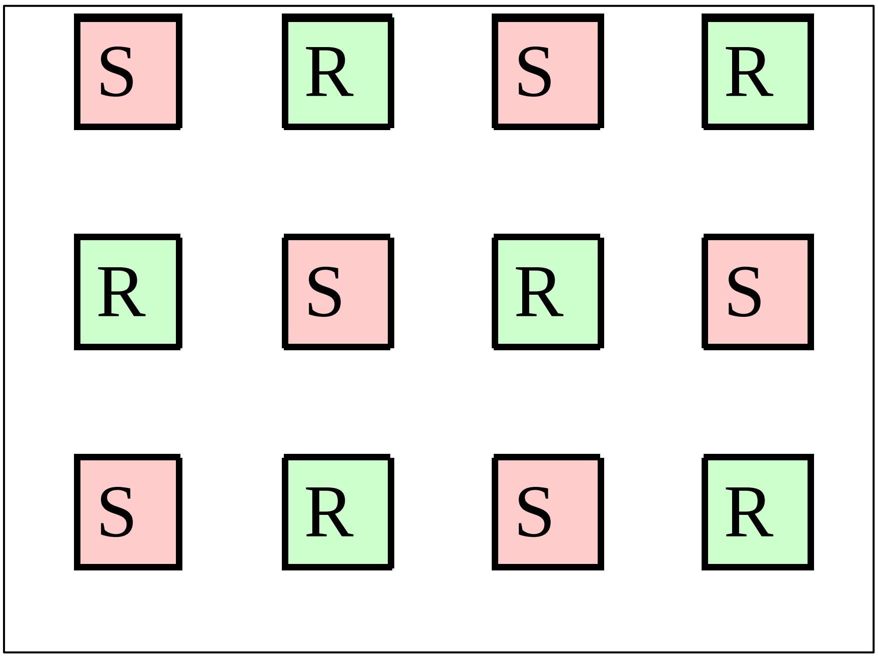
Methods:

The investigations are carried out in four former brown coal mining areas of Lower Lusatia (Eastern Germany) as well as in an undisturbed reference.
The following investigations have already been realized:

- Analyses of vegetation at 112 SUBICON plots in red oak forests as well as in the adjacent open landscape,
- Starting of the experimental approach to recolonization after disturbance.
- Quantitative sweepnet sampling of Heteroptera (30 sites in total, 50 sweeps per 100 qm on each of the sampling sites).
- Heteropteran species sampled by pitfall trapping will be included to analyse biodiversity of different vertical strata.

The influence of soil disturbance on the diversity development of the vegetation in Lusatian post mining areas is analysed by an experimental approach (see figure 1). It is widely accepted that disturbance has a strong influence on biotic communities and their functioning on various spatial scales. In the post-mining landscape of Lusatia an obvious disturbance factor is the wild boar (Sus scrofa) that causes soil disturbances in all vegetation structures by churning up the soil. This kind of disturbance is imitated. The experimental approach is to analyse the mechanisms of colonization of plants and the development of diverse communities.
Three open-cast mines of different ages and three vegetation types (red oak forests, Calamagrostis epigejos stands, psammophytic grassland) are included into the studies, six disturbance and six reference plots per stand are analysed (sum of study plots: N = 108). The following procedure is applied:

- Soil disturbance: Removal of the above-ground vegetation. Digging up of the soil up to a depth of about 12 centimetres;
- Recording of the colonizing individuals;
- Soil seed bank analysis;
- Exposition of seed traps.



(S = disturbance plot, 4 m², R = reference plot, 4 m², Distance between neighboured plots: 2 m)

Fig. 1: Experimental design

The results of the vegetation surveys and the second order consumers studies (TP 4) will be linked in order to generate a general model comprising different functional groups of species.

First Results:

Previous research on open landscape vegetation show that the change of vegetation type is slow. Direct ordination revealed that environmental parameters such as pH, the level of available phosphate and organic carbon as well as the age of the study sites do not significantly account for the variance (Wiegleb & Felinks 2001). For succession in red oak forests no likewise studies are known.

The investigations started in summer 2001. Preliminary results can be presented at this state.

The mean number of plant species in red oak forests of the former coal mining area is 13 (4 - 38 species), in undisturbed red oak forests 17 species (14 – 19 species), respectively, while in Calamagrostis stands 11 species (4 – 17) have been found. In psammophytic grasslands a mean of 9 species (2 – 17) occured.

The number of heteropteran species found on oak trees is low, a very high amount of common species regularly occurring on native oak trees in Brandenburg are missing. This is in contradiction to the sampling results of open landscapes, where species number is high: including results of former studies roughly calculated 30 % of all openland species occuring in Brandenburg established populations at the post mining landscape.

Outlook:

The next steps of the investigations will be:
- Continuing with the data collection,
- Determination of Heteroptera including material collected by pitfall trapping (Tp 4),
- Statistical analyses, modelling,
- Application of the experimental approach,
- Data link between sampling results for different groups of species.

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Project ID: 01LC0018 (SUBICON Subproject 3)
1.3.2001 – 29.02.2004

GENETIC DIVERSITY OF SELECTED PLANTS, PHYTOPHAGES AND ZOOPHAGES IN SUCCESSIONAL RED OAK ECOSYSTEMS

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Key words: Colonization, Genetic diversity, Molecular markers, Population genetics, Quantitative genetics, Succession

Abstract:

The project will analyse genetic diversity of different functional groups (plants, phytophagous bugs, spiders and zoophagous beetles) within a Red Oak chronosequence. Molecular markers will be used to elucidate genetic diversity and population structure as a basis for the understanding of colonization and microevolutionary processes. Genetic diversity within a population and between various populations as well as between different species are analysed in detail and compared to each other.

In plants quantitative genetics of morphological traits will be analysed in order to understand adaptive evolutionary changes due to varying selection regimes (light, competition, nutrients) during the chronosequence.

The results will be used together with those of other subprojects in a comparative analysis of the development of species diversity and genetic diversity through time in a highly disturbed ecosystem. The current state of the project including species selection, site selection, sampling and laboratory progress is reported.

Questions:

The project addresses the following questions:

- *How do different functional groups of plants and animals differ with respect to spatial and temporal population structure?*
- Does colonization take place through continuous immigration or through a single founder population?
- Does genetic diversity change through the course of succession?
- Do molecular markers and quantitative traits differ in their spatial pattern and temporal development?
- Is there microevolutionary change during succession in adaptive traits connected with competition or light regime?

Methods:

The main method of analysis is the Amplified Fragment Length Polymorphisms (AFLP). The AFLP technique is based on the selective PCR amplification of resriction fragments from a total digest of genomic DNA (Vos et al. 1995).

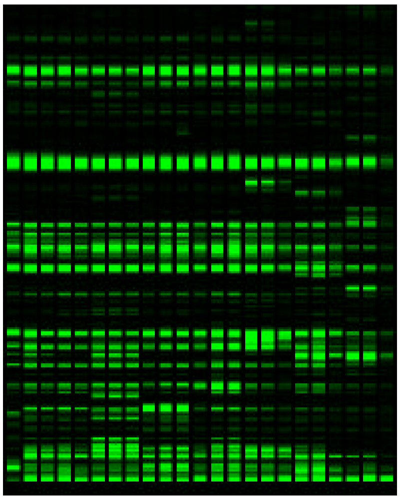

Fig. 1: AFLP (Amplified Fragment Length Polymorphisms) gel image of Rumex acetosella sampled in the Schlabendorf-Süd area.

First results:

Species selection - plants

From a number of potential plant species two species with contrasting ecology and habitat where selected. Whereas a number of species were present either at the beginning or at the end of the chronosequence, only these two were present both early and late in the chronosequence.

(1) Rumex acetosella (Sheep´s Sorrel) a herbaceous pioneer species with low competitive ability, present in 13 sites.

(2) Calamagrostis epigejos (Wood Small-reed) a generalistic stress-tolerant grass, present in 18 sites.

Species selection – animals

Arthropods of different functional groups were selected, namely the phytophagous true bug Stenodema laevigata, the spider Alopecosa fabrilis and the zoophagous ground beetle Calathus ambiguus.

The sampling both for the molecular and the quantitative genetics analyses was undertaken from July to September 2001. For molecular analyses of plants a total of 444 samples from 16 (R. acetosella) and 21 (C. epigejos) sites has been taken. For quantitative genetics 1398 plants from 16 (R. acetosella) and 21 (C. epigejos) sites are being cultivated and cloned vegetatively for experiments to be performed in 2002 and 2003.

Of the target animal species 97 spiders, 173 true bugs and 366 ground beetles in 5 sites were collected for molecular analyses. Next captures will be carried out in spring 2002.

For molecular analyses, AFLP (Amplified Fragment Length Polymorphisms) are currently being developed. Preliminary results are shown in figure 1.

Outlook:

The molecular analyses and laboratory work will be going on in 2002. Focuses on data analysis and modelling of the data will start in autumn 2002.

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Project ID: 01LC0018 (SUBICON Subproject 4)
1.3.2001 – 29.02.2004

STRUCTURE OF THE PREDATOR COMMUNITY IN A RED OAK CHRONOSEQUENCE

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Key words: Araneae, Carabidae, Chilopoda, Coal mining areas, Habitat structure, Red Oak chronosequence, Staphilinidae, Succession

Abstract:

Araneae, Carabidae, Staphilinidae and Chilopoda are studied based on a comparative analysis of different aged red oak stands and grassland of post mining areas. The hypothesis of habitat structure being the most determinating factor of biodiversity of a predator community is tested.

Questions:

In the end of the 19th century, the red oak (Quercus rubra) was imported from North America to Europe as a fast growing tree being able to achieve a high productivity on poor stands. Until now there is only little knowledge about the importance of these forests for indigenous arthropod predators. Several investigations have shown the importance of habitat characteristics such as habitat structure for arthropod colonisation.

In this context, we investigate both the development of red oak forest habitat diversity and the development of predator diversity in a chronosequence of former coal mining areas. Recultivated areas are most suitable for investigations of biodiversity development because any established arthropod populations affecting new colonisators are absent.

- What is the influence of tree species on the predator community?
- What are the differences between forests with indigenous species (Quercus robur, Quercus petraea) and unforested areas on reclaimed soil?
- How much time does it take for establishment of biodiversity in disturbed landscapes?

Methods:

The colonisation of the study areas by predator groups of different mobility and dispersal strategy (Araneae, Staphylinidae, Carabidae, and Chilopoda) is studied. The epigaeic activity of these groups is investigated by pitfall traps and tree trunk eclectors throughout the vegetation period. Additionally, soil cores and sweep-net catches are analysed for arthropod abundance in spring and autumn. Expected results refer to species richness, dominance structure, habitat preference of species, life form diversity, age structure of populations, and also species and individual mobility.

To investigate the influence of habitat structure and vegetation architecture of the forest stands on predators, a method according to Curtis Bignal and Meißner, which analyses habitat structure and diversity of different vertical quadrats, is applied.

The investigations are performed in cooperation with the working groups of the Brandenburgische Technische Universität Cottbus and the Umweltforschungszentrum Leipzig-Halle. The synoptic consideration of the diversity of mycorrhiza (in both their symbiotic and degrading aspect), of primery producers, of selected phytophages, and of zoophages enables a comprehensive picture of the functional relations between spatial structures and biocenotic diversity.

First Results:

In previous studies (Mrzljak & Wiegleb 2000) of open country vegetation of post mining areas it was shown, that all epigaeic arthropod groups being present in the undisturbed surroundings can be found after 20 years in considerable number and species rich community. No specific trend in species number development was detected. Species number of a site is obviously limited by stratification and height of the colonized vegetation type. Differentation among e.g. Calamagrostis and other tall grass stand is not strongly developed. In Europe no comparable data for Red Oak forests exists.

Overview:

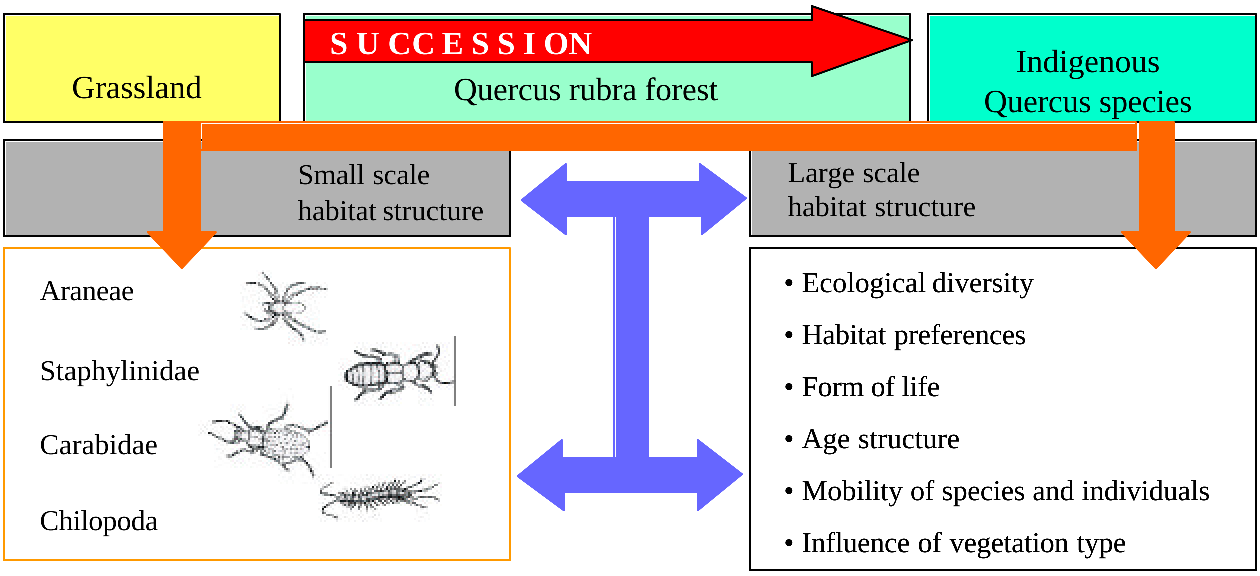

Fig. 1: Investigated arthropod groups and environmental parameters

Outlook:

Outdoor sampling and determination of material was started in July this year and will be continued until end of 2003. First statistical analysis were carried out. Modelling of the data will start after the end of collection.

References:

1. Mrzljak, J. and Wiegleb, G., Landscape and Urban Planning, 2000, 51, 131-146.

Project ID: 01LC0020 (BIOPLEX Subproject 1)
1.10.2000 – 30.9.2003

BIODIVERSITY AND SPATIAL COMPLEXITY IN AGRICULTURAL LANDSCAPES UNDER GLOBAL CHANGE (BIOPLEX) - MODELLING AND GEOSTATISTICS

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Key words: landscape ecology, Geographical Information System (GIS), study site selection, spatially-explicit simulation models, ecological profiles

Abstract:

Among several fields of activity we highlight two examples. First, we introduce PaDS, a tool for objective study site selection for landscape ecology. PaDS showed that the landscape investigated in BIOPLEX can be characterized by mean slope and mean perimeter-to-area ratio of the land parcels. BIOPLEX study sites were selected spanning the entire dimension of landscape complexity. Second, a spatially explicit, multi-species metapopulation model has been developed which will be used to investigate the functional influence of landscape structure on biodiversity.

Results:

BIOPLEX investigates the connections among biodiversity and spatial complexity in agricultural landscapes. This subproject combines the theoretical aspects of BIOPLEX. The fields of activity include (1) the development and application of a standardized procedure for study site selection, (2) the identification of meaningful landscape indices describing spatial landscape complexity as it influences biodiversity, (3) linking geostatistical information of the other subprojects in a GIS, (4) the development of spatially explicit simulation models facilitating a scaling up of findings obtained at small spatial scales to the landscape scale, and (5) the development of hypotheses on the functional influence of landscape complexity on biodiversity using spatially explicit simulation models. Here, we present (1) and (5) in more detail.

Study site selection

In large complex landscapes the spatial representativity of sample sites becomes important as financial and human resources of research projects limit the practible sample size. Therefore, we developed PaDS as a tool for standardised landscape analyses to guarantee reproducible and representative study site selection. The main objective of PaDS is to detect patches that fit user specified criteria based on patch metrics. We explain PaDS using the selection of study sites situated in wheat fields for BIOPLEX subprojects 2 – 4 as an example.

First, PaDS was used to examine 714 Patches of 7 different sizes ranging from $(250m)^2$ up to $(3000m)^2$. For each of these patches a number of landscape metrics and terrain attributes were derived from the DEM (Digital Elevation Model) and the official German land use database called ATKIS; both converted to grids with 20m mesh size. The parameters used in this project were: proportion of different types of land use, acreage/pasture ratio, (total) number of parcels, perimeter-to-area ratio (PAR), Shannon Index, (derived from ATKIS), as well as mean slope, mean global radiation, mean topographical roughness, mean altitude, mean height above drainage channel, proportion of stretched hill slopes (derived from the DEM) and mean precipitation. Using principal component analysis (PCA) this plethora of indices and attributes was synthesized into two compound axes. The two indices describing these axes best are the topographical parameter mean slope and mean perimeter-to-area ratio, a parameter describing land parcel size and shape. Patch size was selected on the basis of parameter distribution. With edge lengths of 2000m or more, land use is usually distributed normally and diversities trend for a maximum. Additionally, PaDS was used to determine, the relevant, structure-controlling landscape parameters for a square patch of 2000m edge length about each of the 6960 arable land parcels. Based on this information 23 study sites were selected which build gradients spanning the entire ranges of slope and perimeter-to-area ratio and therefore represent the entire landscape.

Functional influence of landscape complexity on biodiversity

Agricultural landscapes can be viewed as spatial mosaics of patches of arable land, meadows, and fallow land. We investigate two opposing processes influencing biodiversity in terms of species richness: (1) Species richness increases with patch size because local species-extinction probabilities decrease. (2) Species richness decreases with increasing isolation among patches of the same land use type because recolonisation is more difficult[2]. As a consequence, we predict fairly high species richness at small patch sizes (isolation negligible). As patch size increases, isolation increases as well and local extinctions will be less likely to be counteracted by colonisations, resulting in low species richness. However, as patch size increases further, local extinctions will be rare and species richness very high. Finally, at very large patch sizes, isolation becomes practically perfect and biodiversity is low even though extinctions are unlikely (Fig. 1). The spatial scales at which the hypothesized pattern can be observed are a function of the 'ecological profile' of the species investigated. Ecological profiles differ qualitatively in their dispersal ability and habitat specificity. For example, isolation decreases with increasing dispersal ability and decreasing habitat specificity.

To investigate these hypotheses, we developed a grid-based, spatially explicit metapopulation model. For model development, we had insects in mind. Each grid cell constitutes an area of a specified land use type and may accommodate a number of populations of different 'types' (specific quantitative representation of an ecological profile). All land parcels comprise several cells. Local populations may go extinct and recolonization is possible due to dispersing individuals managing to establish new local populations. We will run simulations for different landscapes using types from within one and all ecological profiles to quantify the specific and overall effect of landscape structure on biodiversity. Simulation results will be compared to the field surveys conducted by subprojects 2 –4. Deviations between field and model results will lead to model modifications and thereby to increasing understanding of the effects of landscape complexity on biodiversity. These investigations will be accompanied by a second, more detailed model restricted to aphid dynamics.

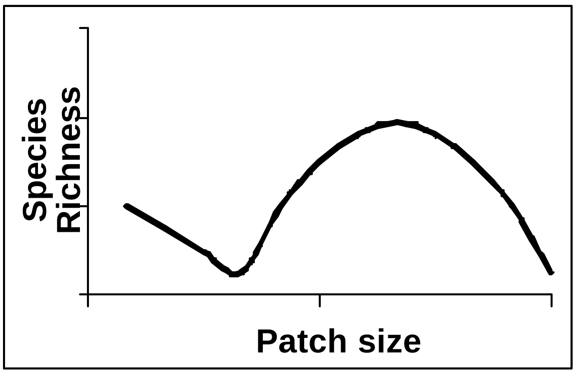

Fig. 1: Species richness as a function of average patch size.

References:

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Project ID: 01LC0020 (BIOPLEX Subproject 2)
01.10.2000-30.09.2003

BIODIVERSITY AND SPATIAL COMPLEXITY IN AGRICULTURAL LANDSCAPES UNDER GLOBAL CHANGE (BIOPLEX) - AGROECOLOGY

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Key words:
biodiversity, ecological functions, landscape structure, landscape complexity, biological control, trophic interactions, top down, bottom up, scale dependence, wheat, cereal aphids, parasitoids.

Abstract:

The Agroecology group investigates the influence of landscape structure and farming management on biodiversity and functioning of ecological processes in agricultural landscapes of northern and middle Germany. The analyses focus on species diversity and species interactions in wheatcrop fields and grasslands. In wheat fields, we address factors that affect the presence, abundance and species richness of natural enemies of cereal aphids (and weeds) as well as the role of pathogens (with project group 3: Phytopathology) and below- and above-ground processes (with project group 4: Soil Ecology) in relation to landscape complexity. We evaluate the ability of ”natural enemies” of pests (and weeds) to act as ”biocontrol agents”, i.e. species which suppress the damage caused to crops by pests below an economic threshold. In grasslands we focus on the combined effects of pollinators and seed predators on plant’s seed set. The analysis of the spatio-temporal variability of these counter-rotating processes will give a deeper insight to multitrophic interactions of important functional groups in terrestrial ecosystems, and to modeling biodiversity (with project group 1: Modeling and Geostatistics) at a range of spatial scales upscaling from microsites, via the field and farm scale to landscapes and the global context.

Results:

Since there is an increasing recognitation that community structure, species abundance and biotic interactions may depend on scales much larger than a single habitat, a landscape perspective considering spatial arrangement, connectivity and environment of habitats may be undispensable in determining local ecological pattern and processes (Kareiva 1990, Kruess & Tscharntke 1995, Roland und Taylor 1997, Thies & Tscharntke 1999). However, landscape context does not influence all species equally, and interacting communities are made up of species with very different spatial strategies. Species show specific responses to landscape structure facilitating or impeding movement among habitat patches, and with a specific perception of spatial scale of landscape complexity (With et al. 1999). Here, we present initial results from herbivore-parasitoid interaction in wheat fields (*Triticum aestivum*) located in 46 landscapes differing in structural complexity. We analysed the most important crop pest on wheat in Germany, the cereal aphid *Sitobion avenae* (Homoptera: Aphididae), and its mortality due to parasitoids (Hymenoptera parasitica). The abundance of the aphid *S. avenae* as well as its mortality due to parasitism was correlated with the perimeter/area ratio (*P/A*). The *P/A* ratio serves as a useful index of shape complexity in a landscape. For a given area, a high *P/A* ratio indicates a complex or elongated boundary shape, and a low *P/A* ratio indicates a more compact and simple shape.

The abundance of aphid *S. avenae* in wheat field increased (slightly) as the *P/A* ratio increased from 0.5 to 1.5, but decreased (slightly) as the *P/A* ratio increased from 1.5 to 3 (Fig. 1A). Mortality of *S. avenae* due to parasitoids increased distinctly, without any evidence of a threshold, from values of 0% to 50% as the *P/A* ratio increased from 0.5 to 3 (Fig. 1B). Our results clearly show, that the efficiency of natural enemies, i.e. their potential to act as ”biocontrol agents”, is generally enhanced in complex landscapes, obviously leading to a tendency of lower pest abundance in landscapes with a *P/A* ratio >1.5-2. The is corresponding to Hawkins & Cornell (1994). They predicted success in classical biological control only above a threshold value of 32-36%, which is the case in our study system above a *P/A* ratio >1.5-2.

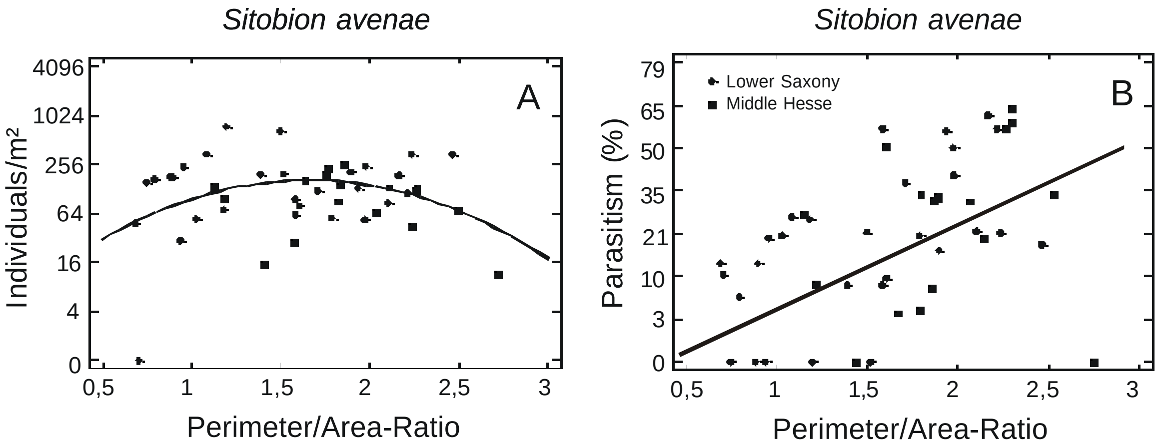

Figure 1: Herbivor-parasitoid interactions in wheat fields (*Triticum aestivum*) in landscapes of different complexity (N= 46) located in Lower Saxony and middle Hesse (Germany). **(A)** Abundance of the crop pest *Sitobion avenae* in relation to the perimeter/area ratio (*P/A*). $Y= 1.55 + 4.19 \times P/A - 1.26 \times P/A^2$. F= 2.74, $P_{Model}= 0.075$, $P_{P/A}= 0.024$, $P_{P/A^2}= 0.028$, N= 46, R²= 11%. **(B)** Mortality rate of *Sitobion avenae* due to parasitim in relation to the perimeter/area ratio (*P/A*). $Y= 3.54 + 15.54 \times P/A$. F= 12.31, P= 0.001, N= 46, R²= 22%. Each data point is based on four subsamples per field (inspection of 4 × 20 shoots per field for aphids and aphid mummies in June). Statistical analyses comprised multiple linear and non-linear regressions with two independent landscape metrics, the *P/A* ratio and the crop area [%] per landscape (see BIOPLEX project group 1 for further explanation) and host plant density (shoots/m²; Fig. 1A) or host density (aphids/m²; Fig. 1B), respectively. Only *P/A* ratio arised as factor of explanation.

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Project ID: 01LC0020 (BIOPLEX Subproject 3)
01.10.2000-30.09.2003

BIODIVERSITY AND SPATIAL COMPLEXITY IN AGRICULTURAL LANDSCAPES UNDER GLOBAL CHANGE (BIOPLEX) - PHYTOPATHOLOGY

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Key words: *Sitobion avenae*, DNA-Fingerprinting, *Septoria tritici*, genetic variability, landscape-structure, agricultural utilization

Abstract:

The ***BIOPLEX*** *subproject Phytopathology aims at evaluating the influence of landscape structure on population processes at the genetic level. Using cereal aphid species and plant pathogens on winter wheat as targets we investigate the genetic diversity of these species within and between fields at a local and a regional scale to evaluate the influence of the structural and agronomical diversity of the surrounding landscape at different spatial scales. The project started with the year 2001. Sampling methods were determined in cooperation with other subprojects. Samples were taken two or three times, respectively (according to specific developmental stages of the wheat) in up to 40 fields in the environment of Goettingen and in the Lahn-Dill-Bergland. The wheat fields were selected by means of GIS-Analysis. During sampling dates additional plants were collected to determine biomass as a covariate. On each field in the environment of Goettingen small areas were excluded from insecticide application for aphid sampling. All farmers were questioned on information concerning agricultural cultivation treatments (tillage strategies, application of fungicides, fertilization, cultivars and crop rotation).*

Insects (L. Reimer)
About 30 to 100 cereal aphids, predominantly *Sitobion avenae*, were collected during two sampling dates from 36 field sites in the region around Giessen and Goettingen. Sweepnet collections were performed along a transect, the length of which was adapted to field size and the number of aphids available. Aphid captures were located at least one meter apart from each other to collect as many clones within one field as possible. >From each sweepnet capture only one nonparasitised individual, identified to species level, was taken for further DNA analysis. Indentifications were verified by Dr. T. Thieme (BTL GmbH Sagerheide). Samples were stored either deep frozen at –20 °C or in 99 % Ethanol. For the analysis of microsatellite length polymorphism (Sunnucks et al. (1)) six primers are actually available. Between 91 and 127 individuals from five field sites of the Goettingen region were screened for five primers and 5 to 25 different alleles were found per locus. The number of alleles so far found is as high or even higher than reported in papers that used a higher number of individuals. The distribution of distinct alleles within a site appears clumped with regard to certain alleles. An example on the allele frequencies at one locus is given in Tab. 1. There are predominant alleles and also rare ones. The allelic distribution seems to be similar at different field sites, but some shifts in allele frequencies do occur (field site 2/1, Tab. 1). The genotypes, defined as individuals sharing the same alleles at all loci, show a high diversity. Only two genotypes were found more than once in the different field sites. These genotypes are homozygous at three or four loci and consist mainly of common alleles.

Table 1: Allele frequencies of *Sitobion avenae* microsatellites at one locus. 125 Individuals were screened and 246 alleles (N) were scored in total.

Allele size in basepairs	Field site 1/1 N = 62	Field site 2/1 N = 26	Field site 9/1 N = 62	Field site 12/1 N = 48	Field site 18/1 N = 48
185	0.79	0.42	0.75	0.75	0.75
186	0.13	0.27	0.11	0.17	0.23
188	0.02	0.04	0.03	0.02	0.00
189	0.00	0.04	0.00	0.00	0.00
190	0.05	0.23	0.11	0.04	0.00
191	0.02	0.00	0.00	0.02	0.02

Additionally, a new primer will be included in further investigations, because certain primers developed from *S. miscanthi* failed to amplify in most cases and two or three PCR runs were necessary to obtain positive results.

The data on the genetic diversity will be analysed for differences between field sites in the Lahn-Dill Bergland and Goettingen. Moreover, these data will be compared with subsamples from Northern Germany and Hungary and also with published data from France and England. The microsatellite data will be also analysed for deviations from the Hardy-Weinberg equilibrium, gene-flow and differences between locations. The data on the population dynamics of the cereal aphids with regard to their spatial and temporal distribution will be covered by other project partners.

Plant pathogenic fungi (J. Morzfeld)

This study aims at analysing the influence of the landscape-structure on the incidence, distribution and frequency of leaf pathogenic fungi on wheat. We will especially analyse the impact of landscape structure on the genetic variability of *Septoria tritici* populations, due to his widespread occurrence. According to the prevailing hypothesis, the distribution and damage of leaf-pathogenic fungi is influenced by measures of agricultural cultivation. Strategies of tillage, application of fungicides, fertilization, cultivars used or crop rotation are regarded of major importance among these measures. An alternative hypothesis states that plant pathogens are less abundant in natural ecosystems compared to agricultural ecosystems. By incorporating both agronomic traits and landscape structure into the analysis of the population genetics of fungi on winter wheat we will be able to separate the importance of either agricultural measures or environmental heterogeneity on fungal biodiversity.

To determine the incidence and damage of plant pathogenic fungi on winter wheat we sampled 50 plants on 28 field sites at three different sampling dates. One leaf of each plant (F-2 or F-1) was qualitatively and quantitatively checked for the following fungal species: *Septoria tritici*, *Septoria nodorum*, *Drechslera tritici-repentis*, *Blumeria graminis* var. *tritici*, *Puccinia striiformis* and *Puccinia recondita.* After visual inspection leaves were collected, dried in the laboratory and then stored at –40 °C. *Septoria tritici* was the most frequent and widely distributed fungi; it was found in both regions in each field. The five other plant pathogenic fungi were distributed in an irregular pattern.

The necrotrophic fungus *Septoria tritici* will be isolated from the stored leaves and grown *in vitro* (Schnieder et al. (2)). The genetic variability of this fungus will be analysed by a fingerprinting-method (MP-PCR: microsatellite-primed-PCR; see Czembor et al. (3)). By means of experiments with different *Septoria*-Isolates (Collection of the institute) ahead of screening DNA-Isolates, experimental conditions, primers for the fingerprinting method, PCR- and other laboratory routines were optimised.

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1.10.2000 – 30.09.2003

BIODIVERSITY AND SPATIAL COMPLEXITY IN AGRICULTURAL LANDSCAPES UNDER GLOBAL CHANGE (BIOPLEX) - Soil BIOTA

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Key words: landscape complexity, soil fauna, ground beetles, ants, wheat, grassland

Abstract:

The character of Central European landscapes is shaped by human land-use, especially agriculture. The continuous expansion of agriculture over the last centuries created open landscapes with new habitats and led to an increase of biodiversity. Therefore biodiversity of Central Europe depends on agriculture. However, industrialisation of agricultural production and intensification of land-use over the last decades led to enormous habitat destruction and thereby to a decrease in biodiversity. The question arising from this development is: What kind of agricultural landscape do we need to sustain high levels of biodiversity? The multidisciplinary project BIOPLEX approaches this question by analysing the relationship between biodiversity and landscape complexity at different spatial scales. The studies focus on wheat fields and managed grasslands in two agricultural regions of Germany (Lahn-Dill-Bergland, Hesse and Southern Lower Saxony). The subproject ***Soil Ecology*** *aims at: (i) recording the species richness of soil living macroinvertebrates (ground beetles, rove beetles, woodlice, diplopods) and soil engineers (ants), (ii) analysing the effect of epigaeic predatory arthropods on cereal aphids in winter wheat, and (iii) quantifying the functional role of decomposers depending on landscape complexity. A comparison between the data derived from these analyses with data on phytophagous insects, plant pathogens and vegetation will reveal some of the relationships between above- and belowground biodiversity.*

Results:

Sustainable management of biodiversity at the landscape level urgently needs simple indicators of biodiversity. Landscape structure affects ecological processes and species richness (Wiens et al. 1993). Landscape pattern descriptors, which correspond to spatial complexity and to varying amounts of land-use types might serve as useful tools to explain differences in species richness across landscapes (Miller et al. 1997). Field experiments and surveys on this topic rely on representative selection of study sites by landscape analyses, taking into calculation the landscape features of interest for the respective survey. Ideally, there is a small set of metrics, which span the important dimensions of landscape structure (Riitters el al. 1995). The selection of study sites in a gradient of landscape complexity is shown in Behrens et al. 2001. Base maps used for the study site selection were a DEM (Digital Elevation Model) and the official German land-use database called ATKIS (Amtliches topographisch-kartographisches Informationssystem). The decision to use these base maps was taken on base of the results of a preliminary study out of which some of the results are presented here:

Species richness of staphylinids, carabids and ants was recorded in a small-scale mosaic landscape. In a complete factorial design we sampled the major land-use types of the open landscape: arable land, managed grassland and fallow land. The study sites were further characterised by different environmental conditions like soil type (dry or moist) and aspect (south or north oriented). We tested the effects of land-use, aspect and soil type by a three factorial ANOVA.

A total of 153 staphylinid species, 100 carabid species and 27 ant species were found. Each land-use type contributed to total species richness of all three taxa at the landscape level. Species richness significantly differed between the land-use types in a taxon-specific way. Mean species richness of staphylinids and ants was highest in fallow land whereas species richness of carabids was highest in arable land. Among the environmental parameters aspect had a significant effect on species richness of staphylinids and ants with staphylinids showing higher species richness at north oriented sites and ants at south oriented sites. Soil type had a significant effect on carabids and ants. Species richness of both taxa was higher on dry soils.

Land-use was the factor explaining the highest proportion of variance of staphylinids and carabids (Fig. 1). Aspect had the highest variance explanation for ants, i.e. a highly thermophilous group. Therefore hot spots of ant diversity in a landscape are to be expected at south oriented slopes. Non-significant interactions indicate that environmental parameters affect species richness of all taxa independent from the land-use. Only species richness of staphylinids was not affected by soil type *per se*, but soil type had a modifying influence on the effect of land-use as indicated by the significant interaction between these two factors. Nevertheless, there still is a high percentage of variance unexplained by the factors considered so far. We expect landscape complexity to be a further significant landscape variable affecting species richness of soil macroinvertebrates.

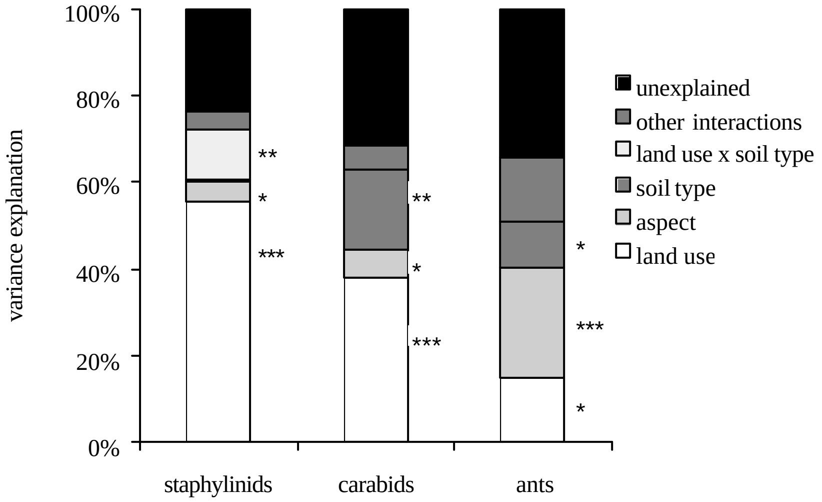

Fig. 1: Variance explanation of the factors land-use, aspect and soil type and their interactions for species richness of staphylinids, carabids and ants as derived from a three factorial ANOVA. *P*-levels: * < 0.05, ** < 0.01, *** < 0.001.

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Project ID: 01LC0020 (BIOPLEX Subproject 5)
01.11.2000 – 31.10.2003

BIODIVERSITY AND SPATIAL COMPLEXITY IN AGRICULTURAL LANDSCAPES UNDER GLOBAL CHANGE (BIOPLEX) - SOCIAL-ECONOMIC EVALUATION AND APPRAISAL WITH RESPECT TO BIODIVERSITY IN AGRARIAN LANDSCAPES

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Key words: system of payment, ecological services, information, contingent valuation method, biodiversity, production value, agriculture

Abstract:

The subproject V is structured into three parts. The part "Result-Oriented System of Payment for Ecological Services“ deals with the development of an economic system of payment for ecological services provided by farmers. These services will be measured by ecological goods arising from plant biodiversity. The part of the project that deals with “The Influence of Information on the Economic Valuation of Natural Resources” has two objectives. On the one hand, it aims at an economic evaluation of ecological goods defined in the first part of the subproject (s. a.). On the other hand, different influences of information that occur during the process of evaluation in a contingent valuation, are investigated in an interdisciplinary approach. Another part of the project concerns „The Impact of Certain Components of Biodiversity on the Production Value in Agriculture“. This aims at assessing the utility certain components of biodiversity and, simultaneously, ecological goods have got for agriculture.

Results:

“Result-Oriented System of Payment for Ecological Services“

Ecological services performed by the farming community are positive external effects. At present some of these ecological services are financed under agri-environmental programs or agri-environmental contracting. In these programs the farmers get paid for acting according to special cropping instructions, e.g. dispensing pesticide use.

In theory, such services could be increased if the financial incentives on offer are improved. Our research project focuses on developing a concept of a regional market and result-oriented system of payment for ecological services provided by farmers. The results of ecological services are ecological goods. Goods arising from plant biodiversity can be considered to be those most suitable for a result-oriented system of payment. These ecological goods should be supplied by the farmers voluntarily and without set regulations. Furthermore, the public demand for ecological goods should be represented by a regional advisory board in the sense of the European subsidiarity principle. This advisory board has to award public contracts for the production of ecological goods.

In this way, environmental programs could be made more flexible and the farmers would receive financial incentives to find innovative solutions for an environmentally compatible management.

The concept further takes into account the preferences of the local population for ecological goods and for the allocation of public funds.

In our transdisciplinary research work we develop this result-oriented system of payment for a representative region in the south of Lower Saxony (County Northeim) and check the possibilities of its application in practice with the relevant institutions of that county. The members of the regional advisory board represent the administrations of agriculture and environment protection, the local affairs, and the associations of agriculture, conservation, and land owners. Up to now we defined regional specific ecological goods associated with grassland use, we worked out management proposals to obtain these ecological goods, and calculated the costs. The award procedures for public orders, complying with the law, were examined with regard to their transferability on a market for ecological goods.

“The Influence of Information on the Economic Valuation of Natural Resources“

Non-market common goods, such as ecological commodities, cannot be evaluated by their market price. To estimate their monetary value, ecological economists have developed several methods of indirect and direct evaluation, for example, the contingent valuation method (CVM), which elicits willingness to pay-values by means of an interview.

In this study, CVM will be applied to estimate the willingness to pay of the citizens living in the representative region, county Northeim (s. a.), for certain ecological goods (s. a.), such as hedgerows in agrarian landscapes. At the same time, the impacts of information imparting and information processing on the valuation of the ecological good in question during an interview situation are investigated. For this purpose, in a first step the findings of other disciplines have been summarised and analysed, based on a common theoretical framework, the Theory of Planned Behaviour. In a second step, hypotheses about information processing and decision making of respondents in CV situations have been derived from this analysis. They will be tested in a study orientated by findings and methods of social and consumer psychology.

“The Impact of Certain Components of Biodiversity on the Production Value in Agriculture“

Local explorations of natural sciences in this field have shown that certain components of biodiversity may be economically important for agricultural production. With the aid of an expert questionnaire, these sporadic results shall be tested by their relevance in different agricultural landscapes, and the capability of generalising them be assessed, respectively.

So far, the recent results presented in literature have been explored and summarised in causes and effects. As the analysis will be conducted according to the Delphi method, the summaries will now be used for developing a standardised questionnaire. With the aid of the Delphi-Questioning, the opinion of a group of experts will be ascertained and structured. As the experts stay anonymous in this kind of questionnaire, biases in the results which may result from the opinions of too strong characters can be avoided. This is, however, often the case in group discussions. Apart from that, various data bases have been checked to find persons with expertise in this field of research. This is crucial as the quality of the results depends substantially on a good choice of experts.

Project ID: 01LC0021 (Subproject 1)
1.1.2000 - 31.12.2003

BIODIVERSITY OF NITROGEN-FIXING MICROORGANISMS

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Key words: Uncultured bacteria, nitrogenase genes, rice roots, DNA-microarrays, mRNA detection

Abstract:

The project aims to analyze the biodiversity of nitrogen-fixing prokaryotes by molecular and classical techniques. During this project, the molecular methods to address questions of terrestrial biodiversity are developed and established: Development of monitoring systems for fast, reliable assessment of the biodiversity of diazotrophic bacteria in association with plant roots, and for analysis of the dynamics of their population structure and their key activities (expression of nitrogenase genes). Protocols were developed to quantify bacterial nifH *(nitrogenase gene) mRNA extracted from roots, and clone libraries of bacterial* nifH *genes completed, demonstrating that the majority of rice root-associated diazotrophs has not yet been cultured. One of the major achievements is the development of a DNA-microarray which can specifically detect and identify a large variety of specific nitrogenase gene fragments amplified by PCR, without the necessity for clone libraries.*

Results:

The diversity of prokaryotic organisms is classically estimated by attempts to cultivate them and by characterization of the isolates. However, during the last decade DNA- or RNA- based techniques led to the conclusion that the organismal diversity is much higher than estimated by these classical techniques: the majority of bacteria present in a given habitat has in most cases not been cultured as yet, and often these bacteria are phylogenetically very distant to known, cultivated bacterial strains [1]. This is also the case for root-associated bacteria [2, 3]. In order to assess the biodiversity and the population structure in a given habitat, their changes in response to environmental changes, and also in order to understand functions of microorganisms in the habitat, culture-independent methods are indispensable.

The most widely used target molecules for molecular ecological studies are ribosomal rRNA genes [1, 4]. This allows an estimation of the biodiversity, but does –in most cases- not permit to link the results to physiological functions of the bacteria. Functions however may be analyzed when key genes for certain metabolic processes are used as target genes. In the global nitrogen cycle, biological fixation of atmospheric nitrogen is an important microbial activity. The availability of combined nitrogen affects plant productivity and the structure of the plant community [5]. Increasing anthropogenic activities result in an increased contamination of the atmosphere by nitrogenous compounds, and in deposition of nitrogen from the atmosphere on soils, even without application of fertilizer [6]. N-deposits are also likely to affect the population of diazotrophs. One of the structural genes of nitrogenase, *nifH*, is particularly suitable for phylogenetic analysis [3, 7].

We established protocols which allow to retrieve bacterial mRNA from soil-grown rice roots. The degradation of RNA was sufficiently inhibited for the detection of *nifH* mRNA by reverse transcriptase (RT) analysis [8]. Template dilution allowed a quantitative analysis of transcript abundance, the application to different rice varieties revealing significant differences. In clone libraries constructed from these amplification products, most sequences analyzed were only distantly related to nitrogenase genes of known, cultured bacteria. Thus, up to now uncultured diazotrophs appear to be predominantly active in rice roots.

A new method for the assessment of biodiversity is being developed which may allow the specific detection and quantification of a large numbers of different *nifH* mRNA fragments without construction and analysis of clone libraries. DNA microarrays or DNA-chips are widely used for highly parallel and high througput analyses of gene expression in genome research. Oligonucleotides or DNA-fragments which are complementary to target genes are linked to carriers such as membranes or glass slides, and used as baits for hybridization with labeled DNA or RNA under study. This methodology is currently adopted by us to construct a „phylo-chip“, a glass microarray for specific detection of the diversity of *nif* genes. Our database of *nifH* genes from cultured diazotophs and fragments retrieved from environmental samples was used to design short oligonucleotides which are specific to single genes or groups of genes with at least 1-2 mismatches to each other. The oligonucleotides were attached to activated glass slides via amino-links at specific postions, hybridized to fluorescence (Cy-5)-labeled amplification products of a *nifH*-directed PCR, and the hybridizations quantified with a microarray scanner. The oligonucleotide design was optimized with respect to the position of hybridization within the fragment and other factors. Using genes of the *Azoarcus* group as examples, a hybridization protocol was developed in which one mismatch was sufficient to result in a specific hybridization signal. Thus from mixtures of DNA of different bacteria, their nitrogenases were specifically identified. The next steps of development will be the detection of root-associated *nifH* fragments using the phylo-chip, and the enlargement of the number of oligonucleotide baits per chip to cover most of the nitrogenase gene diversity.

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Project ID: 01LC0021 (Subproject 2)
1.1.2001 – 31.12.2001

BIODIVERSITY OF NITRIFYING AND SULFATE-REDUCING PROKARYOTES

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Key words: Nitrification, sulfate-reduction, 16S rDNA, DNA-microarray, ammonia-monooxygenase gene *amoA*, dissimilatory sulfite reductase genes *dsrA/B*

Abstract:

Nitrifying and sulfate-reducing prokaryotes catalyze key steps in the nitrogen and carbon-cycle, respectively, and are thus of primary importance for the ecology of most ecosystems. The project aims to develop and adapt methods suitable for cultivation-independent investigations of the diversity and function of nitrifying (ammonia-oxidizing and nitrite-oxidizing) and sulfate-reducing prokaryotes living in the rhizosphere. For both groups of microorganisms 16S rDNA as well as suitable functional genes are used as marker molecules (1, 2 ,4 ,6). Based on encompassing data sets of these marker molecules, oligonucleotide microarrays for highly parallel, high throughput screening of these prokaryotes in environmental samples were developed and initially applied to investigate samples from a Sphagnum bog. These techniques will be supplemented by optimizing the combination of FISH and microautoradiography (3) for its use in rhizosphere and soil in order to determine the links between the availability of specific substrates (for example by plant root exudation) and the microbial biodiversity. These investigations will provide novel insights into diversity and activity patterns of soil and rhizosphere microorganisms and into interactions between plants and microorganisms.

Results:

During the first project phase we have established encompassing 16S rDNA data sets for nitrifying and sulfate-reducing prokaryotes. Based on this information, microarrays for nitrifying and sulfate-reducing bacteria were designed. These arrays, which consist of several hundred oligonucleotide probes, were thoroughly evaluated under different hybridization conditions using reference sets of suitable pure cultures and are now ready for application in environmental diversity surveys. Furthermore, we started to design and evaluate DNA microarrays for ammonia-oxidizing and sulfate-reducing prokaryotes by exploiting the genes encoding the ammonia-monooxygenase (amoA) and the dissimilatory sulfite-reductase (dsrA/B), respectively, as target molecules.

The developed microarrays are now used to investigate the diversity of nitrifiers and sulfate-reducers in a variety of different rhizosphere samples. In collaboration with Prof. Drake and Dr. Küsel (Lehrstuhl für ökologische Mikrobiologie, Bayreuth) we also began to investigate the community composition of sulfate-reducing prokaryotes in different depths of a Sphagnum-bog, a system for which sulfate-reduction rates comparable to those of marine systems have been reported (for example 5).

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Project ID: 01LC0021 (Subproject 3)
1.1.2000 – 31.12.2003

BIODIVERSITY OF METHANOTROPHIC AND NITRATE-REDUCING BACTERIA

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Key words: methane oxidation, nitrate reduction, denitrification, nitric oxide, nitrous oxide

Abstract:

We investigate microbial processes in soils. The research focuses on the question which processes on a microscopic scale are catalyzed by which microorganisms. Besides the functional diversity in soil with respect to processes, there is an even higher structural diversity with respect to the microorganisms that are responsible for the functions. The extent of the soil microbial diversity is completely unknown. In particular, it is unclear how much microbial diversity is required to maintain soil functions. Within BIOLOG we study the biodiversity of methanotrophic bacteria and nitrate-reducing bacteria in relation to their functioning in soil environments. Biodiversity is studied by targeting both the 16S rRNA genes and the structural genes of key enzymes. Here, we targeted the pmoA genes of methanotrophs coding for the particulate methane monooxygenase, and the nirK/nirS and norB genes of denitrifiers coding for nitrite reductase and nitric oxide reductase, respectively.

Results:

We have studied the diversity of the methanotrophic microbial community (i) in rice field soils from different geographic regions[1]; and (ii) in a meadow soil with seasonally changing water table[2]. Furthermore, (iii) the genetic diversity of denitrifiers was explored by PCR amplification of *nirK/nirS*[3] and *norB*[4] genes from pure cultures and environmental samples.

(i) Methanotrophic bacteria play a crucial role in regulating the emission of CH_4 from rice fields into the atmosphere. We investigated the CH_4 oxidation activity together with the diversity of methanotrophic bacteria in ten rice field soils from different geographic locations. Upon incubation of aerated soil slurries under 7% CH_4, rates of CH_4 oxidation increased after a lag phase and reached values of 3-10 µmol $d^{-1}g\text{-}dw^{-1}$ soil. The methanotrophic community was assayed by retrieval of the *pmoA* gene which encodes the a subunit of the particulate methane monooxygenase. After extraction of DNA from actively CH_4-oxidizing soil samples and PCR-amplification of the *pmoA*, the community was analyzed by Denaturant Gradient Gel Electrophoresis (DGGE) and Terminal Restriction Fragment Length Polymorphism (T-RFLP). DGGE bands were excised, the *pmoA* re-amplified, sequenced and the encoded amino acid sequence comparatively analyzed by phylogenetic treeing. The analyses allowed the detection of *pmoA* sequences related to the following methanotrophic genera: the type-I methanotrophs *Methylobacter, Methylomicrobium, Methylococcus* and *Methylocaldum,* and the type-II methanotrophs *Methylocystis* and *Methylosinus*. T-RFLP analysis detected a similar diversity, but type-II *pmoA* more frequently than DGGE. All soils but one contained type-II in addition to type-I methanotrophs. Type-I *Methylomonas* was not detected at all. Different combinations of methanotrophic genera were detected in the different soils. However, there was no obvious geographic pattern of the distribution of methanotrophs.

(ii) Methane oxidation activity and the structure of the methane-oxidising microbial community in a wet meadow soil in Germany were investigated using biogeochemical, culturing, and molecular fingerprinting techniques. Most-probable-number counting of methane-oxidising bacteria followed by isolation and characterisation of strains from the highest positive dilution steps suggested that the numerically dominant member of the methane-oxidising community was a *Methylocystis* strain ($\cong 10^6$ cells g^{-1} d.w. soil). Calculations based on kinetic data support the conclusion that this organism could account for most of the observed methane oxidation activity in the soil. DNA extraction directly from soil and PCR amplification of the *pmoA* gene also recovered *Methylocystis*-like sequences. However, molecular community fingerprinting analyses also revealed a more diverse and dynamic picture of the methane-oxidising community, and there were large variations across samples. Retrieved *pmoA* sequences included, besides *Methylocystis* sequences, others related to the genera *Methylomicrobium* and *Methylocapsa,* and a novel lineage. A combination of classical microbiological methods and molecular fingerprinting therefore gave a better picture of the microbial community in this meadow soil than either method alone, i.e. the molecular methods revealed a higher species richness and uncovered the presence of *Methylocapsa,* but failed to demonstrate the consistently high abundance of *Methylocystis,* and occasionally even failed to detect this organism despite its abundance.

(iii) The genes *nirK* and *nirS* encode two structurally different but functionally equivalent enzymes occurring within the same genus but not within the same strain of a denitrifier. Two classes of *norB* genes exist with low levels of identity: one type with an adjacent *norC* gene and a second type with a N-terminal extension instead. Amplification of *nirK*, *nirS,* and *norB* was successful from pure cultures within the Proteobacteria. Cloning of *nir* genes from environmental samples revealed gene clusters distinct from those of known denitrifiers suggesting novel lineages of yet uncultivated denitrifiers, probably also within the Proteobacteria. Gene clusters were specific for the habitat from which these clones were obtained. Phylogenetic analysis of *norB* grouped genes according to two classes; within the *norCB* class, *norB* genes from isolates grouped together with clones suggesting that most of these environmental sequences might be derived from Proteobacteria. Within the second class, genes from all known isolates except one were grouped in one cluster, clones were unrelated and scattered. Interestingly, in contrast to *nir* genes, which clustered strongly according to the environment from which they were derived, this was not observed for *norB*. With our current knowledge, the origin of novel sequences and their distribution patterns in the environment remain obscure. Future research will focus on exploring denitrification genes from denitrifiers from culture collections and isolates from environmental samples to extend the databases of functional genes by also considering the phylogeny of the organisms.

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1.1.2001 – 31.12.2003

BIODIVERSITY AND SUCCESSIONS IN TEMPORARY TERRESTRIAL-AQUATIC INTERFACES

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Key words: *Actinobacteria*, automated microscopy, substrate gradients

Abstract:

The diversity of microorganisms found in freshwater aquatic habitats is probably a small subset of the total microbial biodiversity of terrestrial habitats. One aspect of the current project attemps to establish the diversity and ecology of freshwater Actinobacteria. This group of gram positive microbes is of considerable biotechnological interest, and many actinobacterial lineages of terrestrial origin are known (5). Some Actinobacteria have recently been discovered to play a prominent role in freshwater microbial communities, too (1), and moreover provide an interesting model for food-web controlled microbial survival in habitats exposed to high and selective mortality (4). Other facets of the project deal with the establishment of high-throughput methods for the quantification of different microbial populations in water samples, and with laboratory models that investigate the competitive performance of individual microbial populations exposed to different substrate gradients (3).

Results:

During the first year, one focus of the project was the development and refinement of appropriate methods for the culture-independent characterization of microbial diversity within one defined phylogenetic group. A PCR-based protocol for the rapid screening of 16S rDNA clone libraries from freshwater systems for comparatively rare actinobacterial sequences (typically 1-10% of all obtained sequences) was developed. So far, 20 almost complete sequences from this lineage could be obtained from several hundred screened clones, which more than doubles the available database for freshwater *Actinobacteria*. After the successful establishment of the screening assay we now progress to produce at least 50 different actinobacterial sequences from 4-5 aquatic habitats that greatly differ in their temporal stability, and to search for eventual biogeographical patterns. In addition, this collection will serve as a base for the design of specific oligonucleotide probe for fluorescence in situ hybridization (FISH), so that the population sizes of different actinobacterial lineages can be followed in selected habitats.

FISH probes are an increasingly popular tool to visualize different bacteria in various environments. So far, the quantification of FISH-stained cells is tedious and time-consuming, and the relative number of different bacteria in a sample have to be established by epifluorescence microscopy and manual counting. This limits the application of the approach to relatively simple ecological questions, and e.g., discourages more comprehensive studies of microbial biogeographical distribution and population dynamics. We are, therefore developing techniques for the automated counting of double-stained bacteria in environmental samples by computer-assisted image analysis. In the first year of the project we have established an image acquisition and evaluation system for the automated microscopic evaluation of comparatively simple samples, i.e. the counting of bacterial cells in suspension that are filtered and immobilized on membrane filters. For this we have developed a robust computerized focussing system that combines a propriatory autofocus with Haralick texture parameters (2), feedback loops for image contrast maximation, and decisions on image content during acquisition. The system is thus capable of excluding inappropriate or badly focussed microscopic fields prior to evaluation without operator interaction with high reliability, and to evaluate >50 FISH stained samples per day at a total of 2000-3000 counted cells per sample. Future improvements are aimed at better discrimination of bacteria and non-bacterial objects in complex (e.g., sediment) samples by means of advanced shape recognition and/or colour.

A third line of research, although originally not explicitely focussed on freshwater systems, is conceptionally nevertheless closely related to one of the basic ecological questions to be adressed in the project. We tested the hypothesis that aquatic bacteria found in different niches in the natural habitat (particle-attached and planktonic, respectively), might in principle also differ in their adaptations to substrate gradients. Two bacterial isolates from a previously established culture collection were exposed to different modes of substrate addition in batch cocultures. During cocultivation on a batch of substrates the final cell densities of the free-living bacterial strain were reduced three times as much as of the attached ecotype, as compared to growth yields in pure cultures. In contrast, the gradual addition of substrates to stationary phase cocultures was clearly disadvantageous for the population of the typically particle-attached bacteria (3). A different growth response to substrate gradients could thus be another facet affecting the competition between bacteria at the aquatic-terrestrial interface.

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1.1.2000 - 31.12.2003

INVESTIGATION OF PROKARYOTIC DIVERSITY BY OPTIMIZED CULTIVATION METHODS

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Key words: Not-yet-cultured bacteria, TGGE, dialysis culture, molecular fingerprints, cultivation, dialysis culture, chemotaxis

Abstract:

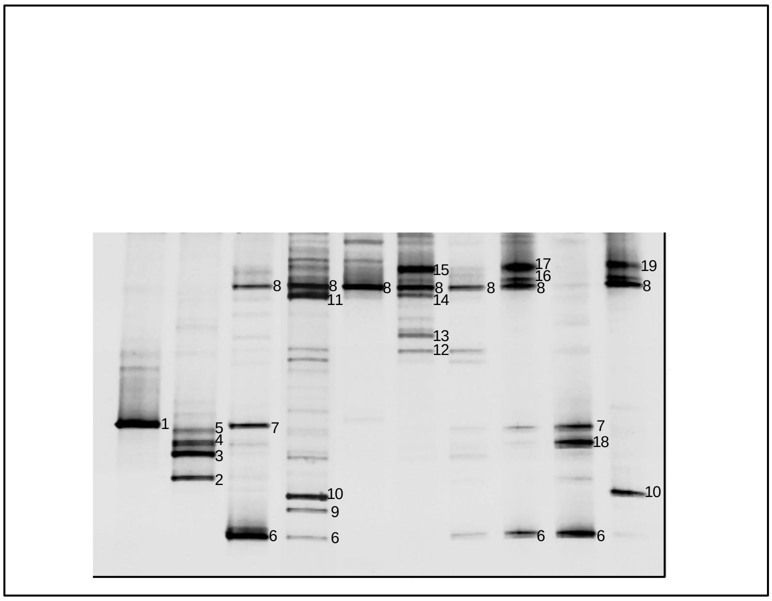
The biodiversity of selected groups of prokaryotes is investigated by a combination of cultivation methods with culture-independent molecular techniques. The target groups are chosen based on their numerical dominance in the natural environment. The present project focuses on those prokaryotes which are not-yet-cultured, but have been shown to occur in large populations in the environment, especially in soil. For a first inventory of the important groups of prokaryotes, group-specific PCR protocols are established and combined with temperature gradient gel electrophoresis (TGGE) to yield typical molecular fingerprints. A suite of novel cultivation methods is employed for the enrichment, isolation and subcultivation of prokaryotes. These methods comprise the formulation of novel mineral media, chemotactic enrichments, growth on inert solid substrates, treatment with specific bacterial pheromones, and dialysis cultures. Cultivation success is monitored by most probable numbers and by molecular fingerprints to establish the most promising experimental strategies for the isolation of certain dominant prokaryotes. By its combination of molecular biological methods with cultivation techniques, the present project offers the perspectivetof ultimately result in the isolation and characterization of ecologically significant prokaryotic isolates and to understand their impact on the performance of the soil ecosystem. We expect that some of the isolates obtained can also be employed as indicators for certain types of ecosystems.

Results:

Culture independent methods have repeatedly demonstrated that the diversity of prokaryotes in the natural environment is unexpectedly high. This is especially true for soil, where the number of bacterial species is estimated to range between 13,000 and 26,000 species [1,2]. By comparison, only 4500 species of prokaryotes so far have been validly described [3]. The diversity in aquatic habitats appears to be lower (~550 species, [4]). So far, only a minor fraction of the diverse and ecologically significant assemblages of prokaryotes can be isolated in pure culture (i.e. 0.3% of the total cell counts [5]) and is thus available for physiological studies. Traditional cultivation techniques have been shown to select for bacteria which appear to occur in minor numbers only [6]. The isolation and characterization of ecologically significant bacteria is thus a prerequisite for an understanding of microbial diversity and the function of microbial assemblages in natural environments.

In the present project eight taxonomic groups of prokaryotes were chosen based on their occurrence in the natural environment: the *Acidobacteria*, *Actinobacteria*, Low GC gram-positive bacteria, α-Proteobacteria, β-Proteobacteria, *Cytophaga-Flexibacter-Bacteroides* Group, nonthermophilic Crenarchaeota, and the Green Nonsulfur Bacteria. Selective PCR protocols for the amplification of 600 bp-long 16S rRNA gene fragments were established. In combination with Temperature Gradient Gel Electrophoresis (TGGE), our technique permits a culture-independent and rapid monitoring of the composition of natural communities. Since the DNA bands generated are available for sequencing, the dominant prokaryotes of each group can also be identified taxonomically in a cultivation-independent manner.

Fig. 1. 16S rDNA fingerprints of the group Green Nonsulfur Bacteria in various environments. Different numbers correspond to different bacteria. All 16S rDNA sequences obtained were previously unknown (after [7]).



Several novel cultivation methods are employed for the enrichment, isolation and subcultivation of prokaryotes especially from soil. Three different soils (fir forest, beech forest, alpine soil at 1400 altitude) located south of Munich were chosen as sampling sites. Our methods comprise the formulation of novel mineral media, chemotactic enrichments, growth on inert solid substrates, treatment with specific bacterial pheromones, and dialysis cultures. Cultivation success is monitored by the most probable number (MPN). We divised a new MICRODROP technique for the automated inoculation of defined numbers of single bacterial cells in liquid media in microtiter plates. To date, a total of 200 bacterial strains could be isolated in liquid cultures with this MICRODROP technique. Employing the group-specific fingerprinting methods described above, the strains obtained are identified and compared to the original composition of the complex prokaryotic community. By the combination of cultivation attempts with culture-independent methods, the most promising experimental strategies for the isolation of certain dominant prokaryotes will finally be established.

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1.1.2001 – 31.12.2001

THE ROLE OF *N*-ACYL-L-HOMOSERINE LACTONE (AHL) MEDIATED COMMUNICATION FOR THE STRUCTURE AND PERSISTENCE OF MICROBIAL RHIZOSPHERE COMMUNITIES

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Key words: Quorum-sensing, rhizosphere, cell-cell communication, *Pseudomonas putida*, *Serratia* sp.

Abstract:

The plant rhizosphere represents a highly complex ecosystem that is influenced by a number of abiotic (soil chemistry, atmos- and hydrosphere, climate, etc.) and biotic factors (plant species, number and diversity of rhizosphere organisms). The bacterial communities of the rhizosphere have strong influence on the growth and health of the plant as well as on their ability to adopt to changed environmental conditions. In recent years it has become evident that a number of bacteria associated with plants produce N-acyl-L-homoserine lactone (AHL) signal molecules that act as chemical communication signals between bacterial cells as well as between bacteria and plants. These interactions appear to be of great importance for the ecology of the rhizosphere. The aim of the proposed project is to investigate the role of AHL-mediated intergeneric communication for the diversity and the stability/dynamic of the rhizosphere ecosystem. These investigations should also allow to monitor changes of the environment by assessing the fluctuations in the communication and population structure of the rhizosphere consortium.

Results:

We have developed and characterized novel Gfp-based monitor strains that allow in situ visualization of AHL-mediated communication between individual cells in the plant rhizosphere. For this purpose three Gfp-based AHL sensor plasmids (1) were transferred into AHL-negative derivatives of *Pseudomonas putida* IsoF and *Serratia liquefaciens* MG1, two strains that are good colonizers of tomato roots. Each of these sensor plasmids is capable of detecting a different range of AHL molecules, depending on the components used for its construction. The resulting strains were rigorously characterized with respect to their sensitivities for various AHL molecules and then employed to visualize AHL-based communication between defined bacterial populations in the rhizosphere of axenically grown tomato plants.

We screened over 300 bacterial strains isolated from the rhizosphere of tomato plants for their ability to synthesize AHL signal molecules. Approximately 12% provoked a positive signal with at least one of the AHL monitor strains used. We selected four isolates for further studies and these were, on the basis of their 16S rDNA, affiliated to the genera *Pseudomonas* and *Rahnella*. The AHL profiles (i.e. the amounts and structure of the AHL molecules) of these isolates were determined by thin-layer chromatography in combination with the AHL biosensor pSB403 (Fig. 1) (4, 2).

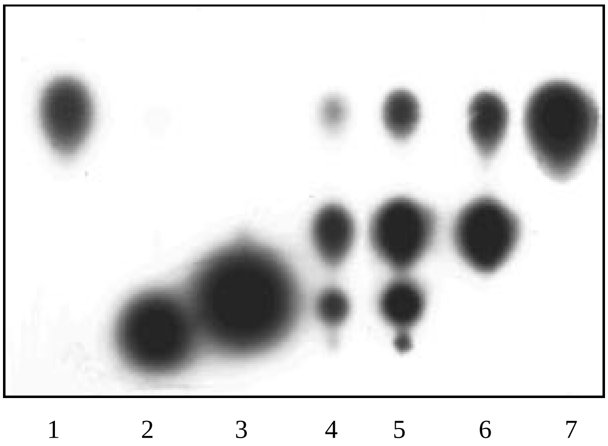

Fig. 1. Thin layer chromatographic analysis of AHLs produced by bacterial strains isolated from the tomato rhizosphere. AHLs extracted from cell-free culture supernatants of *Pseudomonas putida* IsoF (4), *P. putida* Z2D (5), *Rahnella aquatilis* TAA (6), and *R. aquatilis* T13 (7) were separated by TLC, and spots were detected with the aid of the AHL biosensor *E. coli* MT102(pSB403). Synthetic AHLs were included as reference substances as follows: 3-oxo-C6-HSL (1), 3-oxo-C12-HSL (2), and 3-oxo-C10-HSL (3).

To investigate whether these strains do produce AHL molecules when colonizing the tomato rhizosphere we inoculated axenically cultured tomato plants with an AHL monitor strain together with an AHL-producing rhizosphere isolate. When the tomato roots were inspected under a confocal laser scanning microscope, green fluorescent cells could be observed indicating the presence of AHL molecules in the plant rhizosphere. Expectedly, no signals were detected when the sensor strains were inoculated alone. In conclusion, these experiments provide strong evidence that AHLs are produced by bacteria colonizing the rhizosphere of axenically grown tomato plants and that these signals can be perceived by other bacteria (3).

Furthermore, we integrated an AHL sensor cassette, that responds to the presence of long chain AHLs with the expression of Gfp, into the chromosome of the DsRed-tagged *P. putida* strain F117. This monitor strain was used to demonstrate that the indigenous bacterial community colonizing the roots of tomato plants growing in non-sterile soil produces AHL molecules. In a first step this monitor strain was used to inoculate tomato plants grown in non-sterile soil together with the untagged wild type strain IsoF. As for the axenically grown plants we observed that most red fluorescent cells were also green fluorescent indicating that IsoF also produces AHL in the natural root habitat. However, in contrast to the gnotobiotic system, we also detected green fluorescent cells when the monitor strain was inoculated alone. These results clearly demonstrate that the indigenous rhizosphere community produces AHLs at concentrations high enough to activate the monitor strain and thus provides strong evidence that these signal molecules are utilized by the consortium for communication between different populations.

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1.1.2000-31.12.2003

BIODIVERSITY OF PROTOZOA IN THE RHIZOSPHERE OF PLANTS: EFFECTS ON ACTIVITY, PERFORMANCE AND DIVERSITY OF MICROORGANISMS AND ON PLANT GROWTH.

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Key words: manipulation of soil diversity, rhizosphere interactions, plant competition

Abstract:

Competition between plants is high, because plant growth in natural environments frequently takes place in dense stands of established vegetation. Thus both, beneficial and deleterious associations of plants with microorganisms and the regulation of these associations by soil faunal activity may be of fundamental importance for individual plant species, but also for the species composition of the whole community. We investigate the mechanisms and ecological significance of interactions between plants and microorganisms (bacteria, fungi), and their faunal regulation. We focus on three general aspects: (1) the regulation of plant growth by microorganisms and their consumers (protozoa, nematodes, collembola), (2) the competition for nutrients between microorganisms and plants, (3) the regulation of plant-plant competition in the rhizosphere.

Results:

Hypotheses 1.3.1. Protozoa affect size, turnover, diversity and function of microbial communities in the rhizosphere and 1.3.4. Protozoa increase the resilience of the microbial community.

We isolated species of different protozoan taxonomic (amoebae, flagellates, ciliates) and functional groups (bacterial, fungal feeders) from soil. An abundant soil amoebae (*Acanthamoeba* sp.) was selected as model-organism and in cooperation with Prof. M. Wagner, TU-München, TP2) could be genetically related to the *A. castelanii* group. We transferred this naked amoebae with specific soil bacteria in monoxenic cultures. The effects of amoebal grazing on the diversity of rhizobacteria and root growth of experimental plants have to be tested in subsequent experiments.

A first protoype of a new microbial respirometer has been constructed in our department in order to measure microbial activity, biomass, turnover and functional attributes on a microscale.

Investigations of microbial diversity with molecular approaches are currently in progress.

Hypothesis 1.3.2. Protozoa increase plant growth by changing the microbial community in the rhizosphere, by increasing nutrient cycling and hormonal effects.

In cooperation with Prof. I.T. Baldwin (MPI for Chemical Ecology, Jena) and Dr. B.S. Griffiths (Scottish Crop Research Institute, U.K.) we are currently investigating the interactions of protozoa and root-feeding nematodes in the rhizosphere of tobacco plants (*Nicotiana attenuata*). Root herbivores such as nematodes are known as crop pests and may strongly affect plant diversity in the field. Current studies, focussing on effects of visible above-ground herbivory, demonstrated that tobacco plants can discriminate attacks from different above-ground herbivore species. About 500 plant genes are involved in the 'recognition' and specific defense strategies against different herbivores. However, the mechanism of plant response to below-ground herbivores is not yet known. In addition, the interactions in the rhizosphere are complicated by species interactions. Protozoa are known to increase root biomass due to hormonal effects from grazing on rhizosphere bacteria. Root-feeding nematodes commonly have the opposite effect, but leaking of root cell contents due to nematode feeding might fuel growth of rhizobacteria and stimulate subsequent effects of protozoan grazing. We aim to get deeper insight in the molecular regulation of root growth and plant defense to attack from root herbivores.

Hypothesis 1.3.3. Protozoa increase plant growth via interactions with mycorrhiza.

An experiment in cooperation with Prof. G. Bécard (C.N.R.S., Toulouse, France), testing effects of protozoa and AM-fungi on growth of *Plantago lanceolata* is currently in preparation.

Hypothesis 1.3.5. Protozoa affect the competition between plants via species specific effects on microbial communities and root morphology.

In cooperation with Dr. J. Roy (C.N.R.S., Montpellier, France) we investigated the influence of microbial diversity on growth and competition among grasses in experimental microcosms.

The performance of the six different grass species was highly dependent on soil diversity (F = 13.0, p = 0.0001 for the interaction plant species x soil diversity). A subsequent regression of the average shoot biomass per plant species in a sequence of increasing soil diversity (sterile < microorganisms < microfauna < mesofauna) was taken as a measure of plant performance in relation to soil diversity.

The homogeneity of slopes (ANCOVA), gave significant differences for three out of the six investigated plant species. A significant negative slope (F = 4.4, p = 0.04) for *Bromus hordeaceus* indicated a decrease in shoot growth with increasing soil diversity in monocultures. *Bromus* species turned out to be weak competitors in mixtures compared to monocultures. Particularly *B. hordeaceus* gained the lowest shoot biomass in competition with other plant species in the mixture treatment. However, with increasing soil diversity shoot biomass of *B. hordeaceus* increased in plant mixtures (F = 4.8, p = 0.04). This was due to a release of *Bromus* from competition with *Aegilops geniculata* (F = 5.3, p = 0.03) and *B. madritensis* (F = 15.8, p < 0.001) which both were negatively affected by increasing biodiversity. The two strongest competitors in plant mixtures, *Hordeum murinum* and *Lolium rigidum* did not respond to any soil diversity treatment.

In conclusion, soil biodiversity had strong effects on the performance of certain grasses when different plant species were in competition. Apparently, slight modifications in the fitness of a grass by soil organisms multiplied to strong effects when the plant had to compete with other grass species. Since competition among plants is the natural situation in the field, our experiment indicates that effects of soil biodiversity on grassland community structure have so far been underestimated.

Hypothesis 1.3.6. Protozoan effects on plant growth depend on the diversity of the faunal community in the rhizosphere.

This hypothesis is tested by including other faunal groups in experiments with soil protozoa (see examples in hypotheses 1.3.2. and 1.3.5.). Our preliminary results indicate that species interactions in the soil food-web are of major importance for understanding faunal effects on rhizosphere microorganisms and plant growth.

Project ID: 01LC0101 (Subproject 1)
01.04.2001-30.09.2003

AN ANALYSIS OF PREVAILING ECONOMIC AND POLITICAL STRATEGIES FOR THE PROTECTION OF BIODIVERSITY - THE TRADE IN GENETIC RESSOURCES: A VIABLE CONTRIBUTION TO THE PROTECTION OF BIODIVERSITY?

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Keywords: biological diversity; genetic resources; public good; property rights; access and benefit sharing, value, trade

Abstract:

It is the purpose of this sub-project to assess the potential to contribute to the conservation of biodiversity of the international trade in genetic resources (GR). Initial results show that the contribution of the trade in genetic resources to the conservation of biological diversity probably will be limited even without taking into account the concerns unsually cited here, e.g. the incomplete implementation of relevant international legislation or the possibly inefficient use of monetary returns by providers of genetic resources.

Results:

Genetic resources are often considered as one of the major contributions of biodiversity (Swanson 1996). In addition, it is often assumed that genetic resources are the major privatizeable good in the vector of outputs produced by biodiversity. We define, for the purpose of our study, as genetic resources (GR) only biological material the *genetic information* of which is directly used by a potential recipient. The biological material itself (e.g. wood or a medical plant that is used as raw material, i.e. a pharmaceutical is directly extracted) is not regarded as a genetic resource here since it has different economic properties: biological material is a rival, exclusive good. Genetic information, to the contrary, is a public good as soon as the biological material it is embedded in is publicly accessible. Exclusive possession of a biological material implies the exclusive possession of the genetic information contained. Access to a genetic resource in this case can be provided via sale of the material, or via a contract that entitles the providing party to a percentage of the income derived from this genetic information. Accordingly, legal experts discussed as a major problem the implementation of legislation to regulate access and benefit sharing (e.g. Glowka 1997). Economists, on the other hand, tried to assess supply of and demand for genetic resources, including the problem of of transboundary habitats, that may cause ‚races to the bottom‘ of market prices of genetic resources[1]. Recent economic research also focuses on the survey of bilateral contracts in order to examine their design and economic efficiency (e.g. Rausser and Small 2000).

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[1] A related problem is the fact that biodiversity- rich areas amy be substituted, in part, by *ex situ* collections in a partial consideration, i.e. if only the production/conservation of genetic resources is looked at.

We follow a more specific, theoretical approach in the first part of our analysis. We consider appropriabilities in the GR-related industries and markets, i.e. in all phases of GR-related research and development (R&D) processes and marketing of respective R&D results. We examine different institutional frameworks (legal rights of exclusion) and their potential effects on property rights as defined by Barzel (1989). Initial results gained in the area of plant genetic resources for food and agriculture (PGRFA) show that weak property rights have a major impact on the market value of genetic resources. These property rights, however, do not simply depend on an institutional framework (i.e. legal rights of exclusion) that can be created and implemented at the discretion of the national or international lawmaker, since the physical properties of the materials and R&D processes involved largely determine the possibilities of effective legislation, mainly by influencing the enforcability of contracts and/or intellectual property rights. Inherent public good aspects, however, are likely to be much smaller in other industries.

Further study will focus on the assessment of the gap between the social and private value of genetic resources, and on the potential of (international) legislation and implementation of existing legislation to close this gap.

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01.04.2001-30.09.2003

AN ANALYSIS OF PREVAILING ECONOMIC AND POLITICAL STRATEGIES FOR THE PROTECTION OF BIODIVERSITY - THE PROTECTION OF BIODIVERSITY: NEW APPROACHES AND INSTRUMENTS IN INTERNATIONAL LAW

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Keywords: biological diversity; international regimes; international law, economic incentives, transfer mechanisms; institutional coordination

Abstract:

The protection of biodiversity is a relatively new objective for the international community. In 1995, the prevailing international treaty in the field, the Convention on Biological Diversity (CBD), entered into force. Its efficient implementation, however, has yet to be achieved. Another unresolved task is the harmonization of this new objective with related goals (e.g., the protection of species, landscapes, or cultural achievements of indigenous peoples) and the effective adaptation of the existing system of international law towards this objective. The task includes, inter alia, innovative mechanisms with respect to financial transfers. Her, the existing international regime aiming at the protection of biodiversity is analysed. Economic analysis focuses on incentives provided by available instruments. Legal analysis focuses on the identification and examination of existing treaties and regulations that often do not mention ‚biodiversity' but focus on elements thereof. The systematic connection of these international treaties is analysed. Our final goal for this first part of the BIOLOG project is directed towards the description of possibilities of efficient implementation and institutional coordination at the international level.

Results:

The term ‚biodiversity' requires and promotes the joining together of regimes and instruments that have originally been intended to promote the protection either of ‚parts' of biodiversity (e.g., single species) or of areas (e.g., certain landscapes) with existing regimes especially designed to protect biodiversity (maily the Convention on Biological Diversity (CBD, entered into force in 1995), with bodies of the United Nations in charge of environmental problems (e.g., the United Nations Environmental Programme (UNEP) and the Commission on Sustainable Development (CSD)), and with to-be-constructed new instruments.

In the actual phase of the project, we concentrate on an analysis of existing international regimes and instruments. We identified a considerable amount of international regimes and instruments the objective of which is the protection of biodiversity-related elements. The origin of most of these treaties is pre-CBD; they do not usually refer to the ‚biodiversity' directly. Most of these regimes do not have mechanisms for international financial transfer. Reseach with respect to the legal aspects of these instruments has largely focused on problems related to the collision of norms between different regimes (e.g. Raustiala, 1997). Aspects of institutional coordination, however, only rarly have been examined in-depth. Economic research, on the other hand, has analysed incentives provided by these regimes, and incentives of differents regimes have been compared to each other (e.g. Moyle 1998). Results of these economic approaches led to the proposal of potentially more effective new instruments. Aspects of compatibility of these instruments with the existing system of international regimes, however, have been largely neglected by most of these approaches.

We identified as one major goal, at the theoretical/analytical level as well as with respect to the actual implementation of biodiversity-related regimes, the systematic joining together of existing treaties, instruments, and regulations that have potential to contribute to the protection of biodiversity-rich areas with available mechanisms of financial transfer(s). Another major objective, again at the theoretical/analytical level and with respect to the actual implementation, is the analysis and development of possibilities to impose sanctions on countries that do not comply with the objective of the conservation of biodiversity. Both aspects involve very complex problems already at the level of international law and governance. Our preliminary conclusion is that there are serious problems to be solved at the international level, and that the constant degradation and the progressive loss of biodiversity is not a problem of implementation at the national level alone.

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BIOLOG AFRICA

BIOTA

Project ID: 01LC0024 (BIOTA Southern Africa)
01.10.2000 – 30.09.2003

A RESEARCH PROJECT MONITORING AND ANALYSING BIODIVERSITY AND ITS CHANGE ALONG A TRANSECT IN NAMIBIA AND SOUTH AFRICA

BIOTA Southern Africa is located in Namibia and the Republic of South Africa. BIOTA Southern Africa has an integrated interdisciplinary research approach on biodiversity in Africa that includes the following disciplines: animal production, botany, climatology, modelling, mycology, remote sensing, socio-economics, soil science, and zoology.

The project is active along an approximately 2000 km long transect that extends from the Mediterranean Fynbos Biome at the Cape, the semi-arid Mediterranean Succulent Karoo Biome, the arid Desert Biome, the semi-arid tropical Nama Karoo Biome up to the tropical semi-arid Savanna Biome. Based on this transect approach, the target area of BIOTA Southern Africa covers the entire area parallel to the main rainfall gradient, from the temperate Cape with its winter rainfall climate up to the semi-humid Kavango region of north-eastern Namibia.

Within the three BIOTA AFRICA regional projects, BIOTA Southern Africa examines the most arid regions. Hereby, the project activities are located at either margin of the arid subtropical high pressure cell (wider Karoo-Namib region).

Scientific goals of BIOTA Southern Africa

The need to develop new strategies to deal with the dramatic environmental changes in Africa is a fundamental challenge to the scientific community. The protection and management of biodiversity plays a key role in such strategies. The overall goal of BIOTA Southern Africa is to gain knowledge for decision-makers for a feasible and sustainable management of biodiversity. Within the framework of long-term interdisciplinary fieldwork, applicable land use systems are analysed in combination with scientifically based conservation concepts for the resource biodiversity. Socio-economic information is fundamental for the comprehension and the management of the systems.

In order to understand the bio-physical and socio-economic drivers affecting biodiversity, some relevant questions are:

- To what extent are environmental factors responsible for biodiversity?
- How important are abiotic and biotic soil compartments and mechanisms?
- How important are slow processes and preceding environmental and evolutionary history?
- What are the mechanisms by which land use practices control biodiversity and vice versa?
- How important are spatial movements of taxa and environmental factors?
- Are future changes of biodiversity predictable?
- What is the social, economic, and political importance of biodiversity and how can it be valued?

In contrast to dense rainforests, relatively open savanna, shrubland, and semi-desert vegetation allow a more convenient long-term monitoring. In these semi-arid vegetation types, BIOTA Southern Africa has established a standardised monitoring approach that considers the following aspects:

- Based on remote sensing and GIS, a large-scale approach monitors changes to vegetation structures, to soil characteristics, and to biodiversity within a specified transect band.
- More than 30 *Biodiversity Observatories* have been established along the transect band. These *Observatories* represent a large number of major ecosystems and vegetation units.

- Often, these *Biodiversity Observatories* are arranged in pairs, in identical ecosystems, but exposed to different land use practices. This allows the identification of management practices and land use intensities and their impact on natural resources.

Biodiversity Observatories ensure the comparability of research sites within the BIOTA Southern Africa project. The standardisation of scales and applied methods, as well as the integration of different disciplines in a defined research area are the major advantages of this research approach.

Priorities of the first months

Directly after the start in October 2000, and after the formation of the working groups, BIOTA Southern Africa principally focused on the following important issues:

- Strengthening links with the partners and research institutions in Namibia and the Republic of South Africa (MoUs, contracts)
- Strengthening links with landowners and local communities (MoUs, contracts)
- Preparation and carrying out of a first Kick-Off-Trip with all project heads
- Organisation / establishment of the project´s infrastructure (field equipment, cars, weather stations, logistic and research stations, surveyors, permits)

Practical steps of the first months

As a result of these activities, all practical preparations for the field work had been completed by April 2001, and can be summarised as follows:

- Several workshops were organised by our Head office in Hamburg/Germany. Three workshops took place during the Kick-Off-Trip in March and April 2001 in the host countries (two in Cape Town, one in Windhoek). The detailed and multidisciplinary presentation of BIOTA Southern Africa´s intentions and methodology were discussed with the scientific community of Namibia and the Republic of South Africa. The project initiative was welcomed, and in some cases an even stronger integration into the national scientific communities was requested. Based on the motivating spirit of co-operation, clear agreements on the future co-operation were defined. The formation of the "South Africa BIOTA Liaison Committee" (SABLC) will guarantee transparent discussions and support well-founded decisions on the future and joint development of the BIOTA AFRICA project in South Africa.
- A number of more technical matters had to be settled: six cars, technical field equipment, and weather stations were bought. The issues of registration, insurance, and safe storage were solved.
- 30 *Biodiversity Observatories* and a very large number of additional sampling sites have already been established in co-operation with national and local institutions and landowners. For an easy orientation in the field, the *Observatories* have been subdivided into 100 hectares, and numbered. Weather stations were installed and have started with data recording. For all sites, monitoring protocols and general rules were defined, under which field work in the *Biodiversity Observatories* is to be carried out.
- For a large proportion of *Observatories,* first inventories of organisms have been documented. This baseline information can be used by all scientists who work in accordance with the scientific needs as defined by the Namibian and South African scientific community and responsible institutions.
- At several conferences, preliminary field results have been presented to a broad scientific community, and discussion papers are in the making.

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01.10.2000 – 30.09.2003

REMOTE SENSING AND GIS BASED SURVEY OF SPATIAL AND TEMPORAL BIODIVERSITY DYNAMICS AND ANALYSIS OF BIODIVERSITY AND GEODIVERSITY INTERRELATIONSHIPS

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Key words: Remote Sensing, GIS, Biodiversity-Geodiversity, Monitoring, Vegetation Mapping, Capacity Building

Abstract:

This project shall create the basis for a system in which both, remote sensing and GIS applications, form an analysis and monitoring system for the assessment of human impacts on biological diversity. It is our aim to make the existent biodiversity more understandable and predictable, taking into account the UN-Convention on Biological Diversity (UNCBD).

It is planned to establish a coherent GIS along the entire BIOTA transect in order to allow the analysis of spatial patterns of biodiversity, its temporal changes and the mutual dependency of geodiversity and biological diversity. Focus will lie on the comparison of natural ecosystems with those where socio-economic activity has led to various degradation levels of the former natural ecosystems. Furthermore, the detection of indications of spatial patterns of diversity by remote sensing techniques will contribute to future monitoring and conservation concepts.

Further tasks are the "capacity building" for co-operating partners within the fields of Remote Sensing and GIS.

Results:

Within the last 14 months the data base of a Remote Sensing based GIS for the monitoring of present-state biodiversity within the Southern African transect was built up (1). In close interaction with the project partners the different localities of field work were identified during a field trip in March and respective observatories were geographically referenced.

Tasks performed included first of all the investigation of appropriate multitemporal data sets from commercial multispectral remote sensing systems (LANDSAT-7-ETM, IKONOS, CORONA etc.). A set of LANDSAT-7-ETM scenes was acquired, covering the identified biodiversity observatories along the transect. All satellite scenes ordered were georectified to the common UTM system and were integrated as image base into the GIS. Additionally, aerial photogrphs of the Namibian observatories were georectified and added to the data base.

Besides Digital Chart of the World (DCW)-data basic GIS data (topography, infrastructure) were integrated into the spatial database at a scale of 1: 50.000. For Namibia, the integration of farm boundaries, settlements, river and road networks has been completed, whereas Southern African data based on topographic maps at 1: 50.000 are partly still being processed. These primary informations were further used to produce geometrically referenced image maps which are essential as an auxiliary means for the orientation of the fieldworkers. They also act as a base for mapping training samples which form the basis in the supervised classification of vegetation patterns from the multispectral images (2, 3). The maps were enhanced by topological information (roads, settlements, farm boundaries) and were superimposed by a fine resolution latitude/longitude grid in order to facilitate orientation in the field and to enable the direct comparison of GPS recordings with mapped features. The maps were distributed to the project partners in paper printed form. On request, digital maps were also supplied.

An important feature of a spatial database supporting biodiversity analysis in a more indirect way are topographical data (4, 5). They form not only the basis for the absolute geographical orientation of features in space, but are essential to derive topoclimatological information like potential water and solar irradiance distributions in the terrain (6, 7). Due to the lack of fine scale topographical maps, interferometric analysis of European Remote Sensing Satellite (ERS)-tandem data has been performed to derive Digital Terrain Models from the research areas. Respecive data for Namibia have almost entirely been processed. For Southern Africa, topographic information to produce Digital Terrain Models is being purchased at the moment, as appropriate ERS-data are lacking. Due to the importance of spatial climatic data for biodiversity modelling, research had been carried out on downscaling spatially coarse climatic datasets in order to derive climatic information on a spatial scale which is compatible to the scale of the research approach (8, 9).. Up to now, long term (1960-1990) precipitation and temperature data have been downscaled to a spatial resolution of 5km and 2 km, respectively, as long-term monthly means. In the near future it is intended to add additional climatic parameters and to cover the area with non-aggregated monthly mean data.

Resulting from various field campaigns by the project partners of subprojects S05 and S06 vegetation training samples have been integrated into the spatial database for study areas at the Richtersveld/Fish River Canyon, the Knersvlakte and the Wlotzka´s Baken area. Based on these samples vegetation maps have been derived from respective LANDSAT-7-ETM scenes. Validation of these maps is in progress.

To support the use of spatial data and information systems by the project partners two capacity building activities took place at the DLR in Cologne and at the Institute of Botany in Hamburg. Topics of the first course were primarily remote sensing basics with a special emphasis on sensor sensitivity, reflectance of different surfaces, and generation and interpretation of false colour composites. The second course held in Cologne focussed on Remote Sensing basics in combination with GIS architecture for biodiversity research and monitoring (11). Topics like general data structure, the integration of referenced geospatial together with Remote Sensing data and the main steps for building up of an information system were dealt with. Integration possibilities of raster and vector based spatial data with ecological/biological attributes stored in databases were addressed partially.

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EDAPHICAL DIVERSITY AND BIODIVERSITY IN MUTUAL DEPENDENCY

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Key words: soil variability, pH value, Namibia

Abstract:

Soil as one major compartment of terrestrial ecosystems has a significant impact on the composition of terrestrial flora and fauna and vice versa. The soil science BIOTA project aims to analyse the mutual dependency of the soil as a controlling factor of biodiversity along the entire BIOTA transect following a continental climatic gradient of high geodiversity. The documentation of the soil diversity, especially with respect to the interdependency of soil, flora and fauna, requires a standardised and applicable methodology which proofs to be powerful also in the analysis and interpretation of land use practises and management strategies. This includes the selection of useful indicators to document the influence of soil parameters on the biodiversity.

General Aims:

The main focus of the Soil Science BIOTA project lies on the inter-disciplinary approach to analyse the structures, reasons, processes, and impacts of biodiversity along a gradient-orientated transect. The hypothesis that a higher variability in abiotic parameters in a given area will necessarily lead to a higher biodiversity is to be proofed. Considering that abiotic parameters are of varying importance to flora and fauna depending on the biotic group to be analysed, this project does not only focus on a standardised documentation of soil diversity, but also considers the problem of scale. Different methodological scales have to be applied when analysing (a) changes in soil parameters according to changes in vegetation units and/or analysing the effects that single bushes or trees have (b) on animals (shading effect) or (c) on plants (safe sites for germination). Important questions to be answered include whether or not a systematic nutrient or salt accumulation takes place, which effects small burrowing mammals create on soil properties and wether soil crusts by cyanobacterias or lichens have an impact on the nutrient cycle of the soil and thus again on the biotic diversity. Furthermore, the impact of different land use practises on the geodiversity will be analysed. As one major abiotic part of terrestrial ecosystems the soil and thus this project forms an important explanatory and functional link between the various biotic aspects (fauna, vegetation, lichens, crusts, fungi) within the BIOTA project.

Results:

In this first phase main focus lies on the testing of soil spatial variability in the Biota observatories. For the selection of the sampling sites within the observatory a stratified random procedure was developed, in which the observatories are stratified in different habitat types, according to topography, vegetation patterns etc.. Each hectare square is assigned to a habitat type.

During the first field work phase in 2001 seven observatories along the Namibian part of the BIOTA transect were investigated. A total of 134 soil profiles each with a depth of 0,6 to 1,5 m were described by field parameters, documented by photos and sampled for laboratory analysis. The following table gives an overview on the analysed observatories and the number of soil profiles.

Tab. 1: Sampled Biota observatories with number of soil profiles

Observatory	**Number of soil profiles**
01 Mile 46 Research St.	6 (T)
02 Mutompo	20 (R u. T)
03 Sonop Research Station	12 (T)
04 Toggekry 250	40 (R)
05 Otjiamongombe West	26 (R)
10 Gellap Ost	15 (R)
11 Nabaos	15 (R)

R = by ranking T = Transect

Where appropriate, the standardised sampling routine following the ranking procedure was completed by a local transect approach, e.g. when linear dune systems dominate/ characterise an Observatory (Observatory No 2: Mutompo).

First laboratory results of pH values (in H_20) in the topsoil of all observatories show distinct differences in mean values as well as variability along the transect (Fig. 1) from North Namibia with higher rainfall and more sandy soils to South Namibia with lower precipitation. Within one observatory the different habitat types (by topography, vegetation etc.) are characterised by varying pH values of the topsoils, as shown by Fig. 2 for the example of observatory Toggekry. The habitat types with the higher plant biodiversity (Habitat 1 and 2) are associated with topsoil of elevated mean pH-values and larger pH variability than the other habitat types with lower plant diversity and more sandy soils.

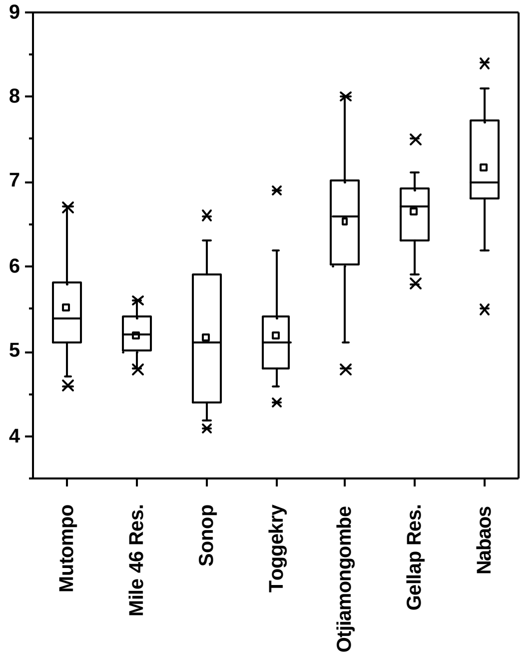

Fig. 1 pH in topsoils: all observatories

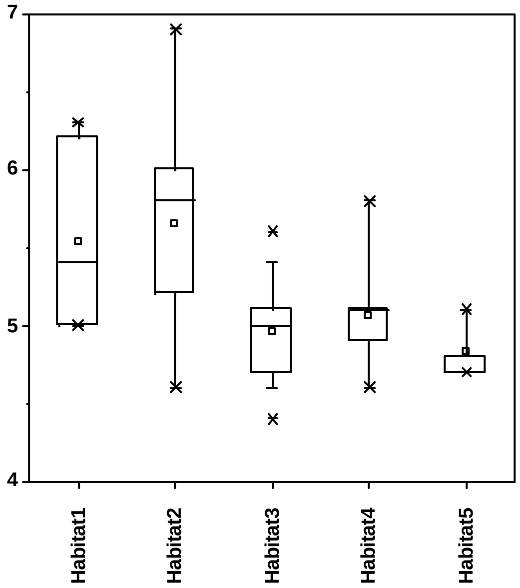

Fig. 2 pH in topsoils: habitats of Toggekry

Project ID: 01LC0024 (BIOTA Southern Africa S03)
01.10.2000 – 30.09.2003

BIODIVERSITY OF SOUTHWESTERN AFRICAN FUNGI: INTERACTIONS WITH HIGHER PLANTS, FUNCTIONAL DIVERSITY AND DNA-TAXONOMY

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Key words: Arbuscular mycorrhizae, Namibia, rust fungi, soil fungi

Abstract:

Our project aims to ascertain data on the biodiversity and ecology of soil fungi, arbuscular mycorrhizae, and plant parasitic rust fungi in important biomes of southwestern Africa. During a first trip to Namibia in March 2001, samples were taken on the observatories Mile 46, Sovo, Sonop 903, Otjiamongombe, Toggekry 250, Gellap Ost 3 and Nabaos 7. First observations and results from this trip are presented here.

Results:

Soil samples examined for the presence of arbuscular mycorrhizal spores revealed differences in the number of spores and – although species identification is still pending – species composition. The dominating spore type in the north (Mile 46 and Sovo) is a small, dark brown *Glomus*-spore, in the thornbush savanna (Otjiamongombe, Toggekry 250) a light brown *Glomus*-spore and in the south (Gellap Ost 3 and Nabaos 7) a small, yellowish-brown *Glomus*-spore. The dominance of *Glomus*-spores is in accordance with the reports by Stutz et al. (1). The number of spores is within the range reported in previous studies from comparable ecosystems (2, 3).

Root samples stained for the presence of arbuscular mycorrhizal fungi were mainly found to be mycorrhizal with the exception of Poaceae in Nabaos 7. As spores were present in soil samples near the plants from which the non-mycorrhizal roots were taken, this warrants further attention. Molecular studies (especially on the samples from Nabaos 7) are under way to check for the presence of non-staining mycorrhizal fungi and to verify the results obtained by microscopic techniques.

The soil samples that were examined for arbuscular mycorrhiza were used for the study of soil fungi as well. Following the procedure of Gams & Domsch (4) the samples were washed with 6 l of water and transferred to isolation media. Over thousand cultures of soil fungi were isolated. A part of the species is already identified, but identification of most isolates is still pending. So far, the isolates that have been identified belong to 20 genera; eight genera seem to be new to Namibia.

The preliminary results confirm the impression gained during the study of arbuscular mycorrhiza, that Gellap Ost 3 and Nabaos 7 are different from the other areas. From the soil in Gellap Ost 3 and Nabaos 7, fewer fungi were isolated. The number of Zygomycetes is especially low, possibly due to the lack of organic litter. The dominating isolate was a Coelomycete. However, in this area samples were taken before the onset of the raining season, while the raining season in the other areas was well under way. Therefore, further sampling is necessary to compare the areas under the same water conditions.

Our work on rust fungi in Namibia aims to contribute to the rust mycota of selected biodiversity observatories and the whole country.

The knowledge about Namibian rust fungi is extremely scanty and mostly derived from the works of Ethel Doidge in southern Africa (e.g. 5). Although the Namibian flora comprises ca. 4.000 species of higher plants (6) our extensive literature search revealed only 13 species of rust fungi (comp. Tab. 1). This species number is extremely low compared with figures available for other African countries [e.g. South Africa ca. 400 (7), Uganda 294 species (8)].

A first species inventory of the BIOTA observatories in 2001 indicates that a considerably higher number of rusts can be expected to occur in Namibia.

Tab. 1: Rust species hitherto reported for Namibia (compiled from literature)

Rust fungi	**Host/Family**	**Host/Species**
Aecidium acanthopsidis H. & P. Sydow	Acanthaceae	*Acanthopsis sp.* Harv.
Aecidium clarum Sydow	Iridaceae	*Ferraria viscaria* Schinz
Aecidium dinteri Doidge	Mimosaceae	*Acacia uncinata* Engl.
Aecidium lebeckiae P. Hennings	Fabaceae	*Lebeckia simsiani* E. & Z.
Aecidium talinophilum P. & H. Sydow	Portulacaceae	*Talinum caffrum* (Thunb.) Eckl. & Zeyh.
Puccinia desertorum Sydow	Convolvulaceae	*Evolvulus alsinoides* (L.) L.
Puccinia chaseana Arth. & Fromme	Poaceae	*Anthephora schinzii* Hack.
Puccinia galeniae Dietel	Aizoaceae	*Galenia africana* L. *Galenia sarcophylla* Fenzl.
Puccinia sorghi Schwein. Syn.: ***Puccinia maydis*** Bereng. Syn.: ***Aecidium oxalidis*** Thuem.	Poaceae Oxalidaceae	*Zea mays* *Oxalis obtusa* Jacq.
Uredo augeae H. & P. Sydow	Zygophyllaceae	*Augea capensis* Thunb.
Uromyces comptus H. & P. Sydow	Convolvulaceae	*Merremia bipinnatipartita* (Engl.) Hallier f.
Uromyces saginatus Sydow	Hyacinthaceae	*Drimia altissima* (L.f) Ker Gawl.
Uromyces trollipi Kalchbr. & MacOwan	Zygophyllaceae	*Zygophyllum* sp. L.

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Project ID: 01LC0024 (BIOTA Southern Africa S04)
01.10.2000 – 30.09.2003

DELVELOPMENT OF AN INTEGRATED SYSTEM FOR THE INPUT, STORAGE AND ANALYSIS OF BIODIVERSITY DATA IN SOUTHERN AFRICA

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Key words: biological soil crusts, checklists, database, ecological and descriptive data, GIS, GUI, interoperability, functional diversity, LIAS, modelling, Mycology.Net, spatial analysis

Abstract:

A central task of BIOTA subproject S04 was the development of a uniform standardized method for data collection in the field. According to the observatory transect method, all data collected in the field were categorized into four different hierarchical levels. The development of the database module "DiversityEcology", which reflects this hierarchical structure, represents the second major achievement of the project. A third major task is the development of a graphic user interface ("DiversityNavigator") for remote editing and analysis of data being stored in Postgres implementations of database modules, based on the "Diversity" data models, which have been developed within the BIOLOG-project GLOPP.

Results:

Three main issues had to be addressed during the first year of the project:

A) Composition of a common method for the data collection in the field
B) Development of a software structure for the recording, storage and analysis of project data
C) Establishment of a Java-based application („DiversityNavigator") for the request and processing of data from the Diversity Database Modules via internet

A) Composition of a common method for the data collection in the field

One main task of the project is the development of a uniform standardized method for data collection in the field to enable interdisciplinary analysis and modeling. According to the observatory transect method, which forms a common standard of the three BIOTA groups, all data collected in the field could be categorized into four different hierarchical levels. The selection and classification of the parameters, which are collected on the different levels, was realized in accordance to the Database-project SOTER (Global and National Soils and Terrain Digital Databases) of the FAO (FAO, 1995). The uppermost level contains data on the observatories as units, like their geographic coordinates, the vegetation type and the local climate. One level below, data on the habitats delimited against each other within the observatories is combined. On the third level, all data on the sites which are investigated by the researchers are combined. The detailed characterization of the investigated sites is a fundamental requirement for spatial analysis and modeling of the distribution patterns of species. On the undermost level, data on all specimens which are investigated or collected in the field and on the applied sampling method are stored. In concordance with all subprojects of BIOTA South the parameters being collected on the two upper levels of the database were determined and their classification adopted to the local conditions. The parameters of the two lower levels were elaborated together with subproject S05. Only such a standardized interdisciplinary approach facilitates detailed spatial and statistical analyses and the yield of new knowledge.

B) Development of a software structure for the recording, storage and analysis of project data

The implementation of a modern networked software architecture with continuous database access and fully developed GIS analysis functionality was another major task of the first project period. The database SQLServer was chosen as DBMS, since this software also allows to process geographic coordinates. A direct database connect of the GIS-software was realized via an ArcSDE gateway. This software architecture facilitates the storage of all data within a geodatabase, which allows an object oriented data structure. ArcInfo was selected as GIS-software, because of the comprehensive analysis and visualization techniques and the new functionalities in the area of geostatistical analysis. For the analysis of remote sensing and other raster data Erdas Imagine is applied. In the near future, the software ArcIMS will be applied to present the results via internet in the form of interactively generated maps.

During the last months, the database module "DiversityEcology" was created, in which the data collected in the field by BIOTA South (data on the observatories and habitats) and all data collected by subproject S05 are stored. The database module was implemented under consideration of the Relational Model by Codd (CODD, 1990) and the normalization rules. The database "DiversityEcology" is an independent database module, that has an interface to the other existing Diversity Database modules. The data input in the database module is realized by a graphical user interface (GUI), that facilitates the input and editing of the acquired data via internet.

C) Establishment of a Java-based application („DiversityNavigator") for the request and processing of data from the Diversity Database Modules via internet

The database modules being developed in the BIOLOG-projects GLOPP (01LC9905) and now being provided to public on the Internet (www.glopp.net) offer suitable tools for the maintenance of taxonomic data (DiversityTaxonomy), literature (DiversityReferences), descriptive data (DiversityDescription) and collection data (DiversityCollection). Their implementation under MS Access will be completed in the near future. The establishment of the Java-based graphic user interface "DiversityNavigator", established in Biota S04, will allow an Internet-based, platform-independent usage of these databases. The first period of this project was dedicated to the establishment of various program technical basics like the definition of data exchange formats, the establishment of data import routines and an experimental prototype network, as well as the establishment of Diversity-compatible Postgres databases. A recently completed draft version of the DiversityNavigator enables the user to import and edit the taxonomic and collection data, stored in Postgres databases. It furthermore allows parallel data queries of databases, which may be located under several domains. The interoperability of the modules could be successfully tested by a configuration with the two database modules DiversityTaxonomy and DiversityReferences which enable users to maintain and query species checklist data. In the forthcoming period of the project the established technique will be used to store and maintain all taxonomic and descriptive data gathered in subproject S05.

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Project ID: 01LC0024 (BIOTA Southern Africa S05)
01.10.2000 – 30.09.2003

BIOLOGICAL SOIL CRUSTS OF TERRESTRIAL ECOSYSTEMS: MODES OF PATTERN FORMATION AND THEIR MODELLING CONCERNING DIVERSITY, STRUCTURE AND FUNCTION IN CRYPTOGAMIC COMMUNITIES

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Key words: biological soil crusts, biodiversity, lichens, algae, cyanobacteria, vegetation ecology, microclimate, dew fall, fog

Abstract

An overview of the field and laboratory work performed so far is given and first results are presented. In almost all observatories along the transect, biological soil crusts, composed of either cyanobacteria, algae or lichens, or a combination of them, have been discovered. Biomass, expressed as milligrams chlorophyll a per m², ranged from 1 to 80 mg/m². So far, 14 genera of cyanobacteria, 21 genera of green algae and 32 lichen species have been determined. A new species of the lichens genus Peltula *was discovered growing underneath translucent quartz pebbles with an inverse internal thallus morphology.*

Special care was given to the establishment of measuring devices for fog and dew fall along a 40 km long gradient from the coast to the inland at Wlotzkasbaken, Namib Desert, in order to correlate this data with the vegetation pattern of lichens.

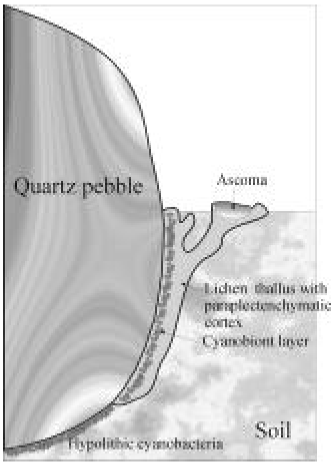
Results

It is the intention of our project to study the species (cyanobacteria, algae and lichens) diversity, pattern formation and biomass of biological soils crusts and their role in the ecosystem. We want to find out their dynamics, their establishment after disturbance and their influence on the diversity of the phanerogamous vegetation (e.g. N input via cyanobacterial N-fixation).

Three of us took part in the kick-off trip and actively participated in the selection of the observatories. A key on the priority of interest was developed and assigned to the newly established observatories. High priority was granted to observatories with well-developed biological crusts and high lichen diversity (12 observatories). Intermediate priority was assigned to observatories without biological soil crusts, but with a rich epiphytic and epilithic lichen flora (8 observatories), where only biodiversity studies are carried out. Observatories without biological crusts or lichens will not be investigated by S05 at this stage.

During this trip, first collections were made and a very rough estimation of the presence or absence of soil crusts of each observatory was achieved. At each investigation site, 4 samples were collected for the following purposes: determination of a) cyanobacterial diversity, b) green algal diversity, c) N- and C-content as well as the isotope fractionation, d) chlorophyll a/b content. Two main classes of crusts can be distinguished 1) pioneer crusts (succession stage after disturbance) and 2) climax crusts (part of permanent vegetation). Further differentiation can be made according to the dominating taxonomical group (e.g. cyanobacterial, algal, lichen or moss crust). Determinations of biomass, expressed as chlorophyll a content per m², resulted in values between 1 and 80 mg/m², with an average of 33 mg/m² for the first 16 samples along the transect. However, this can only be seen as very preliminary results. This is also the case for the first diversity analysis of cyanobacteria and algae. In total, we found cyanobacterial species (free living and in culture) belonging to 14 different genera and green algal species (in culture only), belonging to 21 different genera.

In the Nama Karoo, a new species of the lichen genus *Peltula* was discovered (fig. 1), growing underneath quartz pebbles, exposing its cyanobiont towards the quartz and thus having an inverse internal morphology. The new description of this species is in preparation and will be published in 2002.



An additional transect from the coast 40 km to the inland was established in the lichen field of Wlotzkasbaken, meeting the observatory in the center. Along this transect, measuring devices for fog and dew fall were installed in order to gather data on the events and amount. Those results will be correlated with the very peculiar vegetation pattern of lichens in this area. The biodiversity of the lichen vegetation along this transect was investigated on 21 stations and to a distance of 35 km from the coast. Close to the coast, lichen coverage rises distinctly for a short distance, then diminishes constantly inland along the transect. Most species occur from the coast to the end of the investigated transect section, frequency of some species however changes dramatically. At least one species occurs only at inland stations, several occur only near the coast.

Lichens were collected in the observatories 18 (Koeroegap), 20 (Numees), 21 (Groot Derm 10), 22 (Quaggafontein 478), 26 (Faminkvlakte 111), 27 (Luiperskop 211), 28 (Moedverloren 208) and 29 (Rocherpan) in order to investigate the general biodiversity. In the observatory of Numees vegetation relevés on soil were also carried out by means of a new method. It consists of taking digital pictures of cryptogamic communities on a soil surface of 60 x 60 cm using an aluminum square frame construction. Since May 2001, lichens have been identified in the laboratory. TLC was applied to many samples. Problematic specimens of various genera were sent to specialists. A first list of lichens forming biological soil crusts includes 32 species. Information on lichen characters are entered into a Diversity database module, and those on lichen specimens in the collection database module (http://www.-diversitycam-pus.net). For the analysis of digital pictures, the program PanoramaFactory (freeware) is used to compose the entire relevé of 60 x 60 cm from 36 single digital pictures.

Project ID: 01LC0024 (BIOTA Southern Africa S06)
01.10.2000 – 30.09.2003

CHANGES IN BOTANICAL BIODIVERSITY WITH REGARD TO CHANGES IN LAND USE PRACTICES AND CLIMATE: STANDARDISED MONITORING AND TRANSECT ANALYSIS

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Key words: Phytodiversity, vegetation mapping, community ecology, population ecology, population dynamics, monitoring, land use impacts, desertification

Abstract: *Vegetation plays an important and multidirectional role within the mechanisms that control biodiversity. Firstly, vegetation forms an important resource for humankind and is strongly influenced by land use practices. Secondly, vegetation is controlled by environmental factors and, therefore, is an indispensable indicator for documenting ecological changes. Thirdly, due to its structural, biological, and ecological properties, vegetation itself is an important driver of biodiversity. The botanical subproject S06 aims at long-term analyses and monitoring of the vegetation in over 30 Biodiversity Observatories.*

Results:
Earth's biodiversity includes *"all organisms and species, their immense genetic variation, as well as their complex assemblages of communities and ecosystems..." DIVERSITAS* PROGRAM Based on this broad definition, S06 integrates the assessment and analyses of structures and mechanisms at different temporal and spatial scales. The development of a general working protocol will supply all surveyors with a standardised methodology for all Biodiversity Observatories.

Structural diversity: The mapping of vegetation along the BIOTA transect band, from the Kavango to the Cape, will allow large and medium scale analyses of the vegetation structure. This can only be achieved by the application of remote sensing techniques (S01). The vegetation map is in the validation process. It will serve for an in-depth understanding of the impact of changing natural gradients, e.g. rainfall gradient, as well as the influence of different land use systems [1,2,3].

Community diversity:
The species composition of plant communities reflects environmental conditions. Based on a multi-scale standardised working protocol, a large number of vegetation data were sampled and classified into different vegetation units. Within the 1 km² large BIOTA Observatories, the assessment of the spatial patterns of different communities was carried out on a regular grid of 100 hectare.

Species diversity:
In 2001, for a large proportion of BIOTA Observatories, first inventories of flora and vegetation were documented at four different spatial scales, ranging from 100m², 1,000m², 10,000m² up to 1 square kilometre (Table 1). In some cases, these are linked to demographic analyses of populations and species, focusing on migratory dynamics. Additionally, the monitoring of the BIOTA Observatories also considers the individual and population level (e.g. location, size, number of fruits) [4,5,6]. The long-term monitoring of the permanent plots in the western Richtersveld (South Africa) forms the basis for the simulation models in subproject S10.

Tab. 1: Surveyed Biodiversity Observatories in 2001

Observatory	District, Country	Surveyor
Mile 46 & Mutombo	Rundu, Namibia	B. Strohbach
Sonop 903	Grootfontein, Namibia	B. Strohbach
Otjiamongombe West 44 & Omathako Ranch	Okahandja, Namibia	R. Austermühle
Ovitoto 55	Okahandja, Namibia	B. Strohbach, T. Sheujuange
Wlotzkasbaken, Mile 14	Swakopmund, Namibia	B. Hachfeld
Nico 377 & Reserve	Mariental, Namibia	M. Akhtar-Schuster
Gellap Ost 3 & Naboas 7	Keetmanshoop, Namibia	M. Akhtar-Schuster
Karies 8, Gondwana Canyon Park	Karasburg, Namibia	N. Jürgens
Koeroegap Vlakte	Namaqualand, South Africa	C. Mayer, M. Müller, N. Jürgens
Numees	Namaqualand, South Africa	N. Jürgens
Groot Derm 10	Namaqualand, South Africa	M. Müller, C. Mayer, N. Jürgens
Quaggafontein 478	Namaqualand, South Africa	U. Schmiedel
Leliesfontein 624	Namaqualand, South Africa	U. Schmiedel
Remhoogte 416	Namaqualand, South Africa	U. Schmiedel
Faminvlakte 111	Van Rhynsdorp, South Africa	U. Schmiedel
Luiperskop 211	Van Rhynsdorp, South Africa	U. Schmiedel
Moedverloren 208	Vredendal District, South Africa	U. Schmiedel
Rocherpan Nature Reserve	Piquetberg, South Africa	S. Milton & Co-workers

Intraspecific diversity:

Intraspecific diversity has been established on the level of ITS 1+2 and will be carried out by using AFLP. Samples were taken from the Succulent Karoo Biome (Aspazoma, Cheiridopsis) in August 2001.

Functional diversity:

In 2001, we started with the sampling of diaspore inventories at all BIOTA Observatories in order to understand the dynamics and regeneration capacity of the species. This will be continued. In the Succulent Karoo, recording of ecophysiological adaptations started with regard to salinity stress, ion composition, and water relations at the observatories *Numees* and *Yellow Dune* in the Richtersveld, South Africa.

Further activities: The S06 team is composed of researchers who already have long-term field experience in southern Africa. Due to this, a major part of the organisation and implementation of the project, i.e. the kick-off-trip, workshops, preparation of MoU´s, logistics, and infrastructure was carried out by our team.

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Project ID: 01LC0024 (BIOTA Southern Africa S07)
01.10.2000-30.09.2003

FUNCTIONAL ZOODIVERSITY IN SOUTHERN AFRICA UNDER CHANGING ENVIRONMENTS AND HUMAN USE

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Key words: Functional zoodiversity, food webs, reproduction, population ecology

Abstract:

The main objective of this study is to learn about biodiversity, its composition (taxonomy), how it is functioning and how it can be maintained and managed as seen from a zoologists perspective. In the pilot phase research is focused on small ground living mammals, their reproduction and their interactions with arthropods and plants, especially trophic interrelationships between these groups.

Hypotheses: We hypothesize that

1) specific small mammal communities differ in their direct influence on vegetation and soil characteristics by their digging habits seed dissemination and bioturbation in general;

2) specific small mammal communities directly influence arthropod species richness and abundance mainly due to predation, and thus indirectly affect vegetation communities (consumption of herbivores, pollinators, detritivores...);

3) the differential resource utilisation due to changing nutritional demands of the small mammals in the course of reproduction contributes significantly to vegetation and arthropod community composition;

4) large mammals (in different land use practices) and climate (esp. water availability) influence performance of soil, vegetation, arthropods, and small mammals. Accordingly the functional relationships and ecosystem performance differ between differently managed farms and climatic zones;

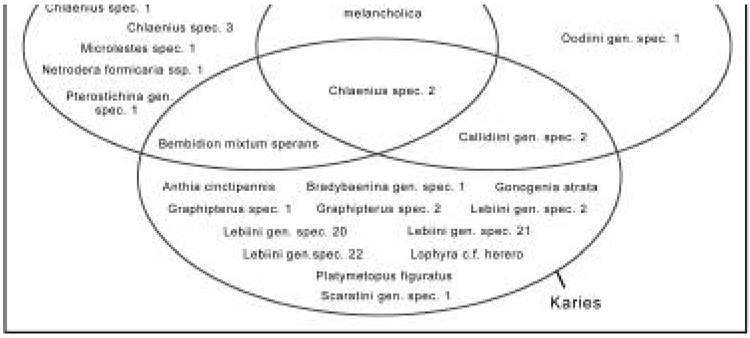
5) the above mentioned indicators of biodiversity can be used for the formulation of management tools with respect to global change.

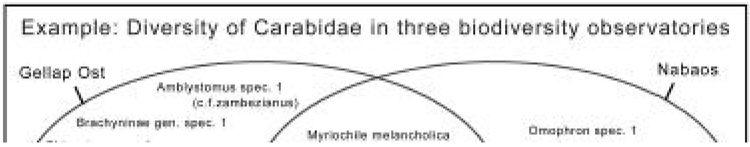
Results:

Investigations took place on iodiversity observatories in Karies 8 (Fish River Canyon), Gellap Ost - Nabaos (Berseba) and Otjiamongombe (Erichsfelde) - Toggekry (Omatako) in Namibia, April - Mai 2001. In South Afrika the biodiversity observatories Yellow dunes, Numees and the Koerogapvlakte at the Richtersveld were sampled in October 2001.

One main goal of the first phase of the project is to develop and optimize adequate methods to long term monitor biodiversity. Plots within the biodiversity observatories were selected according to the ranking method developed by BIOTA-South. A first species inventory was begun. Arthropods were collected with Malaise traps, different light traps, pitfall traps, yellow plates, sweeping nets, pyrethrum fogging and various methods of hand collecting.

A first analysis of the well-known bio-indicator group Carabidae (ground beetles), based on pitfall trap and light trap sampling as well as singling, showed the following results:

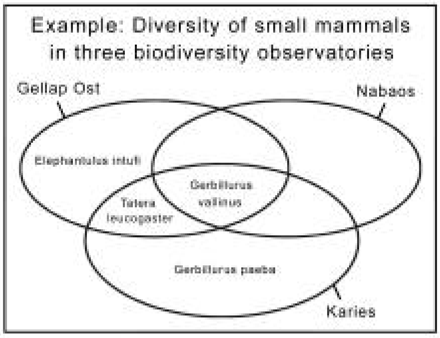




Whereas the differences in species inventory, diversity and abundance of the ground beetles communities between Karies and Gellap Ost are obviously due to meteorological, geological, geobotanical, zoogeographical and geographical factors on the BIOTA transect, the great difference between the Karakul sheep research farm Gellap Ost and the over-grazed observatory Nabaos results from the influence of different land use.

Trapping for small mammals consisted of a 150 m transect holding 30 Sherman traps and three bucket traps with some additional traps selectively placed in bushes and trees. The composition of trapped species reflected the assumption according to literature research; except for *Mus minutoides*, for which the most nothern record could be supplied for the Koerogapvlakte in the Richtersveld.

Comparable to the arthropods, small mammals differ in their species composition and abundance according to the position on the BIOTA transect and the intensitiy of land use. Again Nabaos is impoverished in biodiversity, only the widely distributed *G. vallinus* was trapped.



To analyse trophic relationships, the stomach content of selected small mammals was investigated. For this, the stomach was removed from the dead animal and emptied completely. The volume was measured and the content was first analysed according to volumen relations. A detailled analysis on a more elaborated taxonomic basis followed.

Anatomy of the reproductive tract and embryology of most trapped small mammal species was only poorly or not at all known. First results show that the anatomical structure and reproductive status of the animals deviated from other well documented animals. These data provide a necessary basis for the newly developed method of ultrasonic investigation for the in-vivo determination of the reproductive status in the field.

Discussion and outlook

Monitoring zoological biodiversity is a compromise between effort and results. We can either cover the transect of observatories completely, focus on selected biodiversity observatories to obtain a more comprehensive data set, or record annual cycles.

The last point will be approached for the adjacent biodiversity observatories in Gellap Ost and Nabaos, as here studies on population dynamics on small mammals have started to gather information on population processes and time slots for reproduction. For the main phase, more emphasis will be put on population processes, and functional hypothesis approximated by first models will be tested in the field.

Another point concerns sustainability, which can only be achieved if the project is accepted both in Namibia and South Africa. For this, we are working on the implementation of a MSc-course in "Functional Biodiversity" in cooperation with the University of Namibia. Furthermore, native students are introduced into our project and employed in.

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01.10.2000 – 30.09.2003

DIVERSITY OF NAMIBIAN DRAGONFLIES: EFFECTS OF ANTHROPOGENIC CHANGES AND MODELLING ON DIFFERENT SCALES

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Key words: Odonata, ephemeral rivers, species and community diversity, population diversity, isolation, habitat suitability, population development, distribution maps.

Description of the project and first results

The aim of our project is the development and application of a system for the modelling of Odonata diversity — on population, species and community level — in arid and semiarid regions of Africa. The model-system will help to understand the dynamics of Odonata communities and to evaluate different scenarios of global change and anthropogenic effects for ecosystem-management. Odonate diversity can be used as an indicator in this context.

Faunistic survey, monitoring and experimental studies

The Odonata fauna of Namibia consists of 100 species (Martens et al. in prep.). The highest species diversity – reflecting the presence of permanent rivers – is in the NE (Jödicke & Martens in prep.). To study diversity in arid regions on the species and community level we survey the Odonata of about 250 aquatic habitats in the western catchments, namely the Swakop, Kuiseb, Tschauchab, Ugab, Huab and Hoanib, and, additionally, in the Fish river. We recorded 52 species in these systems. We characterized the environment and the geographical situation of all sites. Based on these data habitat suitability models (see below) will help to evaluate the relevance of factors like habitat duration, vegetation, salinity, altitude and connectivity for the structuring of Odonata assemblages and the distribution of species. A number of sites are selected for long term monitoring to study phenology and variations in assemblage structures. Using artificial pond systems we studied habitat selection, life cycles, phenology, and priority. Our studies revealed clear patterns of habitat choice via oviposition, which effects larval density in different structured ponds (Suhling et al. 2001). All species of these ponds were able to develop within less than two months; *Pantala flavescens* requires only 31 days from oviposition to emergence. The short development allows species to use even short existing habitats and may be a major trait of desert Odonata (Suhling et al. in press). The field studies are accompanied by laboratory experiments, which revealed clear effects of priority, growth rate and intraguild predation in a two species assemblage, combining the widespread species *Trithemis kirbyi* and *Sympetrum fonscolombii*.

Molecular genetics

The molecular genetic analyses of several ncDNA and mtDNA marker reveal first data on the genetic diversity and genealogical relationships of the selected study species. The data provide first insights into spatial and temporal dynamics of selected key-species in correlation to different ecological settings (see below). The latter will help us to identify pathways used by Odonata to colonize the ephemeral desert habitats, which is not possible with traditional methods. The study includes different geographical scales: (a) between habitats in one catchment, (b) between catchments, (c) between the western catchments and other regions of Namibia (such as the savanna regions in the northeast), and (d) between Namibia and other regions like Kenya, in co-operation with BIOTA E07. Based on monitoring data we selected a set of key species, e.g. *Paragomphus genei*, which exclusively colonizes habitats within the floodplains. Others such as *Crocothemis erythraea* and *Anax imperator* are not limited, since they are excellent flyers. We compare the population structures/dynamics of these species in connection with differences in their mobility. Using additional information on environmental stress related genes (e.g. variation in heat shock proteins) provide insights into the adaptive potential of the selected species. Our study also includes genetic information on rare and extremely isolated species, which is a major task when setting up a conservation management plan. For analyses at the genus level we have chosen *Pseudagrion*, *Orthetrum* and *Trithemis*, which seem to be promising model systems to obtain insights into different stages of speciation and differences in species diversity patterns in combination with recent and historical habitat shifts.

Ecological modelling

Modelling is done on different scales. On the habitat scale suitability and population dynamic models will be developed and applied for selected species. We use logistic regression methods to model habitat suitability. These models are based on presence / absence data together with habitat parameters recorded during the survey (see above). As a result we get probabilities of occurrence in a given habitat for each species. Up to now data of the first survey were explored to find species suitable for modelling and to run first suitability models. For population dynamics we used a model based on “delay-differential-equation”, evolved by Crowley et al (1987) for Odonata of the temperate region. This model was fitted to the specific conditions of tropical desert Odonata using literature data as well as data of our own studies (Schroeder 2001). However, since we found that this model will cause some problems while combining it with habitat suitability models we decided to use the Leslie-matrix model instead, which allows the incorporation of more complex data. On the catchment scale different habitat models are coupled by a geographical information system (GIS) to form a multi-habitat model. To do so we take into account the spatial spread of the individuals and the gene flow between different populations. With this model system we will describe the diversity of Odonata under different scenarios, e.g increase of drought, increase of water use, building of dams. We produce distribution maps (basing on GIS), which allows the application of countrywide models the diversity in the second phase.

Identification keys

As a general preparation we produced keys to the adults and larvae of the Namibian Odonata, which will be published with the National Museum of Namibia, Windhoek. The larval key already allows identification of all genera, but not all species, since a number of larvae are undescribed. The adult key already allows identification of most of the species.

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01.10.2000 – 30.09.2003

STRUCTURAL AND SPECIES DIVERSITY IN SEMI-ARID SAVANNAHS OF SOUTHERN AFRICA: THE IMPACT OF LAND USE AND CLIMATIC CHANGE

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Key words: population ecology, extinction risk, spatial-explicit simulation models, remote sensing, landscape structures

Abstract:

In arid and semiarid savannahs species diversity is strongly influenced by the structural diversity (landscape structures at different scales), which in these systems is characteristically formed by woody vegetation. The southern Kalahari based subproject S09 uses an interdisciplinary approach to investigate these structural-dependent relationships, combining field studies (zoological, botanical, genetic and socio-economic), remote sensing, and spatial-explicit simulation models. The aim of the project is to evaluate the impact of current and realistic future land use intensities and climatic change scenarios on the survival of selected animal and plant species and on species diversity in general.

Results:

According to a basic definition of ‘biodiversity’ (UN Environmental Program 1992) biological diversity means the variability among living organisms and the ecological complexes of which they are part. This not only includes species diversity but also the diversity of ecological structures or ‘structural diversity’. Structural diversity encompasses both functional structures such as food webs and spatial structures, i.e. landscape structures at different scales. Both elements of biodiversity – species and structural diversity – are closely interlinked. Any changes in habitat structure inherit the risk of species loss. The aim of this interdisciplinary project is an improved understanding of the complexity of impacts of landscape dynamics (structural diversity) on species diversity under the major driving forces in the southern Kalahari, namely land use and climatic change.

Structural diversity: - In the case of the southern Kalahari structural diversity is mainly formed by woody vegetation. Major impacts on structural diversity in this system can be addressed to land use and climate change. Land use, e.g. in the form of cattle farming or fire wood cutting have evolved major changes of landscape structure. Socio-economic surveys show, among other results, that the majority of farmers are utilizing camelthorn trees, both for domestic and commercial purposes. Roughly about 20 % of the farmers commercially utilize the wood and remove very large quantities. Long- to mid term changes of tree cover ratios have also been quantified by remote sensing techniques using satellite images and aerial photographs covering the last 60 years. An automatic tree detection software has been developed writing a vector database into GIS. These spatio-temporal data of landscape structure can be compared with existing spatial vegetation models (e.g. Jeltsch et al. 1999) and linked to spatially explicit population models under varying land use and climate change scenarios. In this context a new model focuses on the population dynamics of *Grewia flava,* a common shrub in the southern Kalahari. Cattle-induced shrub encroachment – an ecologically and economically important form of land degradation in savannas - is usually explained in terms of livestock grazing altering shrub-grass competition in favour of shrubs. However, empirical studies and modelling results show that under grazing of domestic livestock shrub seed dispersal in cattle dung has a significantly higher influence on *Grewia* encroachment. This has important implications for land use and management since, once young shrubs have established, encroachment is almost irreversible.

Species diversity: - To understand the impact of climate change and land use on species diversity both directly and via structural diversity, several target species were selected that depend on different elements of vegetation structure (trees, shrubs) on different spatial scales. The target species include animal species (tawny eagle *Aquila rapax*, small carnivores e.g. yellow mongoose *Cynictis penicillata*, tree rat *Thallomys nigricauda*, sociable weaver *Philetairus socius* and others) and plant species (*Grewia flava*, *Lycium sp*. and others). For these species field studies on habitat use, population dynamics and population genetics will be linked with population simulation models. For the tawny eagle first model results show that the viability of the Kalahari-population is directly dependent (i) on the mean of annual rainfall and (ii) on the variability and chronological order of rainfall. It is therefore suggested that possible climatic changes will have a major effect on the survival of this population. Future model investigations will show the effect of changes in vegetation structure (mainly large nesting trees), on the survival of the population. For sociable weavers a metapopulation model has been built to investigate (i) the effect of the spatial distribution of rainfall and (ii) the effect of changes in size and distribution of trees on this population. Similarly to the tawny eagle, preliminary results suggest a strong dependence on rainfall patterns. First results of the field investigations on tree rats show a dependence of the population distribution as well as of the individual behaviour of animals on the spatial structure of trees and shrubs. Further investigations on population dynamics and on population genetics were started and data will be used in a simulation model to show the effect of tree- and shrub structure on the population. In a new study on the effects of land use on the biodiversity of small carnivores in three different grazing regimes (cattle vs. sheep, vs. game) first results show, that yellow mongooses strongly depend on vegetation structure: they dig their sleep and reproduction burrows preferably under shrubs of *Acacia hebeclada* and *Rhigozum trichotomum* (>10 m diameter), whereas shrubs of *Acacia mellifera* were rarely used. Density and distribution of shrubs with an equivalent size differ between the three grazing regimes. The aim of our further study is to investigate the consequences of these observed differences on the composition of the small carnivore guild. Data on vegetation patterns show the importance of *Acacia* trees on the overall plant species diversity and abundance: the number of plant species and total vegetation cover were always higher underneath *Acacia* trees than in tree interspaces. In a comparison between three sites of different land use intensities the effect of *Acacia* trees were strongest at the unmanaged site. Increasing land use intensity was correlated with a decline in species/cover of several physiognomic categories. Experimental approaches to test which factor - shading, nutrient enrichment or dispersal - is limiting the occurrence were started with a shrub, *Lycium* sp. First results on shading and nutrient enrichment have shown that germination rate depends on nutrients. Linking of individual population models with models of large scale vegetation dynamics is in progress.

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WHICH PROCESSES AND MECHANISMS DETERMINE THE BIODIVERSITY IN (SEMI-) ARID PLANT COMMUNITIES?

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Key words: allocation, allometric scaling, coexistence, competition, generic plant model, individual-based simulation model, plant functional types, plant species diversity, spatial and temporal pattern, stochastic environment, trade-off

Abstract:

The arid winter-rainfall region of the western Richtersveld (South Africa) harbours an unusually high plant species richness, with maximum values of more than 40 perennials per 100 m^2 [1]. Species coexistence in this system has been attributed to several factors, including the plants' relatively short life span, the high spatial and temporal heterogeneity in environmental conditions, notably water availability, and the compartmentalisation of the shallow soil by rocks, which reduces the spatial scale of competitive interactions between plants.

The aim of the project is to assess the relative importance of these and other factors, using an individual-based, generic plant model. Simulated spatial and temporal dynamics of the plant community under different scenarios are compared with those observed in long-term field studies, and with predictions from general theories of biodiversity.

RESULTS:

In generic plant models, different species are distinguished by only a few characteristics (2-4). In particular, these are the biomass allocation patterns to different compartments such as roots, stem, leaves, seeds and storage tissue. Other characteristics, such as seed size or dispersal distance, may be included. The distinguishing characteristics form a low-dimensional 'design space'. 'Species' are points within this design space and may be best interpreted as representations of plant functional types.

The costs and benefits of biomass allocation to different compartments, in terms of water and photosynthate gain or loss, are based on allometric scaling relationships (5). A sub-model is developed of the dependence of occupied soil volume and water uptake on root biomass.

Model results include characteristic size and abundance distributions of different plant types given specific environmental conditions (cf. 6).

The analysis of the simulation model has two main points of reference: general theories of biodiversity on a more abstract level, and long-term field studies on a more concrete level.

Several 'unified' or 'general' theories of biodiversity and competitive coexistence have recently been proposed (7, 9), each emphasising different possible mechanisms. The simulation model's dynamics will be interpreted in the light of these theories to assess the degree to which they bear on the specific system under study.

The project's empirical basis are long-term observations carried out by Norbert Jürgens and co-workers over the last 20 years, in which location, size and number of fruits of individual plants have been recorded on permanent plots in the western Richtersveld (South Africa).

By mapping real species' allocation patterns into the model's plant design space, the model results can be directly compared to the specific fine scale patterns observed in the western Richtersveld region. However, because of the model's generic structure, key findings of the study are likely to generalise to other ecosystems of similar environmental conditions.

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SOCIO-ECONOMIC ASPECTS OF CHANGES IN BIODIVERSITY IN SOUTHERN AFRICA

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Key words: household, communal and commercial farming, livestock, game, rangeland management, natural resources, agro-biodiversity, property rights, new institutional economics, resource economics

Abstract:

The study aims at giving an overview over past and present livestock and rangeland management strategies in communities and on commercial farms along the BIOTA transect. It also focuses on institutions ruling the management. About 60 households in three rural communities and 20 farm owners in two locations in South Africa and Namibia have been interviewed by structured and semi-structured interviews. RRA tools were used in the communities. Preliminary results indicate that

- *livestock production systems differ along the transect, depending on the environmental conditions, technologies applied, as well as on cultural background and traditions of the different groups,*
- *the production systems have flexibly adapted to changing environmental, economic and political conditions,*
- *water access, water quantity and quality are identified as a key problem for people living in rural areas (esp. communal),*
- *rangeland quality with respect to bush encroachment is an issue for commercial farmers, who take countermeasures, whereas livestock owners in communal areas do not actively react on changes in vegetation composition.*

Results:

Activities of BIOTA S11 started from July 2001 in the four sub-projects (SP)

1. identifying and analysing the actual land use practices and animal husbandry systems,
2. identifying suitable management practices for bio-economic models and rangeland policy,
3. assessing property rights over resources, organisational structure, and national tenure policies,
4. assessing the economic value of savannahs and biodiversity with respect to human use.

Research methods applied included structured and semi-structured interviews, and interviews with key persons.

SP1 and **SP3** did their research jointly in three rural communities (Mutompo; Okamboro, Soebatsfontein). About 40 households were interviewed in a full census in the first two villages, and 50% of all 52 households in the last village. RRA tools such as, resource mapping, and group discussion were applied.

Population density is high in all three villages. Household composition showed a high proportion of old people and children below school age, particularly in Okamboro. Livestock holding is a secondary enterprise, since most of the household income is derived from government transfers or waged labour. Livestock holding differs, since the Herero and Kavango keep mainly cattle, whereas the Nama/Damara keep small stock. Extensive livestock keeping in the communities is less productivity- or market- than security- and savings-oriented. Data on the production of local small ruminants were obtained in progeny histories. The body weight and body measurements of sheep and goats of different ages were taken in more than 20 herds. Most animals were found to be crossbreeds.

A long-term rangeland assessment tool is being developed. It aims at assessing the quality of communal rangeland and at recording the changes from a scientific and farmers' point of view.

Local institutions that regulate access to and use of natural resources characterise all communities, however, the importance of traditional vs. modern institutions and organisations varies considerably. Local committees as resource allocating and sanctioning authorities have usually been implemented by modern organisations or the state. In all communities, former common property resources are partially privately appropriated and fenced in. The extent of this is mapped by GPS and will be integrated in a GIS analysis in future. Migration and absentee livestock ownership is of increasing importance.

SP 2 interviewed farm owners in three locations (18 around Erichsfelde, 3 in the Kalahari, 2 around Fish River Canyon) using a questionnaire on farm practices. Cattle production is the most important enterprise around Erichsfelde, but tourism contributes to up to 50 % of the income. Farmers notified overgrazing and bush encroachment as problems and take countermeasures. Small ruminant production is most prevalent in the two locations in Southern Namibia. All farmers try to make their production more extensive, to lower production costs, and to simplify management.

Data on hunting and tourism operations were also collected on farms and integrated in a Linear Programming model (first LP). It covers range management of wildlife and domestic herbivores. It is temporal, i.e. covers overlapping resource use of several periods, is able to depict the impacts from current grazing on future range quality, and integrates sound practices.

SP 4 is conducted in co-operation with the Dept. of Botany, University of the Western Cape. The project focuses on 4 protected areas (Richtersveld, Namaqualand (Soebatsfontein community), Rocherpan and Riverlands). All stakeholders, such as park management, adjacent commercial farms and communities, will be interviewed to develop an inventory for the consumptive and non-consumptive use of the natural resources in these areas. An online questionnaire will be set up for internet users (especially park managers); tourists and locals will be interviewed by structured questionnaires. A trial questionnaire has been forwarded to a flower tour operator for distribution to tourists (clients) and the data collected. Specific economic valuations methods will be applied. Aspects of the landscape will be modelled within a GIS and future scenarios generated.

Besides the research agenda, contacts to local organisations, extension agents, and research partners were made, covering in addition the Richtersveld and Paulshoek area. A vivid exchange with DRFN, NEPRU, the UNAM (Law Dept.) in Namibia, with the Dept. of Plant Conservation of UCT and with Dept. of Agricultural Economics and Range Ecology, Orange Freestate University Bloemfontein, already exists and is further deepened.

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1.10.2000-30.09.2003

BIOLOGICAL STUDIES ON MYCO-HETEROTROPHIC PLANTS WITH SPECIAL EMPHASIS OF THEIR MYCORRHIZAE

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Key words: myco-heterotrophic plants, arbuscular mycorrhiza, anatomy, Cameroon

Abstract:

The project is carried out in the Southwest Province of Cameroon. 12 species (7 genera; 4 families) of myco-heterotrophic plants could be recorded. A new species of Gymnosiphon (Burmanniaceae) is described. All species were analysed morphologically and anatomically. Mycorrhizal structures were observed. "Trap cultures" were established, using Hieracium pilosella L. (Asteraceae) as a mycorrhizal host plant. "In situ" germination tests were carried out. Observation plots were established near Limbe. Soil sampling, as well as plant monitoring started in October 2001.

Introduction:

The aim of the project is the investigation of the poorly known biology of myco-heterotrophic plants. Myco-hetrotrophic plants receive all essential nutrients (including carbohydrates) from endomycorrhizal fungi, which are colonizing their roots and/or rhizomes [1]. The lack of leaves and chlorophyll, as well as their subterraneous habit lead to the assumption that they live as parasites on their associated fungi [2]. In tropical Africa comparatively few species of myco-heterotrophic plants occur. An exception are glacial refuges like e.g. the rain forests around Mt Cameroon in Cameroon's Southwest Province, which are housing one third of all African species of myco-heterotrophic plants [3].

Data concerning the ecology of myco-heterotrophic plants are very scarce and in the case of most species - especially those from Africa - not existent. The main goal of this project is the registration of the species composition of myco-heterotrophic plants in South-west Cameroon, as well as the investigation of the mycorrhiza and the determination of host fungi.

Results:

Since the beginning of the project in October 2000, three trips to Cameroon were made. Two trips were undertaken during the declining rainy season, that comprises the flowering season of all myco-heterotrophic plants (orchids excluded). The main mission was the registration of myco-heterotrophic plants in the Southwest Province. For this reason the type localities of several species were visited. The rainforests that formerly covered the hills around the village of Moliwe turned out to be completely replaced by oil palm plantations. This area is the type locality of *Afrothismia pachyantha* Schltr. (Burmanniaceae) and *Oxygyne triandra* Schltr. (Burmanniaceae). As the screening of all nearby patches of remaining forest was without any success, it is to be feared that *Oxygyne triandra*, which is only known from a single collection, became extinct. The type locality of *Kupea martinetugei* Cheek ined. (Triuridaceae), that also comprises the only presently known population of *A. pachyantha* (discovered by S. Williams in 1993 [3]) is highly threatened to be transformed into farmland.

The presumably endemic *K. martinetugei* could still be found in abundance. In the Ekundu Kundu community forest near Mundemba a new species of *Gymnosiphon* (Burmanniaceae) was discovered and will be described soon. The taxonomical situation of the African species of *Gymnosiphon* turned out to be very confusing. The careful study of type material might reveal, that another two species (both collected near Mundemba) are new to science. Altogether 12 species (7 genera; 4 families) of myco-heterotrophic plants could be recorded.
All detected species were analyzed morphologically and anatomically using light- as well as electron microscopical (SEM, TEM) techniques. With regard to root anatomy, attention was mainly paid to the endomycorrhizal structures of the involved host fungi. The mycorrhizal patterns of all plants, except *Auxopus macranthus* Summerh. (Orchidaceae), showed the typical characters of an arbuscular mycorrhiza. In order to determine the associated fungus, 'trap cultures' were established, using *Hieracium pilosella* L. (Asteraceae) as a mycorrhizal host plant. Root fragments of *Afrothismia winkleri* (Engl.) Schltr. (Burmanniaceae), *Burmannia congesta* (Wright) Jonk. (Burmanniaceae) and *Sciaphila ledermannii* Engl. (Triuridaceae) were placed onto the living roots of *H. pilosella*. As arbuscular mycorrhizal (glomalean) fungi have no host specificity, it is expected that the hyphae will grow over to the roots of *H. pilosella*. Later on the fungi will be determined by molecular-biological comparison of isolated spores (extracted from 'trap-cultures') and the fungal hyphae within the root tissues. Further on, it is planned to trace the host.-fungus in the roots of adjacent photo-autotrophic plants, with which they perform mutualistic endomycorrhizal relations. This also demands a careful screening of the surrounding photo-autotrophic plant species. For this reason observation plots were established in Bimbia-Bonadikombo community forest near Limbe. Staff members of the Limbe Botanical and Zoological Garden (LBZG) are carrying out a one-year plant monitoring that started in October 2001. Besides this, the abiotic environmental conditions are going to be investigated, especially those concerning the physical and chemical soil composition of the rhizosphere. Soil samples that had been taken at the plots were analysed in the soils research laboratory / Ekona, a facility of the 'Institut de la Recherche Agricule pour le Development' (IRAD). As the reproduction biology, ontogeny and phenology of African myco-heterotrophic plants is completely unknown, several field experiments are performed. "In situ" germination tests are carried out to investigate the ontogeny. For this reason cell sieves (Falcon®), were provided with seeds of e.g. *B. congesta* and buried in the soil. After six months some of the sieves were removed from the soil and examined. The seeds were still vital but no germination process was observed. After 12 months only one seedling of *B. congesta* could be detected within the sieves.

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01.01.2001 – 30.12.2003

BIOTA WEST AFRICA – GENERAL SUMMARY

a) Overall goals

BIOTA West Africa consists of ten subprojects that are part of the joint project BIOTA AFRICA. Each of the three main BIOTA projects aims in its complimentary subprojects at assessing

- dimensions,
- spatial and temporal patterns and
- functional roles

of biodiversity in some of the most important African ecosystems.
The special focus in the upcoming main phase of the BMBF's BIOLOG programme will be on the anthropogenic change of biodiversity in recent times, both in its continent-wide impacts as well as its profound regional peculiarities. The dramatic change is correlated with

- large scale habitat conversion and habitat destruction,
- overuse and mismanagement of natural resources,
- and is also affected by the summed spectrum of small scale human interferences with the environment.

To design advanced management tools, it is necessary to know the *status quo ante*, compare it with the current situation and comprehend the already detectable direct and indirect, immediate and long-term consequences of the change on the ecological and socio-economic stage from the local to the sub-continental scale in West Africa. Such tools will be better suited than any of the presently available management measures for conserving the local and regional biodiversity and for preserving the ecosystems' functional integrity. These scientifically designed tools should allow us to develop wiser and more sustainable forms of use of both the remaining natural as well as converted ecosystems. These goals shall be reached by

- concentrating research on a limited geographical area (see Fig. 1, page 15),
- posing convergent questions and
- applying a harmonised methodology.

The closely aligned, co-operative and interdisciplinary research programme of BIOTA-West integrates the following research areas: remote sensing, meteorology, biogeography, botany (cross-cutting over different fields among those ethnobotany and archaeobotany), zoology (with strong emphasis on entomology, herpetology, chiropterology, and limnology), different subdisciplines of ecology, ethnology, archaeology, socio-economics.

b) Research localities and infrastructure

The studies of the Frankfurt-Group (W11) are being executed in Burkina Faso and in Benin with their counterparts at the Université de Ouagadougou and the Université National du Bénin. A further study (of Barbara Fruth), included under the umbrella of BIOTA-West, will conduct its field work in the Republic of Congo. The main geographic focus within BIOTA-West is, however, on Côte d'Ivoire, with the Centre de Recherche en Ecologie (CRE, Université de Abobo Adjamé) and the Department of Botany at the Université de Cocody as the main counterpart institutions in the country. In Côte d'Ivoire, six of the eight subprojects working in the field are carrying out their empirical studies. During the first year the permanent research camp of the University of Würzburg (originally financed by the Volkswagen Foundation) has served as the already fully functioning infrastructural and spatial pivot, allowing some of the projects a flying start. In due course the newly constructed and now nearly completed permanent Ivoro-German

Field Station in the Comoé National Park will replace the University of Würzburg Field Camp as one of our main infrastructural centres. This new research station will provide excellent working conditions for both, demanding field studies as well as ambitious laboratory research. The station is predominantly financed by (1) a single grant for the construction and most of the general technical and laboratory equipment by the Fritz Thyssen Foundation, by (2) valuable contributions to the infrastructure by the BMBF in the framework of BIOTA West, and (3) by a long-term commitment by the Free State of Bavaria and the University of Würzburg to cover some of the basic running costs. In addition to BIOTA-West, some of the BIOTA-East projects are using this Research Station for comparative investigations. The rights and obligations of the co-operating parties have been stipulated in an exchange of diplomatic notes between the governments of the Federal Republic of Germany and the Republic of Côte d'Ivoire, dated March 3,1997.

The Comoé Research Station allows the lodging and boarding of up to twenty researchers at a given time. There is enough space and all the basic equipment in the laboratory building to allow all accommodated users to perform their research efficiently. Apart from the proper Research Station inside the Park an Information/Education Centre is being built at one of the entrances of the Park. It will serve public relations and educational purposes in a very broad sense and on very different levels (from primary school level to advanced students and scientists) for both, visitors of the Park and residents living in the Park's wider vicinity. Through mediating education-adequate knowledge a widely lacking comprehension for the value of natural resources, for the vulnerability of the fragile web of life, the necessity of nature conservation and of a wise and sustainable use of natural resources shall be roused in the local population and far beyond. To this end much valuable scientific contributions are expected from the BIOTA West projects.

c) The basic natural setting for BIOTA-West's research

There is a steep climatic gradient prevalent along the north-south transect in the investigated part of West Africa (see map, Fig. x), between the arid southern fringes of the Sahara and the humid rain forests on the Atlantic Coast. This offers especially interesting research opportunities regarding a number of aspects of biodiversity alterations within the framework of anthropogenic global change. Most of our subprojects utilise this gradient, at least partly, by focussing on local and/or regional patterns of diversity in different taxa. Comparative studies along this gradient will allow the retrospective understanding of local and regional changes as a consequence of previous natural climate variability within the passed millennia as well as predicting some probable changes in the future under anthropogenicly altered conditions.

d) Understanding the natural background – a highly important objective

All the human-driven ecological changes can only be clearly identified against

- the background of the original patterns of biodiversity, and against
- the dynamic processes in the respective ecosystem not yet under strong pressure of modern man.

Since the necessary previous knowledge that is needed here is not available at present for any of the investigated biomes, basic research requires most of the room in the preparatory phase of the first three years of BIOTA Africa in general and BIOTA West in particular. Such knowledge that can nowadays only be acquired by conducting research in least disturbed systems within protected areas is absolutely unrenouncable. Only with a sound scientific understanding of natural structures and dynamics will we be able to achieve the already mentioned pre-eminent goal of mitigating and eventually bringing to a halt further losses of biodiversity. Also for the additional goal of giving recommendation for enhancing and broadening the wise and sustainable use of organismal diversity, as claimed by the Convention on Biological Diversity (UNCBD), much basic research is required.

The efficacy of all management measurements, be it for conservation or the ameliorated use of biodiversity, will be scrutinised via long-term monitoring. This monitoring will also serve to detect further changes of biodiversity and to recognise their consequences at the earliest possible stage and help to clarify their causes. The latter, however, requires to distinguish natural environmental variability from anthropogenicly caused alterations. Also this task cannot be achieved without a sound knowledge of the natural systems' structural and functional properties. Given the high temporal variability in all natural systems, only long-term research will allow us to gain the necessary insights. Time is running out for effectively curing the problems humans have already inflicted on the worlds ecosystems in general and those of the African continent in particular. We cannot continue to rely further on a pure trial and error strategy when searching for the best means to effectively conserve and wisely use biodiversity.

e) Recognising and understanding biodiversity patterns on different spatial scales

BIOTA West is tackling its scientific problems on very different spatial scales –from subcontinental to regional, landscape and to a more or less fine-grained local level. During the first three years (the preparatory phase that will also serve for capacity building of our counterparts and of our own working groups) we strive among others

- to find patterns of biodiversity at different spatial scales,
- to correlate them with other variables (e.g., climatic, edaphic, orographic, structural, temporal), and
- to observe short-term processes that influence biodiversity patterns and dynamic processes.

At the basis of such correlational data some modelling and up-scaling on larger areas that can only punctually be checked by ground truthing is already possible. This holds especially true when considering what in some instances older data (e.g., former floristic inventories – see the Biomaps project –W03) and remote sensing are offering us as additional information. However, to eventually understand the true cause-effect relationship, which is our final goal, experimental analyses are required wherever possible. Such analyses have usually to be confined to small, exemplary spatial and temporal sectors of the systems and yet are very time-consuming. Such experimental studies have been commenced in a number of subprojects, but they will take their time (and often will need to be extended into BIOLOG's main phase) until one reaches first conclusive results.

f) Achievements up to date

The project BIOTA West started in January 2001. Most subprojects needed some time for practical preparations, for forming or modifying their institutional links, establishing their infrastructure, etc. In the meanwhile this phase has been completed in all ten projects. Several subprojects already started with their scientific work. The hitherto achieved results within all these subprojects are mentioned in the following short abstracts, due to the very limited space, however, only in sketchy form.

Project ID: 01LC0017 (BIOTA West Africa W01)
01.01.2001 – 31.12.2003

REMOTE SENSING AND GIS BASED SURVEY OF SPATIAL AND TEMPORAL BIODIVERSITY DYNAMICS AND ANALYSIS OF BIODIVERSITY AND GEODIVERSITY INTERRELATIONSHIPS

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Key words: Remote Sensing, GIS, Biodiversity-Geodiversity, Monitoring, Vegetation Mapping, Capacity Building

Abstract:

This project shall create the basis for a system in which both, remote sensing and GIS applications, form an analysis and monitoring system for the assessment of human impacts on biological diversity. It is our aim to make the existent biodiversity more understandable and predictable, taking into account the UN-Convention on Biological Diversity (UNCBD).

It is planned to establish a coherent GIS along the entire BIOTA transect in order to allow the analysis of spatial patterns of biodiversity, its temporal changes and the mutual dependency of geodiversity and biological diversity. Focus will lie on the comparison of natural ecosystems with those where socio-economic activity has led to various degradation levels of the former natural ecosystems. Furthermore, the detection of indications of spatial patterns of diversity by remote sensing techniques will contribute to future monitoring and conservation concepts.

Further tasks are the "capacity building" for co-operating partners within the fields of Remote Sensing and GIS.

Results:

Within the last 10 months the data base of a Remote Sensing based GIS for the monitoring of present-state biodiversity within the Western African study sites was built up [1]. In close interaction with the project partners the different localities of field work were identified and geographically referenced.

Tasks performed included first of all an investigation of appropriate multitemporal data sets from commercial multispectral remote sensing systems (LANDSAT-7-ETM, IKONOS, CORONA etc.). A set of LANDSAT-7-ETM scenes were acquired, covering the identified areas. All scenes ordered were georectified to the common UTM system and were integrated as image base into the GIS. Due to the lack of reliable topographical maps, Digital Chart of the World (DCW)-data were used to integrate features like road networks, populated places and river networks into the spatial database. These primary informations were further used to produce geometrically referenced image maps which are essential as an auxiliary means for the orientation of the fieldworkers. They also act as a base for mapping training samples which form the basis in the supervised classification of vegetation patterns from the multispectral images [2, 3]. The maps were enhanced by topological information (roads, settlements as far as available) and were superimposed by a fine resolution latitude/longitude grid in order to facilitate orientation in the field and to enable the direct comparison of GPS recordings with mapped features. The maps were distributed to the project partners in paper printed form. On request, digital maps were also supplied.

An important feature of a spatial database supporting biodiversity analysis in a more indirect way are topographical data [4, 5, 6]. They form not only the basis for the absolute geographical orientation of features in space, but are essential to derive topoclimatological information like potential water and solar irradiance distributions in the terrain [7, 8]. Due to the lack of mid to fine scale topographical maps, interferometric analysis of European Remote Sensing Satellite (ERS)-tandem data has been started to derive Digital Terrain Models from the research areas in the Ivory Coast and Benin.

Due to the importance of spatial climatic data for biodiversity modelling, research had been carried out on downscaling spatially coarse climatic datasets in order to derive climatic information on a spatial scale which is compatible to the scale of the research approach [9, 10]. Up to now, long term (1960-1990) precipitation and temperature data have been downscaled to a spatial resolution of 5km and 2 km, respectively, as long-term monthly means. In the near future it is intended to add additional climatic parameters and to cover the area with non-aggregated monthly mean data.

To support the use of spatial data and information systems by the project partners two capacity building activities took place at the DLR in Cologne and at the Institute of Botany in Hamburg. Topics of the first course were primarily remote sensing basics with a special emphasis on sensor sensitivity, reflectance of different surfaces, and generation and interpretation of false colour composites. The second course held in Cologne focussed on Remote Sensing basics in combination with GIS architecture for biodiversity research and monitoring [11]. Topics like general data structure, the integration of referenced geospatial together with Remote Sensing data and the main steps for building up of an information system were dealt with. Integration possibilities of raster and vector based spatial data with ecological/biological attributes stored in databases were addressed partially.

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Project ID: 01LC0017 (BIOTA West Africa W02)
1.1.2001 – 31.12.2003

BIOPHYSICAL AND HYDROMETEOROLOGICAL PARAMETERS WITHIN THE FRAMEWORK OF TERRESTRIAL BIODIVERSITY RESEARCH

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Key words: abiotic environmental conditions, microclimate, energy budget, water balance

Abstract:

Since many ecological aspects of plants and animals are strongly related to local abiotic conditions, measurements of meteorological and geophysical data provide comprehensive basic information within the discussion of biodiversity stearing mechanisms. The scientific contribution intends to link spatial and temporal variations of abiotic components within dry island forests and savannas in Comoé National Park (Ivory Coast) to actual questions of biodiversity research.

Results:

Two representative experimental sites have been established within savanna and island forest locations in order to determine relevant data concerning the energy- and water-budget, as well as vertical profiles of micrometeorological parameters (Fig. 1). Furthermore, the analysis of digital hemispherical photographs enables us to describe the structure of vegetation within the observed formations (Fig. 2).

In addition, comparative studies will be conducted in the primary tropical rain forest in southwestern Taï National Park. Comprising an area of 457.000 ha this location represents one of the last large humid forest habitats in West Africa. Known as a centre of high biodiversity the Taï Park was declared as a World Heritage Region by the UNESCO in 1982.

In the further course of the project the bioclimatological investigations will be carried out simultaneously within dry forests/savannas in Comoé Park and evergreen forests of Taï Park in order to analyse the largescale interannual precipitation variability and its impact on the different vegetation formations.

Appendix:

Fig: 1: Installation of technical equipment at the savanna station

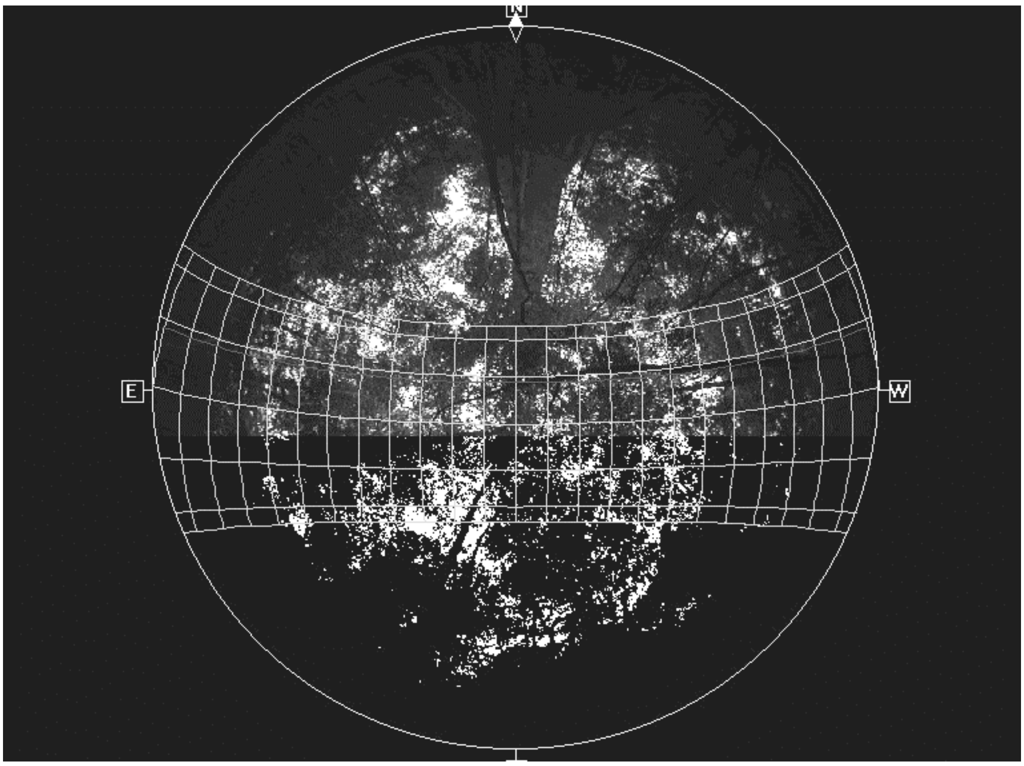

Fig. 2: Partly analyzed hemispherical photography with annual sun-tracks

Project ID: 01LC0017 (BIOTA West Africa W03)
1.1.2001 – 31.12.2003

BIODIVERSITY OF AFRICA IN THE GLOBAL CONTEXT: SPATIAL PATTERNS OF VASCULAR PLANT DIVERSITY IN A CHANGING ENVIRONMENT (BIOMAPS PROJECT)

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Key words: biodiversity mapping, biogeography, vascular plants, geodiversity, spatial analysis, databases, GIS, information system

Abstract:

BIOTA BIOMAPS aims at the analysis of spatial patterns of African phytodiversity at regional to continental scale. Using an inventory-based biodiversity mapping approach, a computer based map of total vascular plant species richness for continental Africa has been generated (using diversity figures for some 470 geographical units). For the first time, detailed statistical analyses of the correlation of total plant species richness with climate, geodiversity and other abiotic parameters are now available on the continental scale for Africa. Additionally, we computed the first continental map of endemism richness. For more detailed analyses using a higher spatial and thematic resolution, we are establishing a database on the distributions of selected plant taxa. Until now, distribution data for about 1600 plant taxa are analysed. The established databases provide a standardised data structure to make the scattered data on floristics, biogeography, and biodiversity of African vascular plants available.

Results:

As a baseline against which the results of more detailed analyses can be tested, we mapped and statistically analysed spatial patterns of overall species richness of African plants on a continental scale [1]. For these analyses, the complete datasets used by Lebrun [2] and Barthlott et al. [3, 4] were revised, significantly expanded and reanalysed using an inventory-based biodiversity mapping approach. The dataset currently includes 470 records of summary data taken from literature on the phytodiversity of geographical units such as mountain ranges, national parks, provinces, and others. Using a new methodological approach, we mapped endemism richness values (an index combining endemism and species richness) for the seed plant flora of the 20 African biogeographical regions [5].

More detailed analyses were started using a taxon-based biodiversity mapping approach. The respective dataset with distribution data for single taxa of African vascular plants allows not only analyses with higher spatial resolution. It is as well the basis for more detailed studies of different aspects of phytodiversity patterns such as endemism, phylogenetic diversity and complementarity analyses. During the first months of the project the basic infrastructure for this approach was established. Using the BioCise data model [6] a database for the management of plant distribution data was developed and linked to GIS. Details of the database and possible co-operation are co-ordinated with W. Berendsohn (BIOLOG Biodiversity informatics). A continent-wide GIS on high-resolution geodata (e.g., DEM, protected areas, climate, geodiversity and vegetation) was established using internet-based information as well as data provided by BIOTA W01. These data are used for the spatial analysis of plant distributions in relation to the abiotic environment to allow predictive modelling of the probable range of a species. In addition, a Gazetteer with more than 1 Mio geographical features on the African continent was compiled using different data sources (NIMA, CIAT, etc.). This reference system facilitates the assignment of exact spatial co-ordinates to plant record localities. Using different online-databases (mainly the Kew Record of taxonomic literature) a dataset on more than 5000 monographs and journal articles on taxonomy, floristics, biogeography and phytosociology of African plants was established and revised for our purposes. Extracts from the dataset were provided for other BIOTA subprojects, as well. Based on our information about available plant distribution data, we are establishing a list of selected species, which are of interest considering our analytical purposes and the work of our co-operating partners. For this work, we specifically co-operate with BIOTA sub-projects W04, W09, W11, E04 and further taxonomic experts.

Until now, two main types of taxon-based data are analysed. The larger dataset at the moment are dot maps of the distribution of some 1240 vascular plant taxa belonging to 124 genera digitised from the Distributiones Plantarum Africanarum. The second dataset is based on the locality descriptions of plant specimens cited in taxonomic revisions. Until now, data on some 420 taxa from 19 plant families have been entered in the database. Furthermore, we are in contact with specialists for various plant groups with the aim of joint analyses of their distribution data. First plant groups to be analysed are Scrophulariaceae, Aristolochiaceae, Melinideae. In addition, we are in contact with working groups (e.g., H.P. Linder, J. Lovett, P. Williams) doing comparable analyses. Altogether, our taxon-based datasets currently include distribution data of some 1600 plant taxa. First analyses of diversity patterns for various plant functional types illustrate the variety of analytical applications of this datasets [7].

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1.1.2001 – 31.12.2003

PHYTODIVERSITY AND DYNAMICS OF HABITAT FRAGMENTS IN THE IVORY COAST: SPATIAL AND TEMPORAL PATTERNS OF BIODIVERSITY CHANGES, EDGE EFFECTS, AND THEIR FUNCTIONAL CONSEQUENCES IN NATURAL AND DISTURBED ECOSYSTEM MOSAICS

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Keywords: forest island, forest regeneration, forest-savanna ecotone, global change, landscape structure, fire, soil properties, sustainable land management, socio-economical conditions, modelling, vegetation map, remote sensing, GIS, Comoé National Park

Abstract:

In the forest-savanna mosaic of West Africa, habitat fragmentation caused by man leads to a decline of natural forests, their increasing isolation, a growing influence of edge effects from the surrounding savanna [1], and an alteration of species composition. As a result, biodiversity, as the most important natural resource of the country and basic foundation for the livelihood of the inhabitants, is declining. In a period of intensification of land use and global change, the consequences of habitat fragmentation on biodiversity are being studied with a focus on temporal and spatial patterns of biodiversity changes, as well as the increasing significance of edge effects. The core questions deal with the consequences for the ecological functioning of natural and cultivated ecosystems [2,3], the quantification of landscape diversity, and the establishment of recommendations for a sustainable land use aiming at a long-term preservation of biodiversity. For this purpose, field data are being assessed in the Comoé National Park and neighbouring utilized areas by use of various transect methods and the newly installed biodiversity observatories. They are being merged with remote sensing data and processed to models using advanced statistical procedures and GIS.

Results:

The analysis is subdivided into five thematic sections:

1. Spatio-temporal analysis of the development of habitat patterns and extrapolation of the results to larger areas. Based on the analysis of new remote sensing data and intensive field work, a map of the important vegetation types of the National Park is being generated. It serves as a basis for the subsequent analysis of landscape structure and diversity. When tentatively related to former data [4], spatio-temporal dynamics of the forest islands become obvious; however, a consistent trend has not been detected yet. The predominance of certain vegetation types in the respective forest islands shows that under natural conditions we may reckon with high beta-diversity among particular forests, whereas the diversity of vegetation types within a forest island is limited. Currently, the data of training areas are being extrapolated onto larger areas within the satellite image in order to generate a GIS vegetation map of the entire region through multiple ground truthing. (Cooperation with W01, W03, W09, W11)

2. Analysis and modelling of edge effects between forest and savanna. Along selected monitoring transects in forest islands of the National Park, botanical and structural relevés are being collected, and the long-term influences of the factors grazing, soil disturbance, and fire are being investigated by means of experimental interference. Furthermore, natural regeneration of woody plants and herbaceous standing crop are being recorded, and experiments on the establishment of transplanted seedlings and in-situ germination of selected woody species are being carried out. Germination characteristics are being compared under controlled laboratory conditions. The biotic parameters are being merged with the determining parameters (microclimate, soil, structure, fire). Though a clear structural and microclimatic gradient was shown to exist along the forest edges during the rainy season, the transplanted seedlings of characteristic tree species showed the same survival rates and relative growth during the first 2 months. Thus, the dynamics of forest edges are presumably determined by the microclimatic conditions of the dry season as well as timing and intensity of the fire events. (Cooperation with W02, W03, W06, W09, W11, S09)

3. Study of the land utilization regime in neighbouring areas of the National Park, comparison of the consequences of habitat fragmentation in the utilized and protected areas. In the cultivated areas, monitoring plots were established in close agreement with the local inhabitants, and the botanical inventory was started. Currently, the vegetation structure [5] and the occurrence of species groups indicating certain types of land use are being analyzed in monitoring transects [6]. It becomes evident that due to utilization, forest edge ecotones are becoming larger at the expense of the forest area. Hence, the effects of abiotic parameters (microclimate, structure, soil, fire) are being investigated. On the basis of extensive polls at local administrative offices and questionnaires of the population in the areas under study, data are being obtained and analyzed on past and present land-use practices as well as the socio-economic conditions of the inhabitants. This in turn will aid interpretation of present and future ethnobotanical developments. Intensive capacity building is being undertaken by an Ivorian PhD candidate working on this topic. (Cooperation with W01, W03, W09, W11)

4. Study of the soil properties. Currently, catenas and chemistry of the soils of the area are being analyzed in order to systematically quantify the impact of soil properties on the formation of forest-savanna mosaics and on the regeneration of forests. (Cooperation with W02, W06)

5. Comparative long-term monitoring of biodiversity changes at monitoring plots in relation to anthropogenic factors. An observatory was installed each inside and outside the Park by means of a DGPS. Its vegetation was assessed and classified in all 1 ha subplots [7]. The subplots to be analyzed by all working teams were determined by means of a stratified ranking procedure. A detailed inventory of the vegetation of the subplots and of additional permanent transects has been commenced. Another pair of observatories will shortly be installed in an adjacent region. (Cooperation with W01, W02, W03, W06, W07, W09, W11)

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1.1.2001 – 31.12.2003

DETERMINANTS OF SMALL-SCALE MOSAICS OF ARTHROPOD COMMUNITIES IN NATURAL AND ANTHROPOGENICALLY DISTURBED HABITATS

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Key words: animal-plant-interactions, arthropod communities, community structure, Comoé National Park, *Dorylus*, local processes

Abstract:

The diversity and structure of ecological communities is determined by many parameters. In order to understand the influence local processes exert on the maintenance of biodiversity in natural and anthropogenically altered environments, two arthropod systems are studied in the West African Comoé National Park. In arthropod communities living on individual savanna shrubs and trees, the role of deterministic small scale variation in plant and habitat characteristics for community composition is investigated. Repeatedly sampled, the arthropod communities of individual shrubs and trees were distinctive even for conspecific plants growing in close neighborhood. Thus, each plant was inhabited by a unique, characteristic set of arthropods. This striking pattern suggested a community organization governed rather by deterministic, small scale environmental variables than by stochastic events. Focal observations on several arthropod species belonging to different guilds supported this interpretation. Driver ants (Dorylus nigricans) are studied as a stochastic disturbance of arthropod communities. Driver ants are considered to be an important, community-structuring source of disturbance especially for ground living arthropod communities. In a first analysis indirect evidence is presented that driver ant raids reduce the abundance of some potential prey taxa as well as that of potentially competing species.

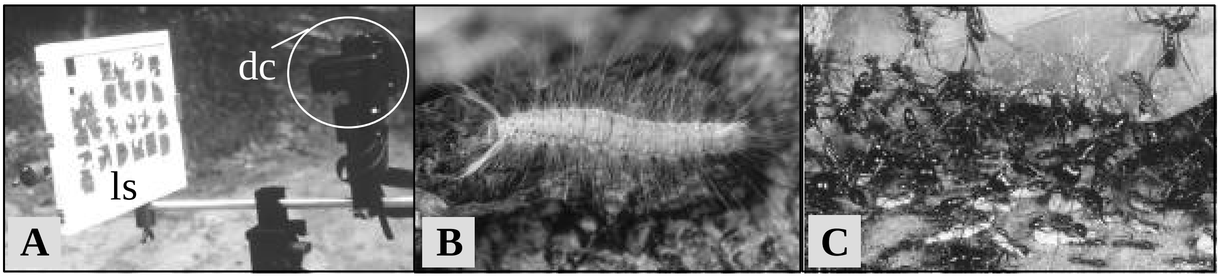

Fig.1: **A**: Apparatus for standardized measurement of herbivory: area of leaf samples (ls) is quantified before and after feeding trials using a digital camera (dc); **B**: Caterpillar of *Chrysopsyche imparilis*; **C**: *Dorylus nigricans* driver ants.

Results:
Repeatedly sampling complete arthropod faunas of individual plants revealed that savanna shrubs and trees are inhabited by distinctive sets of arthropods which turned out to be stable for – at least - more than a year. Such arthropod communities, unique for individual plants, could be found for trees and shrubs exceeding a certain minimum size (Fig.2). This finding could be confirmed even for conspecific plants growing in close neighborhood. Since the species pool for colonization is identical for these plants, it has to be concluded that deterministic habitat characteristics, acting on a restricted local scale, are influential on community composition. Such deterministic habitat parameters could be variable plant characteristics like plant morphology and chemistry or environmental variables like soil heterogeneity (determined in coordination with W02 and W04), generating variation in arthropod-relevant parameters on a local scale [1]. Thus, small scale variability in habitat characteristics seems to be a crucial factor for diversity in arthropod communities. It may play a key role in the interpretation of similarities and differences found for regions or sites differentially influenced by humans and may have profound implications for management measures.

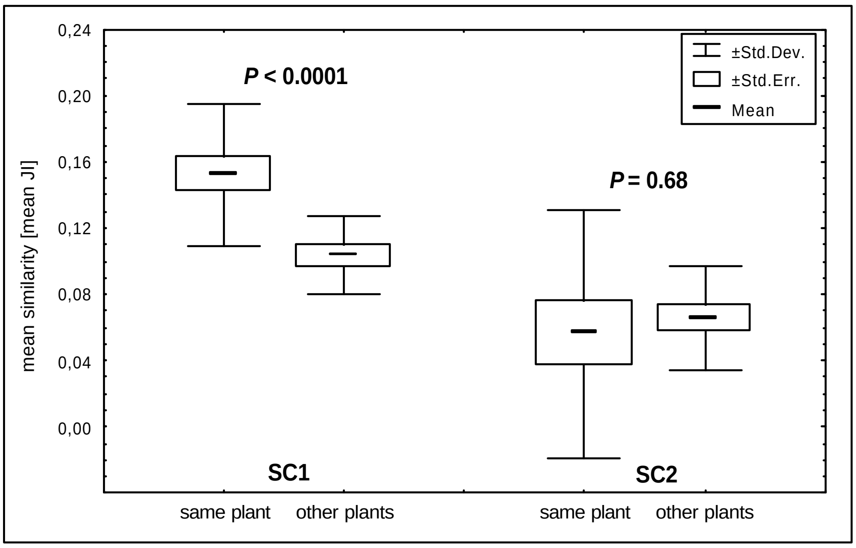

Fig.2 shows similarities in species composition of arthropod communities (excluding ants) eight times sampled from the same and different *Combretum nigricans* plants respectively. It becomes clear that communities obtained from the same plants are significantly more similar than communities from different plants when shrubs of Size Class 1 (SC1: plants with 175 to 1090 leaves) are considered. No difference in species similarity of communities was detectable for small plants of Size Class 2 (SC2: plants with 23 to 94 leaves). Paired t-test; N per size class: 14 plants; JI = Jaccard Index.

The distribution of herbivorous insects seems to reflect the intraspecific variability of plant characteristics mentioned above. This is, as an example, shown in the distribution of the mobile scarabaeid beetle *Apogonia fatidica* and is probably causing food plant changing behavior of less mobile moth caterpillars. *A. fatidica* occurred highly aggregated on certain individuals of the savanna tree *Combretum nigricans* while it was completely absent on some neighboring *C. nigricans* plants (Fig.3A). Feeding experiments (cf. Fig.1A) demonstrated that this characteristic distribution pattern was tightly coupled with leaf attractiveness which significantly varied between individual *C. nigricans* plants for the beetles (Fig.3B).

Caterpillars are limited in choosing between different plants and in reaching the most attractive and best suited plants. However, some caterpillars feeding on *C. nigricans* change food plants regularly. This change of food plants reduces – in view of highly variable plants - the probability of using exclusively unfavorable plants and results in a diversified diet. Feeding on different plant individuals can be positively correlated with fitness which was experimentally shown for *Chrysopsyche imparilis* (Lepidoptera, Lasiocampidae) (Figs.1B&3C).

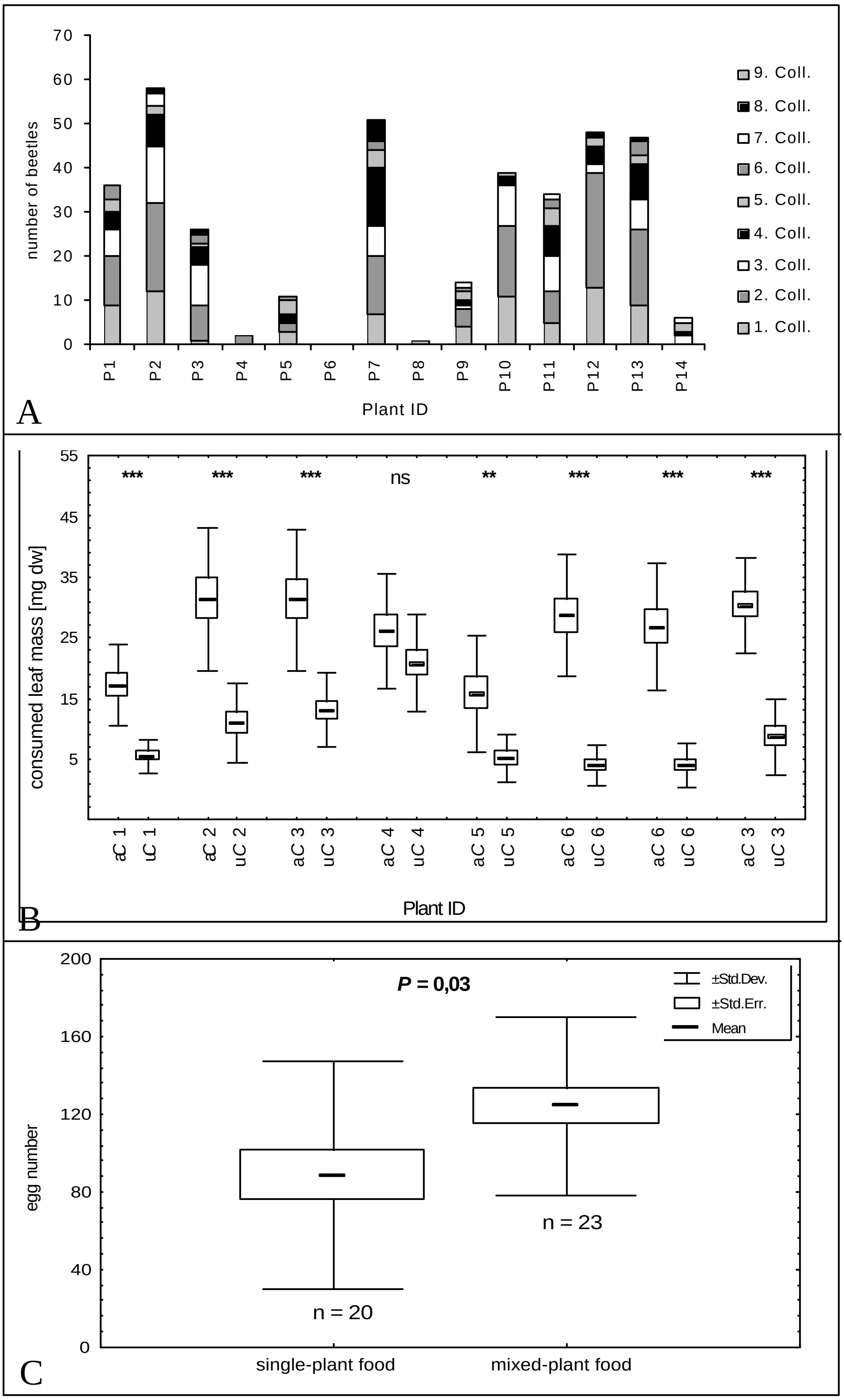

Fig.3 **A**: Aggregated distribution of *Apogonia fatidica* beetles on 14 *Combretum nigricans* plants (P1-P14) which are exemplarily presented for their regularly assessed beetle abundance. Nine consecutive collection events (Coll.) are shown. Differing beetle densities on individual plants reflect variable plant characteristics (attractiveness). **B**: Comparison of leaf attractiveness of paired *C. nigricans* plants (*C*) to *A. fatidica* beetles. Each plant pair tested in the lab contains a plant individual which attracts high beetle densities in the field (attractive *Combretum* = a*C*) and a plant individual which attracts only small numbers of beetles in the field (unattractive *Combretum* = u*C*). Significant differences in consumed leaf mass (dw = dry weight) are indicated (paired t-test): ns = not significant; ** = *P*<0.01; *** = *P*<0.001; Box-Whisker-Plots: Central line = Mean, Box = Std. Err., Whisker = Std. Dev.; N (per plant pair): 12 leaf pairs, 120 beetles. **C**: Comparison of egg numbers laid by *Chrysopsyche imparilis* females raised either on leaves of a single *Combretum nigricans* plant (single-plant food) or on leaves of a mix of six *C. nigricans* plants (mixed-plant food). Females raised on the mixed diet laid significantly more eggs. This indicates that changing food plants can be advantageous in view of variable plants and may evidently enhance reproductive output

Driver ants (Fig.1C) occur in massive densities and show ferocious behavior when on hunting raids. Therefore they are supposed to exhibit a strong effect on arthropod communities in the leaf litter of the gallery forest, leading to the hypothesis that driver ants act as a diversity-enhancing *'intermediate disturbance'* [2]. Besides experimental evidence, two prerequisites would, if well-documented, make this hypothesis plausible: That there is a patchwork of arthropod communities in the leaf litter that is not determined by environmental conditions (vegetation, geo-morphology, humidity, etc.), and that driver ant raids exhibit a relevant disturbance on the arthropod communities. Not enough data have been sampled yet with regard to the first question, but we can present some crude analysis of the effect of ant raids on the abundance of the higher taxa of leaf litter arthropods (Tab.1). For Saltatoria, Hemiptera (mainly Cicada), Collembola and the larval states of Holometabola a significant increase of abundance could be documented during multiple sampling after ant raids (max. 16 days), serving as indirect evidence that abundances are recovering after they were reduced by the raids. For other groups it was not found, in some cases possibly because of small sample sizes or a wrong time-frame (e.g. too short for ant colonies with main losses in the brood rather than in the sampled workers). Interesting is the significant effect on the abundance of non-formicid Hymenoptera which consisted almost exclusively of minute parasitic wasps. This may indicate a second order response on the ants *via* the availability of host species, considering that the tiny, mobile wasps are probably not preyed upon heavily by the ants. The existence of a succession of communities after ant raids is crucial to the proposed effect of driver ants on species diversity in the region. The results presented here are only first cues to assess what taxa are affected by the ants. An analysis of species identities in the samples will help to collect further evidence for an influence of *Dorylus* on the edaphic species communities.

Tab. 1 shows the effect of time after *Dorylus*-raids on the abundance of several groups of leaf-litter arthropods. Six (pit-fall traps), respectively five (Winkler samples) sites were sampled 0, 1, 2, 4, 8, at some sites up to 16 days after ant raids (unfortunately, critical *before-raid* samples can often not be obtained due to the unforeseeable nature of the raids). Trends are indicated as (+/0/-), R-values of significant Spearman-rank correlations are given. Note that in some taxa opposite trends occurred at different sites which requires a more detailed analysis.

Taxon	**Pit-fall traps**		**Winkler-samples**	
Annelidae	0	ns	+	ns
Blattodea	+	ns	+	ns
Coleoptera	+	ns	0	ns
Collembola	-	ns	+*	R=0.390
Diptera	+	ns	+	ns
Formicidae	+	ns	0	ns
Hemiptera	+*	R=0.412	+	ns
Hymenoptera (*non-Formicidae)*	+	ns	+*	R=0.315
Isoptera	0	ns	0	ns
Larvae (*mainly Coleoptera*)	0	ns	+*	R=0.315
Millipedes	0	ns	0	ns
Mites	0	ns	0	ns
Saltatoria	+***	R=0.567	+	ns
Spiders	0	ns	0	ns

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COMPARATIVE STUDIES ON EPHEMERAL SAVANNA WATERS AND THEIR SIGNIFICANCE FOR DIVERSITY AND PRODUCTIVITY OF FISH COMMUNITIES IN NATURAL AND ANTHROPOGENICALLY DISTURBED RIVERS

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Key Words: Comoé National Park, ephemeral waters, fish communities, lateral migration, local processes, spatial-temporal utilization patterns

Abstract:

Freshwaters in tropical savanna biomes are currently subject to massive changes. Deterioration of water quality, elimination of whole spectra of habitats and profound alterations in the basic hydrological conditions are especially serious consequences of human activities. In order to understand the natural organization of local fish assemblages and to assess the effects of anthropogenic influences on the composition and functional characteristics of fish communities, the fish fauna of undisturbed savanna waters in Comoé National Park, Ivory Coast, and in disturbed adjacent areas is investigated. The aim is to describe the spatial and temporal use patterns of savanna waters by age classes, species and assemblages of fish and to understand the factors that are causing these use patterns. In the first year of the project, the main emphasis is put on surveying the composition of fish communities that use ephemeral savanna waters temporarily connected to Comoé river, the only permanent water in the region. 65 species of fish have been caught in these waters so far, among them some new to the fish community hitherto reported for Comoé river. The general composition of fish assemblages of ephemeral waters is comparable to the fish community of Comoé river. However, analyzing parameters of distribution more precisely, a species specific, fine grained use pattern becomes evident. It points to the important role ephemeral waters can play for many species of fish as feeding, growing or spawning sites.

Results:

Our first results indicate that ephemeral savanna waters are an important fish habitat although they are useable only for a limited time of the year. A comparison of the fish fauna of the great river systems of Ivory Coast (Sassandra, Bandama, Comoé) and the fish assemblages of our study area shows that most fish locally occurring in permanent waters can also be found in ephemeral waters. While 91 species of fish are reported for the whole Comoé river system (length: 1,160 km; drainage area: 72,000 km²) [1,2], 65 species of fish could already be recorded in the extremely limited savanna waters studied so far (three 200 m sections of two ephemeral savanna rivers and fifteen ponds with a total surface area of less than 1 km²).

An analysis of assemblage composition indicates that use of ephemeral habitats is not restricted to certain groups but is to be found in a wide range of taxonomic groups of fish (Fig.1). Simply the Cyprinodontidae seem to be relatively rare in ephemeral savanna waters in comparison to the total fish fauna of Comoé river [3]. This might be caused by the existence of many species in estuarine or rainforest waters which contribute to the total Comoé fish fauna. On the other hand, we have recorded one annual cyprinodontid as a characteristic inhabitant of ephemeral savanna ponds which previously has not been reported for Comoé river. Another group of fish, the Cyprinidae, appear, however, especially species-rich in ephemeral savanna ponds and streams. With the documentation of three species, new to the Comoé fish fauna, more species of cyprinids are known from the ephemeral as compared to the river community. This finding stresses the great importance of ephemeral savanna waters to these fishes. It also points to gaps in the current knowledge of the distribution of many fish species in the region. As all fish - with the exception of annual cyprinodontids and *Protopterus*-lungfish which can survive dry seasons without permanent water as eggs or buried in mud holes - have to newly re-colonize ephemeral savanna waters from permanent waters, i.e. from the Comoé river in our case, they have to occur also in the river itself.

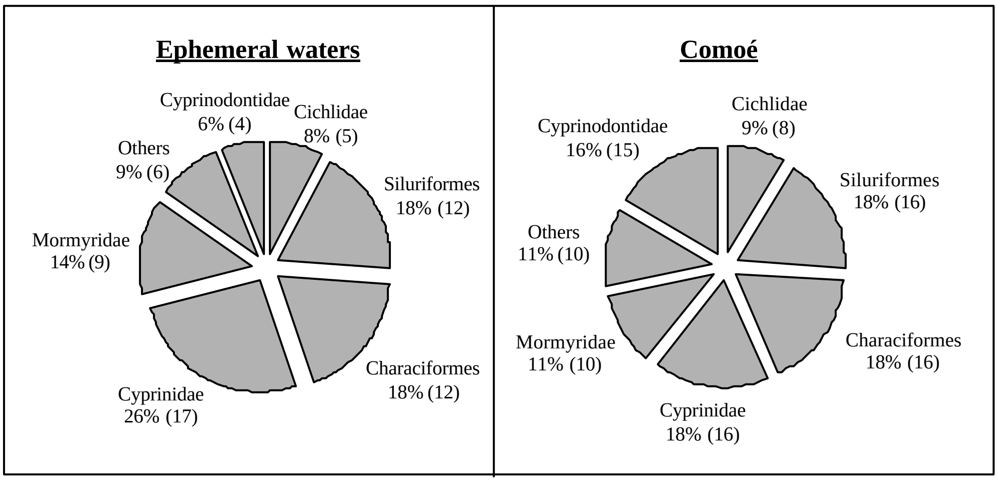

Fig.1: Taxonomic composition of fish assemblages of ephemeral savanna waters (our study) and a great West African river, the Comoé (published data). Total species number for each group mentioned is given in brackets. "*Others*" comprise: Anabantidae, Centropomidae, Channidae, Mastacembelidae, Polypteridae, Protopteridae (for ephemeral waters) and Anabantidae, Centropomidae, Channidae, Clupeidae, Eleotridae, Mastacembelidae, Notopteridae, Polypteridae, Protopteridae (for Comoé river).

Analyzing parameters of distribution and habitat characteristics more precisely (in cooperation with W01, W02, W04), a species specific, fine grained use pattern of ephemeral waters is becoming evident. In dependence of water availability, the composition of fish assemblages in savanna waters changed. On the one hand, species of *Barbus*, *Aplocheilichthys* and *Hemichromis* re-colonized ephemeral waters directly after first rains. They may either try to migrate in savanna ponds far away from Comoé river or to take advantage of low predation pressure by predatory fish in newly developing waters. On the other hand, fish like *Brycinus nurse*, *Labeo parvus* or *Schilbe spec.* started lateral migration much later, entering savanna waters at a time when water level remained high and rather predictable and stable food sources had been established. The different patterns in utilization of ephemeral savanna waters by a species-rich fish community point to the important role these waters can play for fishes as feeding, growing or spawning sites.

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AMPHIBIAN DIVERSITY AND DIVERSITY CHANGES IN WEST AFRICA: GLOBAL, REGIONAL OR LOCAL CAUSES?

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Key Words: Amphibia, bio-monitoring, community ecology, diversity, forest, Ghana, genetics, Ivory Coast, primary habitats, savanna, secondary habitats, West Africa

Abstract:

Amphibian diversity along environmental and disturbance gradients in West Africa has been investigated. Diversity was higher than expected and at least equals that of neotropical regions. Habitat specific anuran communities could be characterized and basic data on life history traits of possible target species for a long term monitoring program have been compiled.

Results:

As a base line for our future research amphibian diversity throughout different West African ecotones has to be documented. So far we compiled species inventories of five national parks in Ivory Coast and the Ghanian Volta region (Fig. 1). By means of standardized sampling techniques we obtained basic data on the amphibian community composition in different habitat types (forest, savanna, primary, secondary). This enables us to detect diversity changes over time, and/or along environmental and disturbance gradients.

In total 96 amphibian species were recorded from Ivory Coast. From 61 species DNA samples have been collected and partly sequenced. For most of the species at least basic biological and ecological data are now available. We were able to document several reproductive strategies so far unknown for African anurans [4, 7], as well as unknown interactions of other groups of organisms with amphibians [5]. By means of morphological, behavioral, acoustical and genetic comparisons we detected five species new to science [6].

Analyses of the leaf litter anuran assemblage of Taï National Park by means of niche overlap analysis, non-metric-multidimensional-scaling, and Mantel-test comparison revealed that the observed multivariate structure is only weakly influenced by biotic interactions and therefore most likely not the sole result of past or present species interactions. Results indicate that different life histories are likely to explain the observed pattern. In primary forests, distinct species assemblages existed but could be explained by geographic proximity and therefore the existence of common local species pools. Assemblages in secondary forests were predictable based on environmental parameters. This can be inferred to be the result of physiologically more restrictive conditions within secondary forest habitats especially due to an altered microclimate. Only highly adapted or tolerant species may be able to cope with these conditions.

These results lead to important implications for bio-monitoring and conservation management and provide useful information, which is urgently needed to assist conservation efforts. Surveys of the populations of selected species may yield information about the state of disturbance of an area. We currently selected several anuran species for further investigations, that proved to be specialized on certain habitat types and/or show peculiar life history traits and therewith represent different ecotypes. These comprise three species with direct development that are restricted to disturbed forests (*Phrynobatrachus alticola*) or occur in varying abundances in primary and secondary forests (*Arthroleptis variabilis, A. crusculum*), as well as three species that all maintain tadpole stages but reproduce in different habitats [*Phrynobatrachus guineensis*: breeds in tree holes in drier parts of primary forest; *Kassina lamottei*: breeds in large ponds in swampy parts of primary forest (Fig. 2); *Cardioglossa leucomystax*: reproduces in slow running forest creeks].

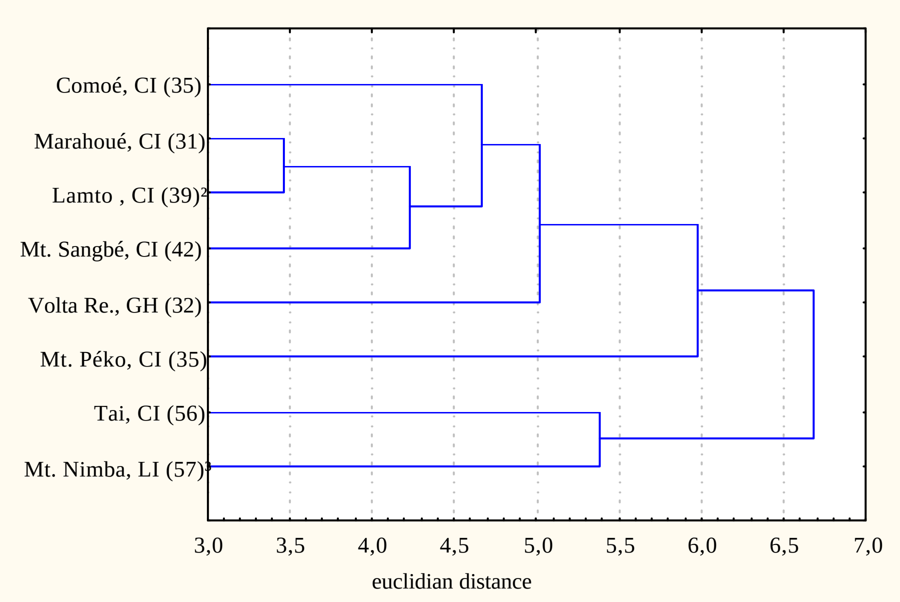

Fig. 1: Similarity of West African amphibian communities; presence-absence data, species numbers in parentheses, CI = Côte d'Ivoire, GH = Ghana, LI = Liberia, [2] = [3], [3] = [1, 2, 8].

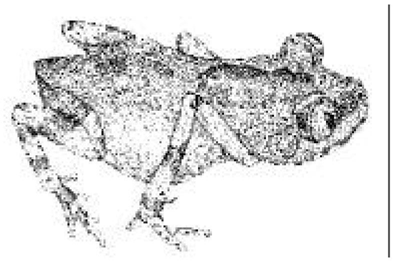

Fig. 2: *Kassina lamottei* an endemic frog of the Upper Guinea forest zone, confined to primary rainforest, drawing: M.-O. Rödel.

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THE INFLUENCE OF LOCAL AND REGIONAL FACTORS ON THE DIVERSITY, STRUCTURE, AND FUNCTION OF WEST AFRICAN BAT COMMUNITIES (CHIROPTERA)

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Key words: local assemblages, community ecology, guild structure, habitat heterogeneity, scale dependency, distribution patterns, regional species pools, GIS, modeling, potential distribution, frugivory, seed dispersal, plant-animal interactions, vegetation dynamics

Abstract:

Using a comprehensive approach, we examine the functional significance of bats for the maintenance of biological diversity in Africa. The project goals are to determine the roles of bats in fundamental ecological processes such as seed dispersal and to assess factors that influence the structure and diversity of chiropteran assemblages on local and regional scales. In a first approach we determine the composition and guild structure of selected bat communities on a local scale (Ivory Coast) by conducting comparative field studies with standardised methodology at two localities contrasting in vegetation composition (savanna and rain forest). In a modelling approach, we analyse the large-scale, regional diversity patterns of West African bats based on data of species distribution as well as biotic and abiotic habitat variables. We study the spatial patterns of bat diversity with the ultimate goal to test underlying factors such as habitat heterogeneity and productivity that might covary with these patterns. In a third approach we examine the role of flying foxes (Megachiroptera) as keystone species in plant-animal interactions and their influence on the spatial and seasonal vegetation patterns within the highly dynamic forest-savanna mosaics of the Guinea zone.

Results:

In our first working package we have established a standardized protocol to sample local bat assemblages. We ask how individual species and entire communities are associated with different habitat types. Until now we have obtained long-term data for two local assemblages, one in the rain forest zone (Taï-N.P.), the other in the Guinea zone (Comoé-N.P.), both of which are fairly undisturbed. The study areas represent important examples of West African biomes that are increasingly threatened by degradation. At present the data set for Taï-N.P. covers 2 years (1999/2000) while the one for Comoé-N.P. was initiated in 1993/95 and now embraces 3 years (1999-2001) of intense sampling, including the Biodiversity Observatory. The preliminary results suggest that the habitat preferences of bats are generally very species-specific, thus making them well-suited candidates to evaluate and monitor the effects of habitat alteration through land conversion and global change. Furthermore, the structure of the assemblages (species and guild composition, abundance patterns) reflect the different habitat types that have been sampled. These data will serve as a base-line against which the effect and magnitude of land alterations can be tested in the main phase of BIOLOG. So far, a total of 53 species which represent 84% of the estimated 63±4 species (calculated with EstimateS, © R. Colwell) have been found in Comoé-N.P. In Taï-N.P. we have recorded 37 species, representing 80% of the expected 46±2 species. These preliminary data support our initial assumption (see BIOTA application) that the diversity peak of bats in West Africa is not found in the rain forest zone but in the adjacent forest-savanna mosaic of the Guinea zone. This diversity peak is caused by the exceptional habitat richness which fosters an influx of species from habitats adjacent to the ecotone. The species richness of Comoé-N.P. by far surpasses all other African bat communities that have been studied in the past. It underlines our general hypothesis [1] that African bat communities are not depauperate as proposed by FINDLEY [2] but attain levels comparable to the Neotropics. We conclude that habitat degradation – especially in highly dynamic mosaic systems – is likely to negatively affect species richness, composition and community pattern, potentially altering the function of dependent ecosystem levels. This latter question will be addressed in the main phase of BIOLOG.

While our first working package focuses mainly on the local factors determining bat assemblages, we investigate in our second working package the spatial patterns of bat diversity on a regional / subcontinental scale and its interdependency with the local scale. For this approach we model the habitat preferences and potential distribution patterns of all bat species occurring in West Africa. To build species-specific habitat models, the known occurrences of each species (verified point localities only) are superimposed onto biotic and abiotic variables (vegetation, topography, climate) already implemented in the GIS of BIOTA-subproject W01. By superimposing the modelled distribution patterns we identify the regional diversity patterns and regions with exceptionally high species richness and / or endemism (hot spots). We have already established a data base which comprises all known point localities of West African bat species (121) that have been published (ca. 470 publications) and where specimens (about 20.000) are available in museum collections in Europe and North America. It is the most comprehensive data set for any group of African vertebrates. The modeling approach will allow us to overcome many of the sampling biases by building species-specific habitat models and extrapolating them into space. For this working package we are collaborating closely with BIOTA-subprojects W01 and W03.

Finally, in our third working package we study the role of flying foxes on the vegetation dynamics of the Guinea savanna by determining their influence as seed dispersers. We investigate their importance in detail by focusing on the tree species *Cola cordifolia* (Sterculiaceae) and *Milicia excelsa* (Moraceae). First results indicate that both species are dominant elements of island forests but with varying densities and/or patchy distribution within these forests. This pattern might be caused by the activities of highly mobile seed dispersal agents. We therefore test the assumption that flying foxes significantly influence seed distribution, having a high potential for long distance dispersal. Direct observations at three fruiting tree species (*C. cordifolia, Syzigium guineense* and *Uapaca togoensis*) suggest that flying foxes mainly feed by shuttling between resources and feeding roosts. In an island forest, dominated by *C. cordifolia*, a high number of feeding roosts (46) with seeds of this species could be identified within a small area of 2 km². The distribution of feeding roosts appears to be concentrated in areas of least fruiting density. Although initial seed deposition is high, germination rate appears to be moderate yet yielding a high density of seedlings per area. Surprisingly, very few older age classes could be found so far. In close cooperation with BIOTA-subproject W04 we have established ten 100 m² plots in which seedlings will be individually marked and monitored over the next years to determine seedling establishement, survival, and the resulting spatial pattern. In addition, we measure seed rain as well as seedling density along transects oriented away from parent trees to assess distance effects.

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PHYTODIVERSITY IN THE WEST AFRICAN SAHEL AND SUDAN ZONE – DEVELOPMENT AND EVALUATION

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Key words: Phytodiversity, land use and changes in phytodiversity, ethnobotany, archaeobotany, Poaceae, digitalization of herbarium collections.

Abstract:

In the Sahel and Sudan zone of Burkina Faso and north Benin, biodiversity observatories according to BIOTA-standards, based on satellite images and on observations in the field have been selected and established (Fig. 1). For each of the 3 principal regions (representing Sahel, North and South Sudanian zone), a pair of plots was selected, differing principally in the intensity of land use, especially cattle grazing. A floristic inventory as well as relevés of the subplots were realized during field work. The ethnobotanical studies concentrated on the perception/observation of changes in flora and vegetation by local people and knowledge about relevant species. The field work was performed in close co-operation with the local counterparts (see above). The required contracts with the relevant local institutions and counterparts where signed, serving also as research permits. The program BRAHMS was installed on a new computer (financed by the project) in the national herbarium at University Ouagadougou, BF. Digitalizing of collections was started and further training of staff is to take place at the end of 2001.

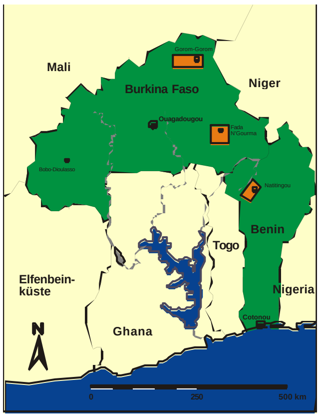

Fig. 1. 🟧 = Study sites

Results:

As the field campaign will only finish in the beginning of November and the diversity data acquired (inventories, reléves etc.) have not been analyzed yet in detail, the following results can only be very preliminary and fragmentary. BIOTA W11 is an interdisciplinary research project. Its objective is the analysis and evaluation of recent and historical changes in plant diversity following a climatic gradient and varying land-uses. Better foundations for sustainable utilization concepts and protection measures will be developed. A further objective is the extension and cross-linking of West African plant collections to make the analysis of collection data more efficient. The project is to be executed in co-operation with counterparts at the Universities of Ouagadougou/Burkina Faso and Cotonou/Bénin and with the SFB (collaborative research project) 268 „Westafrican Savanna“ of the University Frankfurt/Main.

Especially the contacts, installations and scientific results of the SFB 268 and the excellent co-operation with the counterparts were of great help to deal effectively with the authorities as well as to locate and design the study plots for the BIOTA project.

For the selection of the plots, besides studies in the field satellite images proved to be highly informative and helpful. For each of the 3 principal regions (representing Sahel, North and South Sudanian zone), a pair of biodiversity observatories were selected. Floristic inventories of vascular plants and relevés of subplots were realized. In co-operation with the ethnobotanists, the kind, extent and duration of human impact on the study areas were determined. The plots of each pair differ principally in the intensity of cattle grazing. Of special interest is the fact, that we were authorized to establish one observatory in a reserve strictly protected from grazing and agriculture since about 50 years. Designation and investigation of plots took place in close co-operation with the scientific counterparts (see above). PhD students from Burkina Faso and Benin are actively involved in the project and partly also participated in the first field campaign.

The increasing intensity of grazing and agriculture have led to changes in the flora and vegetation also realized by the local people [1], [2]. As expected, alpha-diversity alone cannot serve to describe the changes: While species diversity seems to be lower in the least disturbed habitats than in the moderately disturbed ones, the changes are considerable as far as the grass layer is concerned. Besides the overall phytodiversity studies in the plots, special topics are the diversity changes in selected groups assumed to be of special indicator value. While the counterparts will in part concentrate on the woody plants, we will in the first period pay special attention to the Poaceae. Height and structure of grass layer as well as species composition vary considerably according to type and intensity of land use. Striking is the decrease of abundance and diversity of perennial Poaceae and increase of annual grasses with increasing grazing pressure [3], [4]. Dynamics in the distribution area of these indicator groups are to be detected by the investigation of (especially historical) herbarium collections. As part of this analysis, relevant material of the selected indicator groups in the herbarium collections in Berlin (B) and Brussels (MEISE) were digitalized, and the entering of these data in a BRAHMS database has begun. In order to facilitate the access to and exchange of diversity data, the national herbarium at University Ouagadougou was provided with a new computer which was installed together with a version of the program BRAHMS. This is to serve the digitalizing of the herbarium collections to facilitate access to and exchange of phytodiversity information. The same program has already been established in the course of a Dutch project in the national herbarium of Benin in Cotonou. The training of the staff in BRAHMS has commenced in October and will be continued in December 2001.

For the study of historical changes of the Sahelian phytodiversity, samples of charred wood from the Sahel of Burkina Faso were identified, recovered from 20th century archaeological sites. These include a large number of species, some of which have become rare in the modern flora [5]. Comparison with the modern woody vegetation is done at present.

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Project ID: 01LC0022
1.1.2001 - 31.12.2003

THE CUVETTE CENTRALE AS RESERVOIR OF MEDICINAL PLANTS

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Key words: flora, Congo basin, Cuvette Centrale, medicinal plants, ethnobotany

Abstract:

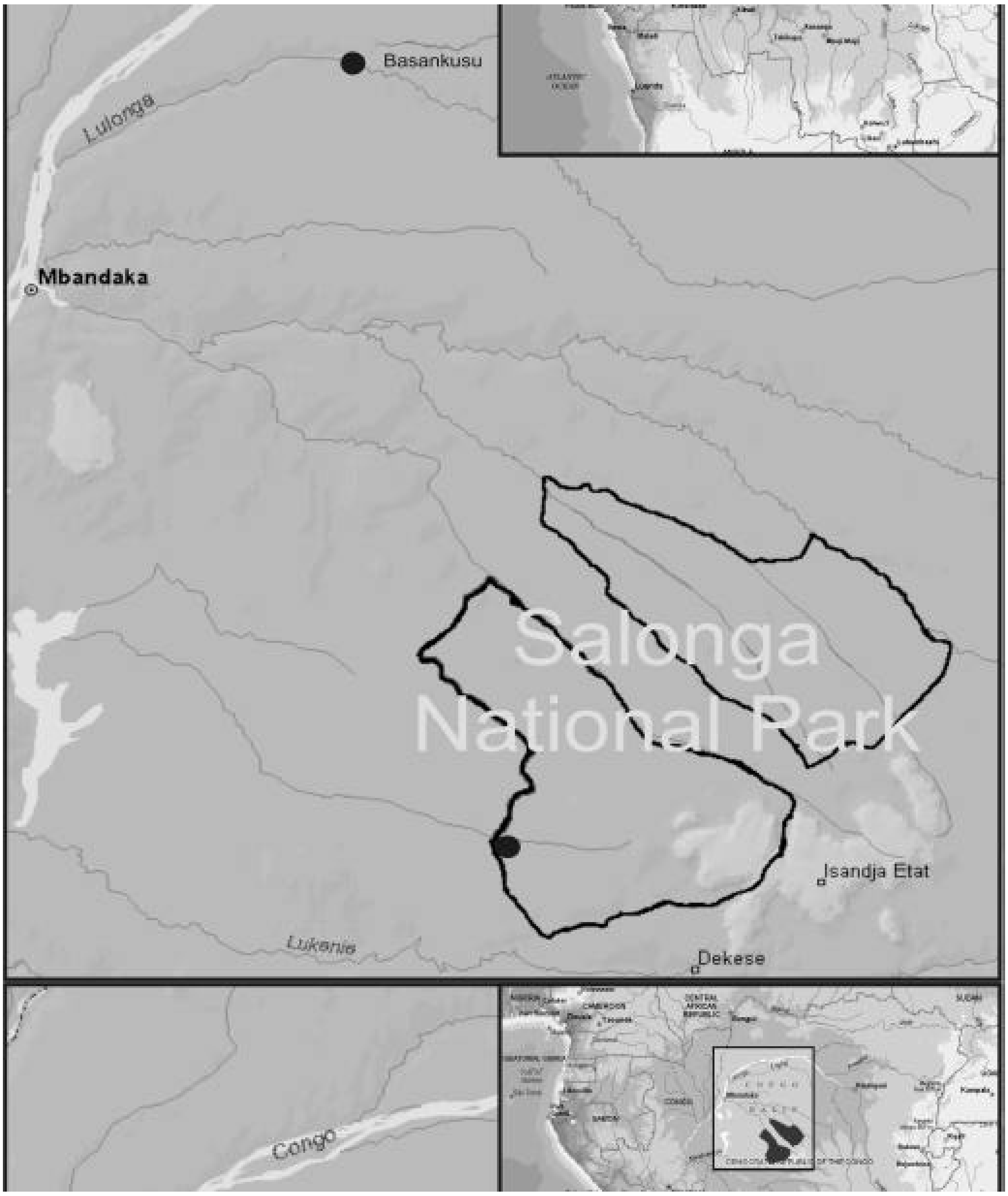
We wish to conduct a long-term project on plant diversity in the central region of the Congo Basin, the Cuvette Centrale, Democratic Republic of Congo. During the initial phase (3 years) we seek to establish the personnel and infrastructural foundations. This implies the project-oriented education and training of technicians and young academics at the University of Kinshasa as well as the collection and determination of the flora of this area with specific focus on natural medicinal plants. In order to characterise the study area in terms of it's plant diversity and abundance, parameters such as measures of size (dominance), numbers (density) and distribution (frequency) will be investigated. In addition, the historical and current significance of natural herbal plants for the medication of both humans and animals and their phytochemical characteristics will be documented. High priority will be given to the evaluation and projection of possibilities of economic use of natural herbal plants within and by the country of origin.

Results:

In the initial proposal, data collection was planned to be conducted at Basankusu (see figure), Province of Equateur. This area was occupied by rebels opposing the official government based in Kinshasa and thus became inaccessible for scientific research. Therefore, we explored other areas within the central Congo basin and decided to establish a new site for field research situated at the south-western border of Salonga National Park (see figure), Province of Bandundu. The Institut Congolais pour la Conservation de la Nature (ICCN) has been requested to grant permission to conduct field research within Salonga National Park and the contract is now ready to be signed by the Minister of Environment.

During a pilot study in spring 2001, 15 transects (200 x 10m) were established for habitat characteristics using methods established during earlier studies (Boubli et al. *submitted*). Along these transects, 170 specimens of wild plants were collected. Reference copies of this collection were stored in the herbaria of Kinshasa and Brussels University for identification. Out of these, 42 species are already identified. About 50% of these plants are reported to be used as medicinal plants by the local population (Bakundu).

Interdisciplinary cooperation with leading officials of Kinshasa University, environmental organisations and NGOs was established. By the end of 2001 a small crew of graduates will be trained and ready to start data collection in the upcoming year. A systematic investigation of both quantitative and qualitative data in the field will put light on the floristic diversity of the area and filter out plants of potential pharmacological interest. Goal is to obtain base-line information for long term data collection and to present a comprehensive documentation of the flora in form of an archive of plant taxonomy accessible to the public that will be backed up by specimens in both Congolese and European herbaria. The historical and current significance of the recorded medicinal plants for both humans and animals will be investigated and presented as monographs.



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Project ID: 01LC0025 (BIOTA East Africa E01)
1.04.2001-31.03.2004

BIOTA EAST AFRICA: BIODIVERSITY IN CONVERSION – THE INFLUENCE OF FRAGMENTATION AND MAN-MADE EXPLOITATION ON THE BIODIVERSITY OF TROPICAL MONTANE FORESTS

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Introduction

BIOTA East Africa links a set of thematically and geographically strictly coordinated analyses of biodiversity conversion in the East African highland and montane rain forests. Analyses of biodiversity and its change are carried out mainly at Mt. Kenya and Kakamega forest (Fig. 1), Kenya. The latter represents the eastern-most branch of the Guineo-Congolian rain forest block, situated at 1400 to 1700 m a.s.l. in western Kenya. The area has protected status as National Forest Reserve and includes both primary and secondary rain forest, as well as several isolated fragments. It is perfectly suited to conduct comparative analyses of biodiversity within the mentioned habitat types. The efforts are centred on the comparison of primary and secondary highland rain forests with small isolated fragments. The developing open area habitats (farm land, grazing areas, waste lands etc.) and the communities forming within them are included. Comparative studies are carried out in other forest regions in Kenya, Tanzania and Uganda.

In addition, five representative palaeo-african refugial areas have been selected to investigate plant diversity and structure of xero-tropical montane communities in southern Yemen and on Soqotra. obtained ecological data will help to estimate the present state of desertification and to develop management plans for the preservation and sustainable use of unique xero-tropical communities.

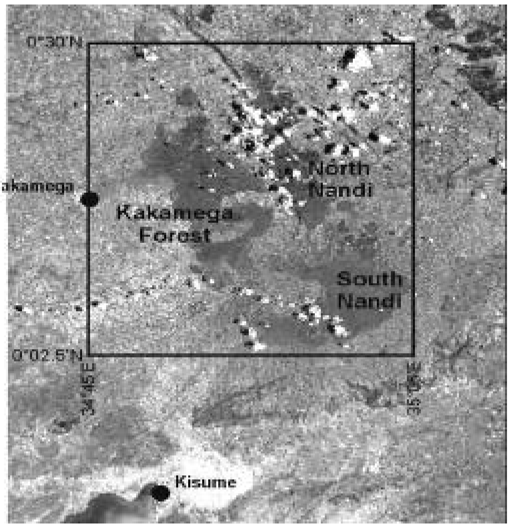
Scientific goals of BIOTA East Africa

Principal goal is the establishment of biodiversity observatories for long term monitoring, with main focus on the effects of man-made changes in biodiversity. To achieve this aim, significant interfaces of the trophic network of the tropical rain forest and its replacement communities have been critically selected: plant-pollinator systems, forest fragmentation and seed dispersal, exchange of atmospheric compounds, regeneration of tree species, decline in anurans, diversity of coprophagous beetles, dragonflies, and Lepidoptera. The use of modern remote sensing techniques and the collection of local and historical information on environmental change will be used to establish a local information system in the study areas. Experiments are carried out using standardised plots and sampling methods. The potential of forest and savannah ecosystems for sustainable land use are investigated. As a result, we expect a better understanding of the complex consequences of evolutionary change on the different hierarchical levels resulting from degradation and fragmentation, especially at the level of critical trophic and reproductive interfaces. In addition, we expect to be able to provide useful tools and methods for rapid assessment procedures for selected systems.

Steps of the first months

The BIOTA East Africa project started in April 2001 with preparations for the Kick-Off-Trip to Kenya which took place in May and June 2001. On this trip, all necessary formalities to receive working and research permissions from Kenyan governmental officials were arranged and numerous scientific cooperations with local and international institutions were established through signing bilateral Memorandums of Understanding (MoU) and contracts. At the same time, we took the first steps towards an establishment and improvement of research logistics (field equipment, vehicles, research station, weather station, field assistants) and identified certain areas to which the BIOTA East Africa research design should be applied. As a result of these activities, all involved subprojects already conducted their first campaign of field research and data sampling (mainly at Kakamega Forest and Mount Kenya).

Fig 1: satellite image of western Kenya, including the Nandi escarpment and Kakamega Forest, the main study site of BIOTA East Africa.



Established Cooperations

Beside the network of internal BIOTA cooperations, BIOTA East Africa established the following cooperations with local and international counterparts (e.g. exchange of data, joint education and training of students/para-taxonomists):

- National Museums of Kenya (NMK), Nairobi
- Kenya Wildlife Service (KWS), Nairobi
- International Centre for Insect Physiology and Ecology (ICIPE), Nairobi
- International Centre for Research in Agroforestry (ICRAF), Nairobi
- Maseno University, Maseno
- Kenyatta University, Nairobi
- Makerere University, Kampala
- EAFRINET (East African LOOP of BioNET International)
- African Pollinator Initiative (API)

In addition, internal communication with BIOLOG biodiversity informatics projects (e.g. EDIS, DORSA) revealed the necessity of linking voucher collections obtained through BIOTA research with a sustainable data management for efficient use and long-term accessibility of information.

Project ID: 01LC0025 (BIOTA East Africa E02)
1.4.2001 – 31.3.2004

IMPACT OF BIODIVERSITY CHANGE ON THE EXCHANGE POTENTIAL OF TRACE GASES BETWEEN ECOSYSTEMS AND ATMOSPHERE

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Key words: surface fluxes, atmosphere, trace gases, VOC, agroforests, GIS, remote sensing, geo-spatial data

Abstract:

Tropical ecosystems produce a variety of trace gases playing decisive roles in the atmosphere by triggering the oxidation power as well as the warming potential. Despite their relevance for the regional and global atmosphere a sound understanding of the effect of tropical agroforest-ecosystems, showing different grades of plant diversity, on trace gas emission is lacking. To close this gap, interdisciplinary research enterprise is necessary by coupling plant and soil documentation with a satellite imagery-based geographic information system supplemented by ecophysiological studies related to the production of the trace gases and canopy modelling. New airborne surface flux measuring platforms will be developed and used to investigate the air surface exchange of trace gases of ecosystems of different biocomplexity. For up-scaling from the plot scale to regional scale ground as well as airborne measurements will be used to develop a trace-gas-surface-flux model for the different land use types. The proposed activities will further serve to document the effect of anthropogenic activities on the biodiversity of tropical forest ecosystems as well as on the chemical composition of the tropical atmosphere, taking the Kakamega Forest area and its change over the last thirty years as example.

Results:

(1) General tasks

- For an effective project performance, cooperations with institutions in Kenya (ICRAF, ICIPE, ILRI, NMK, DRSRS, LPR) plus setting-up of geo-spatial data sharing agreements (with ICIPE, ICRAF) supplementing memoranda of understanding were arranged. The contract negotiation procedures with the BMBF, DLR and ICRAF have been finalised.
- During a first visit o the test area possible experimental plots were identified by overflying Kakamega Forest and the surrounding.

(2) Development of an airborne surface flux measurement platform

- For airborne surface flux measurements a platform with a 5-holes-probe coupled with a relaxed eddy accumulation device recently developed and quality assured is under construction.

(3) Experiments at the Kakamega Forest site

- A replicated spatial analogue survey designed to assess the impacts of forest conversion on soil productivity (greenhouse bioassay), carbon and macronutrient (C, N, P, K, S, CEC), stocks soil physical properties (bulk density, water stable aggregates, texture) has been completed. One hundred geographically paired sites contrasting primary/secondary forest with subsistence maize agriculture were surveyed across the Kakamega and South Nandi forest ecotones in Jul-Aug. 2001. All sites were georeferenced. Diffuse reflectance measurements (350-2500 nm range) and physicochemical analyses of topsoil samples are underway. A selected number of samples will also be analyzed for ^{210}Pb (210-Lead) and ^{137}Ce (137-Cesium) inventories, to contrast soil erosion-deposition rates between agricultural and forest sites.

- A protocol for rapid assessment of soil productivity was tested in Kisumu. Topsoil samples were screened in a pot study using maize as an indicator species. The spectral and physicochemical analysis of plant and soil samples is still underway.
- A meteorological station has been set up in the Kakamega forest and is operating since mid of September.

(4) Setting-up of the BIOTA-East-GIS

- First GIS-application in order to support the BIOTA-East kick-off trip to the Kakamega Forest: combining topographic maps (1:50'000 scale), a vegetation map compiled by M. Haupt, and photographs taken from an aircraft during the IFU kick-off trip
- Intensive search for available geo-spatial data by contacting different Kenyan, Swiss and German institutions as well as for relevant literature, resulting in orders of relevant maps and literature.
- Setting-up the BIOTA-East-GIS-structure considering different levels of detail: a) Africa, b) Kenya, c) Kakamega Forest and associated forest areas, d) Kakamega Forest, e) observation plots
- Integration of ready-available geo-spatial data sets of African or Kenyan extent from DCW (PSU), DLR (Oberpfaffenhofen), ESRI (Redlands), FAO (Rome), ILRI (Nairobi), UNEP/GRID (Geneva), UNEP/GRID (Nairobi), as well as of topographic maps covering the Kakamega Forest and associated forest areas
- Ordering fine-resolution Landsat satellite imagery time series: 2001, 1995, 1989, 1984, 1979/80, 1975, 1972/73
- Presenting the BIOTA-East subproject E02 at international conferences (see references)
- Preparation and presentation of a seminar “GIS in Biological Sciences” at the NMK (Nairobi) as a contribution to capacity building.

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Project ID: 01LC0025 (BIOTA East Africa E03)
1.3.2001 – 31.3.2004

REGENERATION OF TROPICAL MONTANE TREE SPECIES – SPATIAL AND TEMPORAL DYNAMICS OF FEED BACK PROCESSES

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Key words: Dispersion, diversity and composition of tree species; spatial variation of canopy throughfall, nutrient elements and soil characteristics; regeneration of tree species; light climate; growth;

Abstract:

The plot-based study is embedded into a research network which investigates different levels of disturbance/fragmentation on processes which may influence changes in biodiversity. This study focuses on processes which regulate the regeneration of tree species. Abiotic processes like water and nutrient input via canopy thorughfall, biotic processes like growth of trees are intercorrelated with changes in canopy structure, light climate and soil properties. All these processes controll the regeneration of trees. Necessary cooperations with other research groups investigating dissemination, diversity of tree species on larger scales give BIOTA the change to analyse spatial and temporal changes. Close cooperations with Kenyan institutes helps to reach the aim of observatorial areas in East Kenya.

Results:

Aims of this project can be divided into four main aspects:
1. Detailled description of tree species composition, dispersion and diversity in different sites of the Kakamega forest in Kenya. This includes measurements of the incremental growth of tree species measured with dendrometers, which gives the chance to analyse the influence of climate on growth of tree species over a long period of time
2. Analysis of the spatial and temporal variations of rain fall and canopy throughfall as one example of an element flux which could influence the species composition of trees.
3. Analysis of spatial variations of pH, EC, total element content and water extractable element fraction in soils. The aim is the determination of spatial variations of soil nutrients at horizontal and vertical dimensions at different sites in the Kakamega forest.
4. Analysis of the regeneration of tree species within the forest in 1 squaremeter plots.

Parameters which are measured: Species composition, dispersion and diversity of tree species, incremental growth of trees, diversity and dispersion of seedlings and saplings, analysis of canopy throughfall and rain fall in high temporal resolution, analysis of canopy structure using hemispherical photographs, analysis of soil samples; in all samples (rain water, soil samples) main nutrient elements, pH, EC and selected trace elements are to be analysed.

All investigations in this forest are plot-based which gives us the possibility to analyse spatial patterns. The research area is influenced by the rural population at varying levels of selective logging, collection of fire woods, sampling of medicinal plants and fragmentation into smaller forest compartments. This allows the analysis of processes along an desturbance gradient.

The **main idea** behind the project: Soil and forest in Kakamega have developed over a long period but during the last ~100 years the forest is influenced by the population. Different levels of influence may have caused different changes in vegetation, changes in soils. Spatial variations in canopy throughfall, light climate and changes in soil nutrient availability may have resulted in changes in vegetation. All this processes are interrelated and have feed back effects on each other. Analysing processes in water and nutrient input via canopy throughfall in dependence on the structure of the vegetation, the light climate, soil properties and tree species regeneration can help understanding the underlying processes and can be used as biodiversity observatorial sites of changes in climate.

State of affairs (first field trip from August to November)**:**

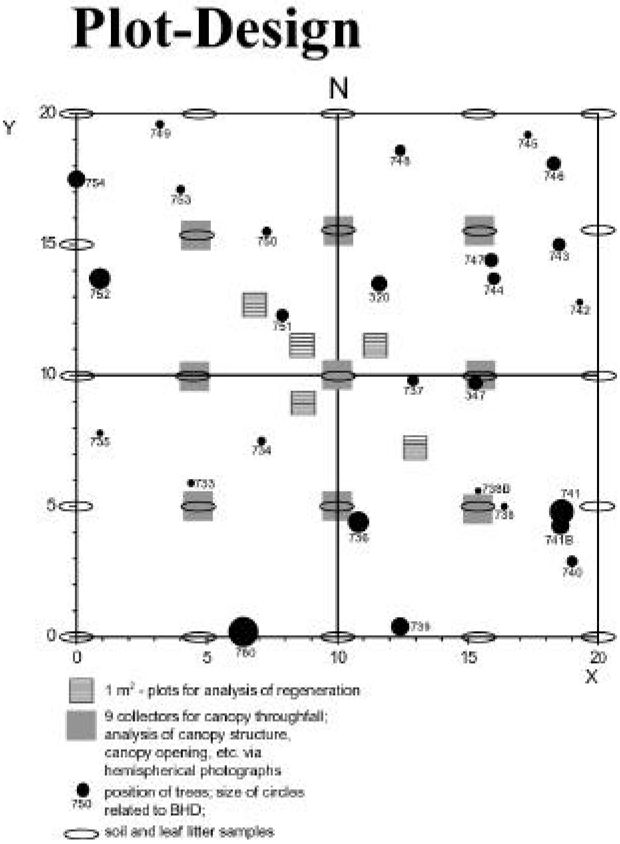
Since project start we had fixed problems concerning research permits; initiated close cooperations with the ICRAF soil department (Dr. Alain Albrecht) and with the Herbarium and Botanical department of the National Museum of Kenya (Dr. J. Mutanga).

Demarcation of 12 plots at four different sites in Kakamega (GPS data available): Colobus trail, Buyangu Hill, Salazar circuit, Isecheno. Plot size 20 to 20 m (see sketsch).

At 25 points per plot at 7 depths soil samples were collected (2100 samples). Additionally 600 samples of leaf litter (two samples per soil auger hole) were collected.

In all plots tree species are determined, tree height measured, BHD determined and dispersion measured. 198 tree now have dendrometers which allows the analysis of incremental growth.

In 6 Plots we have installed collectors for canopy throughfall. At 12 dates we have already collections of rain fall and canopy throughfall (daily readings).



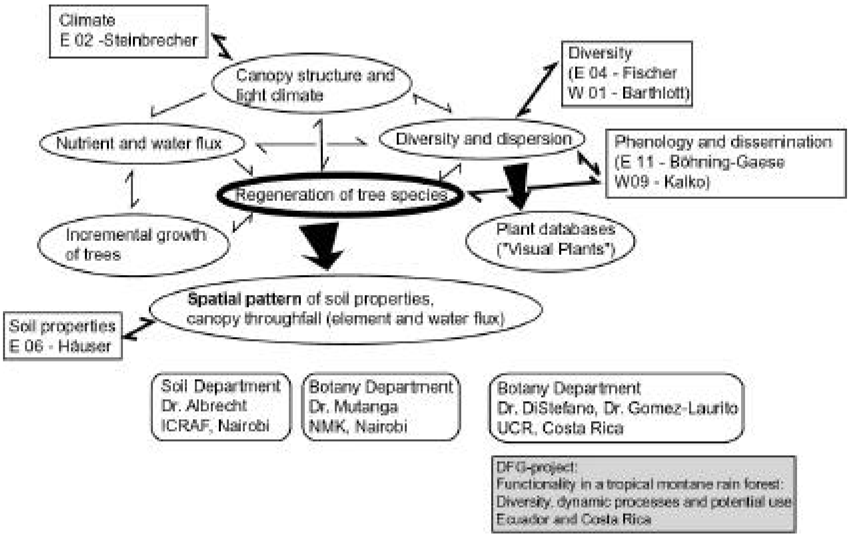


Illustration of main aspects of the project (ellipses), cooperations with other BIOTA-groups (boxes) and other cooperations (rounded boxes). The project is closley related to the DFG-project group in Ecaudor, which allows comparisions of processes between Costa Rica, Ecuador and Kenya. In all three countries we work with similar project designs in tropical (pre-)montane rain forests.

Project ID: 01LC0025 (BIOTA East Africa E04)

1.4.2001-31.3.2004

INFLUENCE OF NATURAL AND ANTHROPOGENIC FRAGMENTATION ON THE VEGETATION IN MONTANE RAINFORESTS OF KAKAMEGA AND MT. KENYA

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Keywords: Kakamega Forest, Mt. Kenya, primary forest, secondary forest, vascular plants, stem epiphytes, bryophytes, lichens, Kenya

Abstract:

In Kakamega Forest, 35 plots of vascular plants and 130 plots of epiphytic bryophytes and lichens have been studied in primary and secondary forest types. The primary forest stands are characterized by a tree layer of 25-35 m, a dense shrub layer with dominating Dracaena fragrans and a low coverage of herb layer. The secondary forests show a tree layer of usually less than 10 m and a dense herb layer. In primary forests, hygrophytic bryophytes are dominant on stems, while lichens are represented mainly by crustose species. Secondary forests are characterized by the abundance of desiccation tolerant bryophytes and foliose and fruticose lichens.

Results:

First field investigation in the northern part of Kakamega Forest revealed that large parts of the forest are degraded and primary forest stands are restricted to only a few sites. 35 phytosociological relevés of vascular plant vegetation have been studied at Buyangu Hill, near the Colobus-Trail, along the Isiukhu-River, around the KWS-Camp-Site and in the northern Kisere fragment. At Buyangu Hill and near Colobus-Trail, the forest shows rather few older trees but many secondary forest species. Probably there has been selective logging in the past. The upper tree layer reaches 25-30 m and the following primary forest tree species have been observed, e.g. *Prunus africana*, *Diospyros abyssinica*, *Chrysophyllum albidum, Markhamia lutea* and *Aningeria altissima*. A rather dense shrub layer consisting mainly of *Dracaena fragrans* is however typical for primary forest. The herb layer generally shows only low coverage. Dominant taxa are *Pollia condensata*, *Dorstenia brownii* and the gap species *Desmodium repandum*. In the rather abundant gaps at Colobus-trail, additional species are *Brillantaisia madagascariensis*, *B. vogeliana*, *Oplismenus hirtellus* and *Renealmia engleri*.

The Forest in the northern Kisere fragment seems to be much more undisturbed. Here large trees of nearly 35-40 m including *Manilkara butugi*, *Diospyros abyssinica*, *Prunus africana* could be recorded. Also a dense shrub layer of *Dracaena fragrans* and *Acanthus eminens* together with a low cover of the herb layer are characteristics for primary forest. Along the Isiukhu river typical riverine forest with dense herb layer, the abundance of gap species and a high bryophyte cover are typical features.

The investigated relevés in the secondary forest are characterized by an open canopy usually less than 10 m tall and a dense herb layer with a high coverage. Typical trees or shrubs for this forest type are: *Rapanea melanophloeos*, *Acacia abyssinica*, *Acanthus pubescens*, *Polyscias fulva*, *Neoboutonia macrocalyx* and *Croton megalocarpus*. In the herb layer, *Aframomum zambesiacum*, *Achyranthes aspera*, *Desmodium repandum* and *Pavonia* *urens* are abundant. Also several terrestrial orchids like *Eulophia streptopetala*, *Habenaria malacophylla* and *Disperis aphylla* have been observed, which could not be recorded in primary forest plots.

Parallel to the investigation of vascular plants 130 phytosociological plots of epiphytic bryophytes and lichens in the lower stem parts have been studied in the same areas in Kakamega Forest. At Buyangu Hill and Colobus-trail, epiphytic vegetation was dominated by hygrophytic bryophytes (Hepatics like *Plagiochila* spp., different Lejeuneaceae, e.g. *Lopholejeunea* spp., *Lejeunea* spp. and mosses like *Porothamnium* spp., *Neckera* spp.). Lichens were represented mainly by crustose species (e.g. *Lepraria* ssp.). Similar observations could be made in the Kisere fragment.

The more open habitats along the Isiukhu-River allow the occurrence of crustose and foliose lichens as well (e.g. *Sticta* spp., *Lobaria* spp., *Leptogium* spp.). Among the bryophytes pendant species like *Pilotrichella ampullacea* are dominating.

The secondary forests studied are characterized by a high diversity of foliose and fruticose lichens (e.g. *Parmotrema* spp., *Heterodermia* spp., *Usnea* spp., *Leptogium* spp.). The epiphytic bryophyte flora consists mainly of desiccation tolerant taxa like *Frullania* spp., *Brachymenium* spp. and *Orthotrichum* spp..

Diversity in epiphytic relevés is much higher in secondary forest than in primary forest. In the latter usually not more than 10 species were observed in a 50 x 20 cm plot while in secondary forest up to 25 species occurred.

Additionally 40 relevés of epiphytic bryophytes and lichens have been recorded on Mt. Kenya. The study sites were situated in the montane *Olea-Podocarpus* forest at 2500 m a.s.l., the bamboo-zone (*Sinarundinaria alpina*) at 2700 m and the *Hagenia*-zone at 3000 m. In contrast to Kakamega Forest the more open montane forests are dominated by large *Usnea* species. Generally natural disturbance by Buffalos (*Syncerus caffer*) and elephants (*Loxodonta africana*) occurs in all forest types.

Project ID: 01LC0025 (BIOTA East Africa E06)
1.3.2001 – 31.03.2004

LEPIDOPTERA AS INDICATORS OF HUMAN IMPACT ON TROPICAL RAINFOREST ECOSYSTEMS IN EASTERN AFRICA

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Key words: biodiversity, rainforest, Kenya, butterflies, moths, Lepidoptera

Objectives:

Afrotropical rainforest habitats have changed rapidly due to anthropogenic influences over the last centuries, and have become increasingly fragmented and disturbed with growing demands on land use by the local population. The effects on insect biodiversity and, in particular, Lepidoptera are poorly known, as basic faunistic data about such groups are still scarce [1,3].

Diversity and subsistence of phytophagous insects like Lepidoptera depend on various abiotic and biotic parameters such as microclimate, soil-characteristics, vegetation composition and structure, and availability of specific larval and adult food resources, which all are directly influenced by the different forms of historic and current land use.

The project aims to describe, characterise and compare the alpha- and beta-diversity of selected families of diurnal and nocturnal Lepidoptera in natural, semi-natural and disturbed habitats in standardised BIOTA biodiversity observatories for the area of Kakamega Forest in western Kenya. This approach should allow to identify suitable sets of indicator species for effectively assessing the relative impact of different land use patterns on insect (Lepidoptera) rainforest communities in the region. At a later stage, it is intended to expand the obtained results by comparative studies planned at Côte d'Ivoire (Comoe N.P.) and in combination with data from related BIOTA projects (E05, E07, E09, E10) to become applicable for tropical rainforest ecosystems throughout eastern and western Africa.

For the starting phase of the project, the focus is to refine methodological standards for the required field surveys, including techniques for recording, determination of taxa, and data analysis. For the entire duration of the project, the following steps are considered:

- Inventorying the Lepidoptera diversity (8-10 families) for selected plots
- Characterisation of the Lepidoptera community for every selected plot, in relation to past and present human impact
- Comparison of Lepidoptera communities between different habitats, in relation to abiotic and biotic parameters and human disturbance factors
- Identification of indicator species for different types of forest habitats / land use impact
- Development of assessment schemes for evaluation of land use patterns on the current state of insect biodiversity in (East) African forest ecosystems

For this project, it is necessary to rely on comparatively well known groups. The following Lepidoptera families have already been identified as promising candidates in Eastern Africa: Papilionidae, Pieridae, Nymphalidae, Saturniidae, Sphingidae, and Arctiidae [2]. In addition to recording Lepidoptera, soil samples will be taken for all sample plots and jointly analysed (BIOTA E02, E03) to recognise historic changes in land use patterns.

Methods (field surveys):

Standard protocols and techniques for recording and monitoring Lepidoptera diversity are refined to be used in different forest habitats [4]. Intense fieldwork will be carried out at the selected plots/observatories twice in a year during a period of 4-6 weeks, around the beginning and the end of the rainy season, which will later on be supplemented by monitoring activities throughout the year.

For recording diurnal Lepidoptera, transect walks will be conducted periodically (three times a week) at definite times during daylight. All butterflies seen within the bounds of the trail and within a distance of 5 m ahead of the observer are recorded. For recording fruit feeding Nymphalidae, baited traps will be used additionally along the transect routes.

Nocturnal Lepidoptera are recorded by light using both standardised automatic (15 W) as well as manual light traps (125 W) (figs. 1, 2). Recording occurs three times a in periods ranging from 3 hours to the entire night. All species of the selected Lepidoptera families are recorded quantitatively, and individual records will be stored in a central database for further statistic and biometrical analysis of diversity.

Furthermore, small soil samples (100 ccm) taken from homogenous patches within the observatories will be analysed for physical properties and chemical composition following standard procedures.

Fig.1: automatic light trap

Fig.2: manual light trap ('tower')

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Project ID: 01LC0025 (BIOTA East Africa E07)
01.05.2001-30.04.2004

DIVERSITY AND SPECIES COMPOSITION OF ODONATA AS INDICATORS OF BIOTOPE QUALITY OF EAST AFRICAN RAIN FORESTS AND THEIR REPLACEMENT COMMUNITIES

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Key words: dragonflies, Odonata, biodiversity, Kenya, Tanzania, Uganda, wetlands, coastal forests

Abstract:

The principal aim of this project is a comparative study of ecology, diversity and biogeography of dragonflies (Insecta: Odonata) in primary, secondary and fragmented rain forests and different wetland habitats in East Africa. To achieve this an identification key for the dragonflies of eastern Africa is prepared and distribution data as well as data on species specific habitat requirements are collected. These will be used for further applied studies, e.g. the development of indicator systems for environmental disturbances.

Results:

Utilising both, aquatic and terrestrial habitats, the large, predominantly diurnal dragonflies, who can be readily observed and in most cases easily identified in the field, can contribute much to the evaluation of environmental quality. They are known to be very sensitive to structural habitat quality and thus can be a valuable tool to evaluate landscape degradation and have been used as indicator species. The amphibious larvae of dragonflies are critical in regard to water quality and aquatic morphology of streams. The adults are sensitive to habitat structure and are excellent indicators of river disturbance, e.g. changes in habitat structure. Within this project a throughout inventory of East African dragonflies in various habitats and the collection of species specific ecological data is aimed at.

Current activities

Data collection has been started in different areas in Kenya, Uganda and Tanzania. In most areas visited, new records for the could be made and a lot of data on various ecological aspects could be collected. The PhD student John Joseph Kisakye, (Makerere University, Kampala, funded through the BIOTA programme) works on dragonflies in different forests. In cooperation with a GEF project in southern Tanzania it is planned to have Master's projects on the impact of habitat degradation on dragonflies from 2002.

Coastal forests in Kenya

During the last year coastal forests of Kenya were surveyed to a large extend. Coastal forests are listed as important areas in terms of conservation for East Africa [1] and are a major centre of endemism in Africa [2, 3]. Coastal forest areas of Kenya and Tanzania are the primary habitat for a number of highly localised dragonfly species (endemics and/or of unique taxonomy). Detailed studies were carried out on the ecology of the two dendrolimnetic species *Coryphagrion grandis* and *Hadrothemis scabrifrons.* Dragonfly communities relative to different habitat types from indigenous forests to cultivated landscapes were described.

Most of the forest species are confined to coastal forests of East Africa, being stenotopic and highly sensitive to disturbance. With increasing habitat disturbance eurytopic species which are common and widely distributed in Africa colonise the habitats. The species assemblages between different habitat types (stream, swamp, pool) in the disturbed landscape are identical, the β-diversity being very low, although the diversity of single localities may increase after habitat disturbances.

Publicity work
Species check-lists for several National Parks and other protected areas of Kenya have been prepared and were presented to the corresponding authorities. Information boards on the local dragonflies were prepared for some visitor centres (Saiwa Swamp NP, Mt. Elgon NP, Arabuke Sokoke Forest, Nairobi NP). For 2002 a small dragonfly workshop is planned in the Institute of Environmental and Natural Resources, Makerere University, Kampala.

Cooperations
Dragonflies are included in a Wildlife Conservation Society (WCS) project in Tanzania "Southern Highlands Conservation Programme" and in a DANIDA funded project on IBA's in Uganda. Within all projects national reference collections are build up and local scientists trained. First negotiations have started with Ethiopia to include dragonflies in a planned inventory of insects. Together with BIOTA S08 species assemblages in arid habitats, colonisation strategies in seasonal habitats and population genetics of species with a panafrican distribution and different dispersal types are comparatively studied.

Odonatologists working in Africa are linked through the recently started PHAON (Pinhey's Heritage African Odonata Network), which proves to be an excellent tool to exchange views and data, discuss results and present projects. In cooperation with other scientists an atlas for African Odonata and a mapping programme are long term aims.

Publications
The identification key of East African dragonflies will be published in 2002 or 2003. A regional report on dragonflies of Eastern Africa for the IUCN Odonata Specialist Group has been recently prepared. At least one new species waits for description, while a number of other projects need more field work. Following recent manuscripts could be finished:

Clausnitzer, V. 2001a. Notes on the species diversity of East African Odonata, with a checklist of species. Odonatologica 30:49-66

Clausnitzer, V. 2001b. Notes on *Trithemis bifida* and *T. donaldsoni* (Odonata: Libellulidae). The International Journal of Odonatologogy 4:179-189

Clausnitzer, V. in press. Reproductive behaviour and ecology in the dendrolimnetic *Hadrothemis scabrifrons*. The International Journal of Odonatologogy.

Clausnitzer, V., Lindeboom, M. submitted. Natural history and description of the dendrolimnetic larvae of *Coryphagrion grandis.*

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Project ID: 01LC0025 (BIOTA East Africa E08)
1.4.2001 – 31.3.2004

MEASURING AND MONITORING AMPHIBIAN DIVERSITY IN EAST AFRICA: SEPARATING GLOBAL FROM REGIONAL AND LOCAL CAUSES

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Key words: global amphibian decline, community ecology, global ecotypes, indicator species, monitoring, population structure, molecular genetics, standardised methodology, Kenya

Abstract:

Global amphibian decline is currently a controversial issue. However, to judge upon a world-wide phenomenon needs world-wide monitoring. The Global Amphibian Diversity Analysis Group *(GADAG) is setting up a long-term monitoring of circum-equatorial anuran communities. It focuses on ecologically similar species in comparable habitats. Under a GADAG framework, BIOTA E08 studies amphibian communities in eastern Africa (Kenya) along a transect of isolated rainforests of different degrees of fragmentation. This research is methodologically equivalent with analogous projects in West-Africa (BIOTA W08) and Borneo and ally coherent with other BIOTA projects in Kenya. Amphibian diversity is measured at three different levels: the community, the species, and the population level. Species for monitoring are identified, different field methods are tested and compared with other projects (e.g. BIOTA W08). A molecular genetic database of African amphibians is being established and distribution data are implemented in a BIOTA-compatible GIS.*

Results:

For more than one decade now, scientists have noticed tremendous population declines in amphibians all over the world. It is controversially discussed if these observations correspond to a global *biodiversity crises* – or if local or regional causes are more responsible [1, 2].

The project BIOTA E08 has the intention to contribute to resolving this controversial. It is part of a world-wide measuring and monitoring network for amphibian diversity at different levels, incorporated in the *Global Amphibian Diversity Analysis Group* (*GADAG*). This group currently operates in East and West Africa under BIOTA as well as in Borneo. Additional projects are being added to run long-term observations of amphibian populations at the global scale after the current three projects will have provided methodical standards. Only a world-wide diversity analysis system dealing with similar methodology on comparable species ("ecotypes") can provide an answer to the question "global or local?" [3]. The BIOTA framework is especially suitable for *GADAG's* goals, because of the inter- and trans-disciplinary character of BIOLOG. BIOTA E08 focuses on three different levels of amphibian diversity, the community, species and population levels. The specific goals are

- to long-term monitoring of amphibian communities and relative abundance of species.
- to detect anuran species and populations to be monitored (indicator species)
- to define monitoring standards for amphibian populations.
- to analyse the diversity change of all occurring species and the demographic and genetic development of indicator species with respect to environmental (human-caused) change.

Main study area of BIOTA E08 is the Kakamega Forest, added by four additional sites for comparisons: Mount Elgon, Aberdares, Mount Kenya and Runda. We share the Kakamega Forest with all BIOTA projects dealing with E Africa. Mount Kenya is also shared with BIOTA projects E04 and E06. Study sites used by all three projects are already determined.

In 2001, all study sites have been surveyed for amphibians. Data from scientific collections (i.e. National Museums of Kenya, Nairobi; California Academy of Sciences, San Francisco) were added. We can already tentatively provide species lists for Kakamega Forest (21 spp.), Mount Elgon (10), Aberdares (13), Mount Kenya (10) and Runda (15). The total number of species found is 39. Relationships between the localities mentioned is shown in Fig. 1. Field and museum data are currently made GIS-compatible.

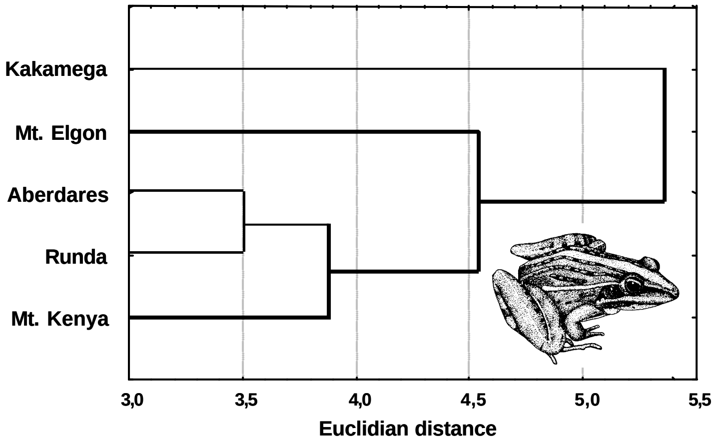

Fig. 1: Comparison of five East African amphibian communities, based on presence-absence data.

Miscellaneous life history and syn-ecological data were recorded for most species (e.g. circadian activity, vocalisations, reproductive modes, predators, prey, climatic preferences). These data are important to taxa that are suitable as. We preliminarily identified potential indicator species for long-term monitoring: *Hyperolius viridiflavus*, *H. pantherinus*, *Ptychadena mascareniensis*, *Phrynobatrachus natalensis*, *Xenopus borealis.* They refer to amphibian ecotypes, currently being defined for the entire tropics by *GADAG* [4].

Field methods for amphibians monitoring have been tested at Kakamega Forest, including opportunistic, quadrate and transect sampling [5]. Field methods are being evaluated, and extrapolation of species richness of communities is tested (cooperation with BIOTA W-08 and the *GADAG* Borneo project).

Molecular methods are used in two ways:

- Molecular taxonomy: Unambiguously IDs of hardly determinable species, species complexes and larvae through DNA sequencing. A molecular database has been established. It presently harbours DNA data of 123 African amphibian taxa.
- Monitoring of genetic population characters: Genetic erosion starts prior to population decline. Therefore, all occurring species are currently screened to identify taxa with high genetic variability for later long-term observations.

A GIS for amphibian distributions is currently being set-up in cooperation with BIOTA E02 to link former and current distributions of species with geo-spatial landscape information.

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Project ID: 01LC0025 (BIOTA East Africa E09)
01.03.2001 – 31.03.2004

THE INFLUENCE OF LAND USE MODES ON DIVERSITY, ABUNDANCE AND GUILD STRUCTURE OF COPROPHAGOUS BEETLES IN THE AFRICAN FOREST-SAVANNA-MOSAIC

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Key words: dung beetles, pasture, agriculture, forestry, fire ecology, community ecology, species diversity

Abstract:

Dung beetles (Scarabaeoidea) show their highest global diversity and abundance in African forest-savanna mosaics. They are responsible for the largest portion of dung decomposition and, thus, take part in the maintenance of soil fertility. The habitats of the forest-savanna mosaic are subject to increasing man-made change and degradation. In this project we analyse changes of a- and ß-diversity, abundance, and guild structure of coprophilous beetles caused by different modes of human land use. Based on quantitative comparative data to be collected in Kenya and Côte d'Ivoire we will analyse to which extent the most important influences, i.e. decrease of autochthonous game fauna by poaching, traditional extensive cattle farming, forestry, agriculture and bush fires, affect the species composition, guild structure and abundance of coprocenoses and, consequently, soil fertility. In addition, we will investigate the historical reasons for the origin and the maintenance of the high diversity of Afrotropical dung beetles to develop strategies for the conservation of this unique, diverse fauna.

Results:

Dung beetles assemblages are an ideal model system for studying effects of human influences on natural habitats because they respond to changes of vegetation structure and microclimate. During the pilot period of the project (2001-2004), we are focusing on the effects of bush fires, poaching and extensive cattle farming. Bush fires are traditionally lit to clear forest areas for agriculture and plantations, and to burn savanna areas to improve extensive cattle farming and hunting.

We established study sites at the border between forest and savanna in the V-Baoulé in Côte d'Ivoire (near the Bringakro research station of the Centre Suisse de Recherches Scientifiques), and in the forest-savanna mosaic region (near the research station of the Universität Würzburg in the Parc National de la Comoé). We sampled at a savanna site that is regularly used as cattle pasture, a savanna site without cattle grazing (*Imperata* grassland), forest islands in the grazed savanna, in a secondary forest, a coffee plantation (burned 17 years ago) and in a yams field in the forest (freshly burned; Fig. 1). Plots of 20 m^2 protected from grazing and protected from fire (Fig. 2), respectively, were installed in the grazed savanna of Bringakro. Additional unburned plots are chosen in the Comoé Park to be established during the next dry season.

Fig. 1: Yams field (*Dioscorea* sp.) on a recently burned secondary forest site; Bringakro, Côte d’Ivoire.

Fig. 2: Firebreak around a 20 m^2-plot of savanna parkland, regularly used as cattle pasture; Bringakro, Côte d‘Ivoire.

The first samples indicate that abundance and diversity of dung beetles is lowest in the secondary forest, higher in the open degraded areas in the secondary forest (coffee plantation and yams field) but highest in the grazed savanna. However, compared with the Parc National de la Comoé, that has still a rich autochthonous game fauna, the species number in the grazed savanna of Bringakro seems to be lower. Baseline data on the dung beetle fauna of the Comoé Park are already available [1, manuscripts submitted].

Our prospecting trip to Kenya is scheduled for October 2001. The sampling programme in Kakamega forest (different forest types and degraded areas around) will start in 2002. Also in 2002, we will start sampling the third study area in Côte d’Ivoire, the Reserve d’Aboukouamekro (a former cattle farm where native large mammals have been reintroduced). Comparing dung beetle assemblages of a region with persistent autochthonous game, fauna with an area with secondary introduced game and with a region where big mammals are extinct and have been replaced by cattle herds, may indicate the relation between mammal fauna and dung beetle assemblages. To evaluate the importance of coprophagous beetles for soil fertility, we started measurements of the amount of buried dung for the species responsible for the highest percentage of dung beetle biomass. Comparisons between dung beetle assemblages of geographically distant regions of the Afrotropical forest-savanna mosaic (Kenya and Côte d’Ivoire) will indicate which of the effects of human land-use on these organisms are general and which are determined by regional parameters.

In addition, we will investigate the history of the present scarab fauna of East and West Africa using phylogenetic and biogeographic analyses. This will elucidate how taxa and zoogeographical elements react to man-made habitat changes. Comparing dung beetle faunas of regions with and without species-rich autochthonous large mammal faunas we will draw conclusions on the importance of the latter for developing the extraordinary diversity of dung beetles in African forest-savanna mosaics. In the long term we will develop conservation strategies for maintaining dung beetle diversity, as well as an indicator system for rapid evaluation and assessment of biodiversity, and for estimating the degree of its endangerment.

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Project ID: 01LC0025 (BIOTA East Africa E10)
1.4.2001 – 31.3.2004

EFFECTS OF HABITAT FRAGMENTATION ON PLANT-POLLINATOR INTERACTIONS IN EAST AFRICAN RAINFORESTS

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Key words: pollination, plant-pollinator interactions, habitat fragmentation, Kenya

Abstract:

The project analyses the influence of forest fragmentation on plant-pollinator interactions. First results indicate a significant difference in flower visitation rates between different forest plots for the understory shrub Acanthopale pubescens. *However, a clearcut pattern between continuous forest and forest fragments cannot be shown as yet.*

Background:

It is widely recognized that fragmentation of natural habitats not only affects the distribution and the abundance of organisms, but that it may disrupt the important biological processes that maintain biodiversity and that are of high importance for the functioning and the longterm existence of ecosystems. The pollination of plants by animals represents such an integrative process - almost 100 percent of the flowering plants in tropical rainforests are pollinated by animals. The main aim of this project is to analyse the alterations of plant-pollinator interactions caused by habitat fragmentation and the consequences for the long-term maintenance of tropical biodiversity.

Cooperation:

The cooperation with the National Museums of Kenya and the International Centre of Insect Physiology and Ecology, both Nairobi, were firmly established. As pollination is a very important integrating process within and among natural communities, ecosystems and agricultural systems, the project is highly appreciated by our counterparts and Kenyan officials. Furthermore, a close connection to the African Pollinator Initiative (C. Eardley, South Africa) was established, resulting in the participation in the First Pan-African Pollination Workshop in February 2002.

Results:

The study is carried out at the Kakamega Forest Nature Reserve, which forms the easternmost part of the afrotropical, guineo-congolian rainforests. During the first field stay (June – October 2001) we established one study site in the northern part of the forest, and another site in the southern part, each consisting of continuous forest (Colobus, Salazar, Isecheno) and different forest fragments (Kisere and Malawa in the north, Yala, Kaimosi and Ikuywa in the south). In order to tightly connect the pollination project to the project on seed dispersal (E11) both groups use exactly the same study plots. Due to logistic problems, forest fragments in the eastern part of the nature reserve are to be excluded from the study.

Contrary to the preliminary studies in 2000, and due to the exceptionally high rainfalls in early 2001, flowering in general was sparse and so was pollinator activity. So far, our studies concentrated on *Acanthopale pubescens* (Acanthaceae), an understory shrub that – with one exeption – occurs in all forest fragments. *Acanthopale pubescens* flowers from July to August and is abundant enough for statistical purposes. Its showy white flowers are quite attractive to a variety of insects and are most probably pollinated by bees (e.g., naturally occuring honeybees). More than 150 individual plants were selected for different purposes. In all forest plots we collected data of the different levels of pollination (i.e., frequency of flower visits, pollination success (pollen tube counting), fruit and seed production) and sampled possible pollinators by standardized methods like sweep netting and malaise traps. Here, the help of Caleb Analo is highly acknowledged. Comparative data on pollinator diversity is, however, not yet available, as we began trapping insects regularly just in October 2001.

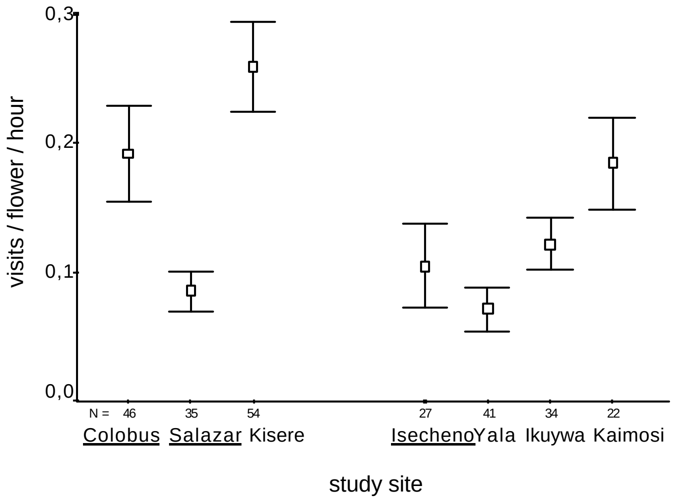

Fig. 1. Insect visitation rate (mean ± s.e.) of flowers of *Acanthopale pubescens* at different forest fragments and continuous forest (underlined) in the north (left) and the south (right) of Kakamega Nature Reserve.

Based on about 300 one-hour observation sessions we can demonstrate significant differences (one-way ANOVA) in flower visitation rates between study sites (Fig. 1). However, no pattern that holds generally for differences between fragments and continuous forest can be shown so far. This is certainly due to the fact that only a single plant species was included in the study. The data on fruit and seed production that are presently analyzed will surely reveal important additional information. Furthermore, forest fragmentation at the Kakamega site obviously is strongly overlayed by other processes like present-day anthropogenic disturbance, above all logging and grazing. The Kaimosi fragment, for instance, although privately owned, is an extremely degraded forest where *Acanthopale pubescens* is superabundant. On the contrary, the Kisere fragment with its not too abundant *A. pubescens*, is one of the best maintained forest fragments of the north. Among other reasons, at both sites, the high visitation rates may be directly related to the plants abundance or, alternatively, may be the result of the lack of alternative resources. To address these uncertainties it is necessary to incorporate other plant species in the study. We already selected the abundant *Dracaena fragrans*, *Acanthus eminens* and *Coffea* sp. for our further investigations that will supposedly start in January 2002.

Project ID: 01LC0025 (BIOTA East Africa E11)
1.1.2001 – 31.12.2004

EFFECT OF FRAGMENTATION ON SEED DISPERSAL, REGENERATION AND DYNAMICS OF KAKAMEGA FOREST, KENYA

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Key words: biodiversity, ecosystem processes, fragmentation, frugivores, fruiting plants, regeneration, seed dispersal, seedling recruitment

Abstract:

This project investigates the influence of forest fragmentation on biodiversity and ecosystem processes related to seed dispersal and forest regeneration in Kakamega Forest. Data on the diversity of frugivorous animals as potential seed dispersers and on the diversity of fruiting trees, shrubs and lianes are currently gathered comparatively in four continuous forest and five forest fragment plots. In a first inventory, seedling recruitment of primary forest tree species was mapped at the same sites to obtain a first understanding of the influence of fragmentation on forest regeneration. Seed dispersal, seedling recruitment and regeneration will now be studied in depth in a few selected tree species (i.e. Prunus africana, Olea capensis, Antiaris toxicaria*).*

Results:

The greatest threats to the biodiversity of tropical forests are habitat loss and forest fragmentation. Understanding how fragmentation affects ecological processes that involve animal and plant populations and how this influences species and habitat persistence in the long term is particularly important but hardly understood [1,2,3]. Seed dispersal by animals is one mutualistic interaction which is essential for the long-term maintenance of populations of tree species in tropical forests. Fragmentation disrupts animal populations and might lead to a decline in frugivore diversity in forest fragments. Consequently, this might result in a break-down of dispersal processes influencing the regenerative potential of forest ecosystems, leading to changes in abundance and spatial distribution of plants [4,5] with far-reaching consequences for the diversity, dynamics and stability of forest ecosystems [6,7]. However, despite its importance there has been relatively little work on animal-plant interactions in tropical forest remnants [but see 1].

In this study we investigate seed dispersal and regeneration processes of forest trees comparatively in continous forest and forest fragments in Kakamega Forest, Western Kenya. In our first field season 9 study plots of 1 ha each were established with four situated in the 8600 ha continuous main forest block and five situated each in one of five peripheral forest fragments with sizes ranging from 100 ha to 1500 ha. Three of the study plots are situated within the biodiversity observatories of BIOTA East (i.e. Buyangu Hill, Mukanku and Kisere).

Our first aim is to document changes in diversity and abundance of animal dispersers focusing mainly on birds. Kakamega Forest is well known for its rich and unusual avifauna, with the 194 forest-dependant bird species including 40 Guinea-Congo Forest biome species and 33 Afrotropical Highland biome species [8]. A recent study showed that Kakamegas peripheral fragments have already lost several forest bird species since their separation from the main forest block [9]. For our study we started a monthly monitoring scheme of the diversity and abundance of the frugivore community using point counts, both in our continous forest and fragment plots. With these data we will be able to understand whether important functional groups such as certain frugivorous dispersers are missing from forest fragments [10]. Parallel, we have started monitoring the diversity, abundance and phenology of fruiting trees, shrubs and lianas at the same sites. So far, fruiting has been low with mainly *Ficus* trees being a major fruit resource for the frugivore community.

Beyond the diversity level, we secondly seek to determine whether forest fragmentation affects seed dispersal and regeneration of tree species. Because the youngest plants in a previously fragmented forest are mainly the result of regeneration from seeds after the fragmentation process has occurred, density and pattern of seedlings may provide clues to the possible effects of fragmentation on tree regeneration. Therefore, a first inventory of forest regeneration was carried out by mapping seedling recruitment and regeneration in 90 1 m^2 seedling plots in each of the continuous forest and forest fragment plots. Seedlings were identified and counted and their age estimated using the number of leaves, stem height and stem characteristics. First results indicate that seedling diversity appears not to be related to fragment size or time of their isolation from the main forest block. However, there seems to be a relation to management system (with higher diversity at sites under Kenyan Wildlife Service compared to under Forest Department) and to disturbance level with highest seedling species numbers in the low disturbance - sites Buyangu and Kisere Forest.

In a next step, we will now look behind the potential causes for differential seedling recruitment and study seed dispersal and regeneration of a few selected primary tree species such as *Prunus africana*, *Olea capensis* and *Antiaris toxicaria*. We will will carry out tree observations, identify seed dispersers, and quantify dispersal rates of individual trees in the same continuous forest and forest fragment plots. We will also quantify seedling recruitment and mortality due to predation and herbivory.

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Project ID: 01LC0025 (BIOTA East Africa E12)
01.04.2001.-31.03.2004

MONTANE FOREST ECOSYSTEMS IN KENYA - DIVERSITY AND POTENTIAL FOR USE

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Key words: Montane forests, ecology, regeneration, vegetation, ethnobotany

Abstract:

Objectives of the proposed project are: First the investigation of the dynamics and stability of the montane forests. How do different types of disturbance (timber extraction, and slash- and burn, high game and livestock populations) affect biodiversity. The second focus centers on the current land-use practices and attempts to evaluate which sustainable use of these resources would be possible. Special attention will be given to the use of non-timber products (particularly medical plants), and the carrying capacity with relation to game and livestock populations.

Project and first Results:

Despite their enormous biological diversity and their exceptional economic and ecological importance as water catchments, erosion barriers and source of timber and non-timber products, tropical montane forests have so far been overshadowed by the interest of governments, public and scientific community in tropical lowland forests. Apart from the Biodiversity Convention, the “Mountain Agenda“ of the 1992 Rio Conference indicated the high priority in mountain region conservation. Little information however exists about this ecosystem. Few neotropical studies have been compiled. Most research focuses still on lowland rainforests or the alpine zones. Even large studies as „Ecoandes“ in Colombia touch the mountain forests only marginally. Our own long-term studies about the phytosociology and regeneration of the forests of Eastern Africa are a sound base for further ecological investigations. The research deficit in tropical mountain forests becomes apparent particularly with regard to forest regeneration. There are almost no studies on regeneration- and succession processes after natural or human disturbances. Only in Eastern Africa, our previous work provides detailed information about forest regeneration. and the germination and growth of important tree species.

Kakamega and Mount Kenya were declared forest reserves in 1933 and 1932. At this time, there were still about 24000ha primary forest in Kakamega. Meanwhile, only 13000 ha (1988!) of fragmented forests are left. 10-20% of the fauna are regarded as endemic. Kenya Indigenous Forest Conservation Project (KIFCON) estimated a value of US$ 2.000.000 for annually harvested forest products, leading to high overharvesting. In the last 26 years Kakamega lost about 50% of its standing timber. 60 years of absolute protection would be necessary to reach the 1965 level again – impossible in a region with high demand for forest products.

Little knowledge exists about Kakamega. Few data on vegetation, tree species diversity and fragmentation are available, and little data on regeneration processes.

Research on use of non-timber products, particularly medicinal species is extremely important to indicate alternatives to timber use and mining, and can thus provide a base for sustainable use projects. Such studies need a high degree of trust from the side of the local population, and thus should be conducted by students from the host country.

Main topic of research are the disturbance of the dynamic species composition in various forest communities, the regeneration potential of the biocoenoses and the way of regeneration, and the use potential of the mountain forests for the local population. The succession processes are studied on selected plots with clear natural (treefall, wind, fire) or human (cutting, slash- and burn, pasture use) disturbance. Main focus are anthropogenous disturbance, as natural processes have been studied by our group already in detail. Particularly important will be to focus on possibilities for sustainable use – how fast can forests regenerate to a climax community? Is high species diversity necessary for maintaining stable forest communities? Fire is of special importance, as this is the most common mean of forest destruction. Timber use and pasture are additional focuses. The possibility for regeneration of disturbed areas are studied with fencing experiments and grazing of selected plots. This will give base data about the vegetation and its possible uses, and will lead to suggestions for management. Additionally, population structure, Regeneration and Ecology of important timber and non-timber species are investigated along altitudinal transects.

The intense use of non-timber products is extremely important for rural populations in large parts of the tropics. Apart from forest products providing food, building materials or fodder, many species serve as medicinal plants. 80-90% of the population uses such traditional medicines. The knowledge about the use is handed from Generation to generation. In recent times, this knowledge transfer is interrupted more and more often, as old healers die, and no apprentices are available. This is particularly pitiful as this sector provides very interesting potential for the sustainable forest use. The documentation of medicinal plants, their uses, possibly contents and their ecology are the second part of the research project. Two Kenyan Ph.D. students funded by the project conduct this work in the Kakamega and Mount Kenya Regions. A final goal of the work is to provide a public medicinal plant herbarium and a “medicinal plant guide“ for the training of health assistants in the local communities. This is an important focus in the establishment of a Botanical Garden at Maseno University, for which Maseno University has set aside 15 hectares of land. Maseno University contributes to this task not only by providing the land but also by its pertinent botanical and horticultural knowledge, by investment of manpower and by offering facilities for external researchers to use the plant material and other facilities in the garden. The goals of Maseno University Botanical garden are to grow, study and promote tropical flora with emphasis on woody native Kenyan species in an educationally useful setting as teaching field laboratories for students‘ individual ecological and conservation projects and to provide an information resource for government, industry, science and the community for practical utilization of forest resources in human development. This is in particular necessary because of the almost complete deforestation of the country, leaving not more than 2% of the country as living and/or gazetted forests. The destruction of plants with high medicinal value is taking place at faster rate. This needs to be mitigated by ex-situ culture of medicinal plants which after developing appropriate cultivation techniques could then be made available to the traditional healers, thus Ethnobotany are one of the major goals of the garden.

Project ID: 01LC0025 (BIOTA East Africa, Yemen E13-E16)

BIOTA-EAST
YEMEN-PROJECT-GROUP:

BIODIVERSITY AND ECOLOGY OF THE PALAEO-AFRICAN REFUGE AREAS IN SOUTHERN ARABIA AND ON SOCOTRA (REPUBLIC OF YEMEN)

Since the Arabian Peninsula was separated from the African continent not earlier than in the Oligocene, E Africa and the Arabian Peninsula had a common tropical flora, vegetation and fauna for a long time. At the same time, migration and exchange between the xerotropical floras and palaeotropical faunas of Asia and Africa were possible across the Arabian Peninsula. Due to the aridisation of the entire region in the late Tertiary, the palaeo-African vegetation and its fauna was then forced into the south of the Arabian Peninsula, isolated from Africa, with increasing aridity finally fragmented and delimited to refuge areas. In the monsoon-affected mountainous areas of the south coast of the Arabian Peninsula and on the island of Socotra, such island-like relict vegetation complexes rich in endemics and with close floristic affinities to NE tropical Africa have survived to the present. They are bioclimatically and ecologically conspicuously differentiated and comprise shrub formations, as well as deciduous and semi-deciduous woodlands of various composition. Similar to the situation regarding the flora, the fauna of S Arabia consists of a unique and complex mix of widespread afrotropical species, highly specialized endemics and remnant populations of palaearctic species.

Five representative palaeo-African refugia have been selected to investigate plant diversity and structure of xerotropical montane communities in southern Yemen and on Socotra by means of standardized monitoring sites. A main objective of the Yemen project group is to obtain information about the history of habitat fragmentation and its present effect on genetic diversity in selected groups of plants, insects and vertebrates. Genetic comparison of isolated populations is used to estimate the time frames of their historical dispersal and diversification. The floristic and vegetational data will provide new insights into the biodiversity and biogeographical position of this little known but biogeographically very important region. A first documentation of the value, importance and ecology of these ecosystems finally will help to estimate the present state of desertification and to develop management plans for the preservation and sustainable use of these unique xerotropical communities.

The selected areas are:
(1) Hawf Mountains, Governorate Al-Mahra: The coastal escarpments shelter the most extended closed woodlands in Yemen, partly comprising endemic *Anogeissus* woodland. As a species rich area with considerable regional endemism it has been recommended by the Environmental Protection Authority of the Republic of Yermrn for protection. Important rural economy.
(2) Ras Fartak Mountains, Governorate Al-Mahra: A climatically transitional mountainous area with very sparse and low woody, partly succulent vegetation cover, but with patches of semideciduous *Anogeissus* woodland in the most favourable sites in the summit area at altitudes of 700-950 m. Extensive pasture economy.
(3) Kor Seiban area, Governorate Hadhramaut: A summit plateau at altitudes of 1800-2000 m with sea facing vertical escarpments and furrowed by numerous wadis. Remnants of semi-deciduous woodland have survived on some slopes and in wadis. Pasture economy.
(4) Jabal Urays, Governorate of Abidjan: The climatically most favoured mountainous area in the coastal SW of Yemen, with important relict communities and high local endemism. Pasture economy.
(5) Socotra, Shihali Peaks, Governorate of Hadhramaut: Species-rich, climatically favoured woodland communities. Pasture economy.

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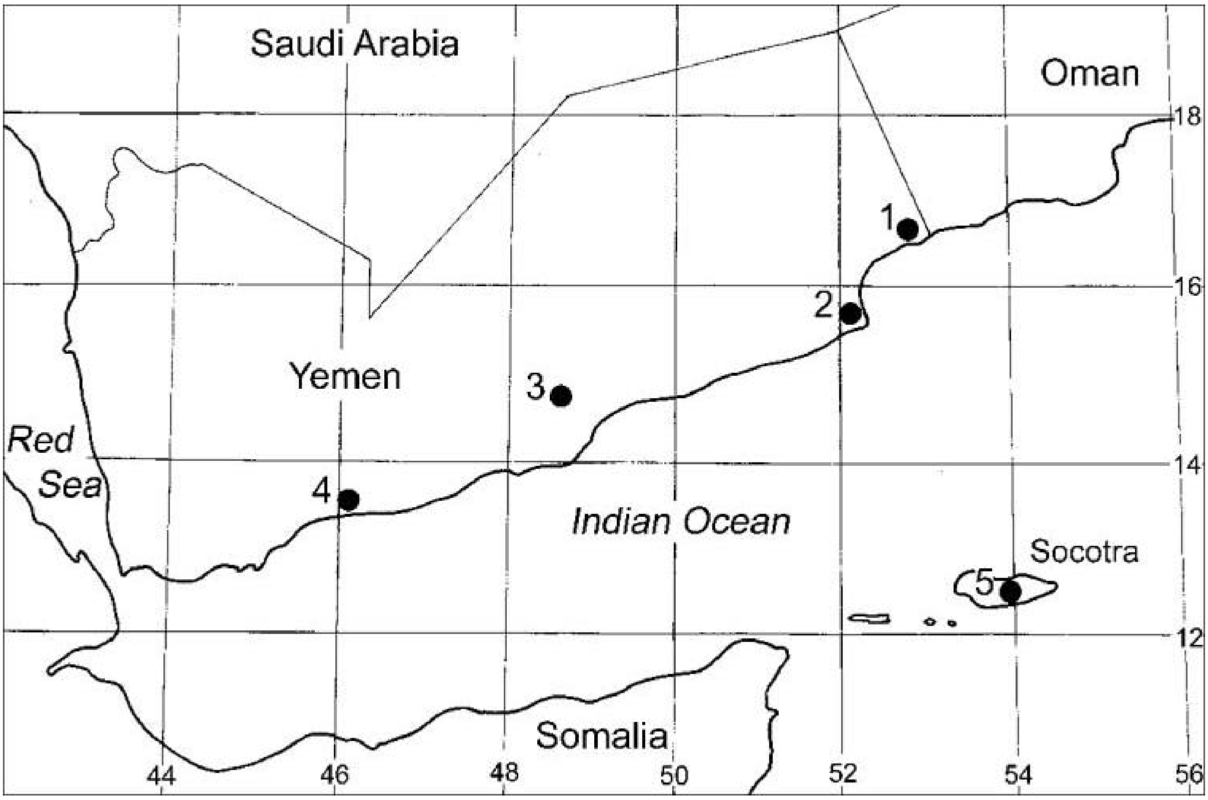

Fig. 1. Map showing the five selected refugia in the coastal mountains of southern Arabia and on Socotra (1 = Hawf Mountains, Gov. Al-Mahra, 2 = Fartak Mountains, Gov. Al-Mahra, 3 = Kor Seiban area, Gov. Hadhramout, 4 = Jabal Urays, Gov. Abyan, 5 = Socotra, Shihali Peaks, Gov. Hadhramout).

Project ID: 01LC0025 (BIOTA East Africa, Yemen E13)
1.3.2001 – 31.3.2004

PHYTODIVERSITY AND VEGETATION TYPES OF REPRESENTATIVE PALEO-AFRICAN REFUGIA IN THE COASTAL MOUNTAINS OF SOUTHERN YEMEN AND ON SOCOTRA (REPUBLIC OF YEMEN)

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Key words: Yemen, *Anogeissus* woodlands, tropical vegetation relics, fragmentation, flora.

Abstract:

As the results of the first six weeks' field campaign in September and October, first standardized monitoring sites on which the Yemen Project Group combines their research were established in three of the five selected refugia, and 650 plant samples for the molecular analyses of subproject E15 were provided. Determination, analysis and documentation of the floristic inventory as well as the present vegetation complexes of the palaeo-African relict vegetation in the S Yemeni-Socotran refugia was started, focusing on the Bauhinia-Tarchonanthus *woodland relics in the Kor Seiban refugial area in the governorate of Hadhramout and on the closed* Anogeissus dhofarica *woodlands in the two refugia in the governorate of Al-Mahra. Instructively illustrating the post-Tertiary fragmentation of the xerotropical plant cover in southern Arabia, preliminary results of the vegetational and floristic study of the* Anogeissus *monsoonal woodland remnants in the Hawf and Fartak mountains are provided.*

Results:

The monsoonal woodland on the Arabian Peninsula is restricted to a small area along the central south coast. It extends from Jabal Samhan, at c. 55°E, in the province of Dhofar of the Sultanate of Oman to the Ras Fartak mountains, at c. 52°10'E, in the Governorate of Al Mahra of the Republic of Yemen. The still little known main part of c. 10 000 ha in Yemen is confined to the coastal escarpments of the Hawf Mts. between Al Fatk at 52°44'E° and the border to Oman (our selected refugial area no. 1). To the larger extent it is an *Acacia-Commiphora* woodland, only on the climatically and edaphically most favoured sites, at altitudes of 300-900 m and in about a fourth of the total woodland area, a closed woodland dominated by the endemic Combretaceae tree species *Anogeissus dhofarica* and with a closed canopy at about 7-8 m height exists. All eight species of *Anogeissus* are trees of rain green tropical woodlands and forests. *A. leiocarpa* occurs in Africa from NE Ethiopia to Senegal, five species occur from India to SE Asia, two species are endemic to S Arabia. Besides *A. dhofarica* this is *A. bentii,* which is restricted to gallery woodlands of wadis in Hadhramout. Both species are relics of the Tertiary belt of (semi)deciduous tropical forest and woodland ranging from S Asia to Africa across the south of the Arabian Peninsula.

According to our preliminary results, the *Anogeissus* woodland is the by far most species-rich woodland community in the Arabian Peninsula, with c. 90 species per 1000 m^2

Table 1. Tree and shrub species of *Anogeissus* woodlands in Al-Mahra, Yemen.

	Hawf	Fartak
Acacia senegal	+	+
Acacia etbaica subsp. *uncinata*	+	+
Acacia nilotica subsp. *indica*	+	
Acokanthera schimperi		+
Allophyllus rubifolius	+	
Anogeissus dhofarica	+	+
Azima tetracantha	+	+
Blepharis dhofarensis	+	
Blepharispermum hirtum	+	
Cadia purpurea	+	
Carissa edulis	+	
Cocculus balfourii	+	+
Commiphora kua	+	+
Commiphora gileadensis	+	+
Cordia perrottetti	+	
Croton confertus	+	
Delonix elata	+	
Dichrostachys cinerea	+	
Dodonaea angustifolia	+	+
Euclea schimperi	+	+
Euphorbia smithii	+	
Ficus ingens	+	
Ficus sycomorus	+	
Ficus vasta	+	+
Flueggea virosa	+	+
Grewia bicolor	+	
Grewia villosa	+	+
Hildebrandtia africana	+	+
Hybanthus durus	+	+
Jasminum grandiflorum	+	+
Jatropha dhofarensis	+	
Justicia areysiana	+	+
Lannea triphylla	+	
Lantana sp. YP460	+	+
Maytenus dhofarensis	+	+
Olea europaea subsp. *cuspidata*	+	+
Pavetta longiflora	+	+
Pistacia falcata	+	
Premna resinosa	+	
Rhus flexicaulis	+	+
Rhus somalensis	+	+
Ruttya fruticosa	+	
Tarenna graveolens	+	+
Woodfordia uniflora	+	
Zygocarpum dhofarense	+	

Fig. 1. Small *Anogeissus* woodland patch on Jabal Fartak.

on average (Table 1). Towards the upper edge of the woodland belt, evergreen tree species are mixed into both the *Acacia-Commiphora* and the *Anogeissus* woodland. A separate sclerophyllous woodland belt as, e.g., the *Olea-Barbeya* woodland in the Asir Mts. of Saudi Arabia is not formed in Al-Mahra. A hundred km farther west and entirely isolated from these main stands, the Fartak mountains (our refugial area no. 2) shelter some outposts of *Anogeissus* woodland. The effect of the SW monsoon is drastically reduced there and the semi-deciduous *Anogeissus* woodland type (Table 1) is confined to small or even tiny patches (ranging from 80 to c. 2000 m^2) in moist niches at altitudes of 700-950 m (Fig. 1), which are, however, similarly species-rich as in the Hawf Mts. Initial floristic analyses of the Al-Mahra refugia result in a number of species not hitherto known from Yemen (Table 2).

Table 2. Initial list of new records for the vascular plant flora of Yemen; 1 = Hawf area, 2 = Fartak area; vouchers at B.

Alectra parasitica Hochst. (1), *Becium dhofarense* Sebald (1), *Blepharis dhofarensis* A.G. Mill. (1), *Blepharispermum hirtum* Oliv. (1), *Centaurea dhofarica* Baker (1), *Ceratopteris cornuta* (P. Beauv.) Lepr. (1), *Cibirhiza dhofarensis* P. Bruyns (1), *Dhofaria macleishi* A.G. Mill. (1), *Dichrostachys cinerea* (L.) Wight & Arn. (1), *Dyschoriste dalyi* A.G. Mill. (1), *Euphorbia orbiculifolia* S. Carter (1), *E. smithii* S. Carter (1), *Gladiolus ukambanensis (*Baker) Marais (1), *Gossypium stocksii* Masters (1, 2), *Habenaria malacophylla* Reichenb.f. (1), *H. myodes* Summerh. (2), *Jatropha dhofarensis* Radcl.-Sm. (1), *Kleinia saginata* P. Halliday (1), *K. squarrosa* Cufod. (1, 2), *Lannea triphylla* Engl. (1), *Lavandula dhofarensis* A.G. Mill. subsp. *dhofarensis* (1, 2), *Maytenus dhofarensis* Sebsebe (1, 2), *Portulaca dhofarica* M. G. Gilbert (1), *Poskea socotrana* (Balf.f.) Taylor (2), *Pulicaria nobilis* Gamal-Eldin (2), *Remusatia vivipara* Schott (1), *Rungia parviflora* Lindau (1), *Suaeda moschata* A.J. Scott (2).

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1.3.2001 – 31.3.2004

ECOLOGICAL CAUSES OF BIODIVERSITY IN THE COASTAL MOUNTAINS OF SOUTHERN YEMEN AND ON SOCOTRA (REPUBLIC OF YEMEN)

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Key words: South Arabia, vegetation, relic forest, *Anogeissus dhofarica*, microclimate, dew-fall, ecology, ecophysiology

Abstract:

The ecological analyses of the vegetation types aim at morpho-functional adaptations and general patterns concerned with the xerotropical plant cover. These concern especially water economy, phytomass and specific productivity of the vegetation types. Pedological examinations complete this view determining the influences of edaphic factors to vegetation. The causal explanation of vegetation ecology results in the explanation of the actual desertification facing the thread of habitat destruction and loss of biodiversity. This gives a scientific basis to assist an ecologically sustainable development. An evaluation is aimed at the ecological potential of nature resources and the intensity of human use or exploitation. It reveals the qualification of vegetation types important to an indigenous economy and to the influences on specific degradation states as well as the actual risks for the ecosystems (fig. 1).

Results:

During the South Arabian Field Campaign in Oct. 2001 and at the end of the monsoon season, microclimatic parameters and respective plant responses have been measured. Field Measurements were taken at the sights of permanent plots agreeing to the flora and vegetation studies of Sub-Project E13. Primary data add some insight into the puzzle of understanding and approaching an ecosystem undergoing desertification. As rain-fall was exceptionally low in 2001 - and the local population could not even yield one drop of cistern water - dew-fall seemed to provide the regular precipitation and to contribute a major supply to the vegetation. This subsidized pre-project measurements from Soqotran mountain ranges (fig. 2). The extensive use of the chlorophyll fluorescence technique enlightened photosynthetic responses on individual and vegetation level. Diverse ecological patterns have been studied in detail at an *Anogeissus dhofarica* spot at Site 1 in the Hawf area. Further field data have been recorded in the coastal mountain ranges at Ras Fartaq and at Damqaut.

Representative plant and soil probes have been taken for laboratory measurements. Plant material was dedicated to quantify its contents of chlorophyll and minerals, soil samples to their textures, nutrients and to the C/N analysis. Some representative specimens of dominant species have been transplanted to the greenhouses to give access to more sophisticated ecophysiological studies.

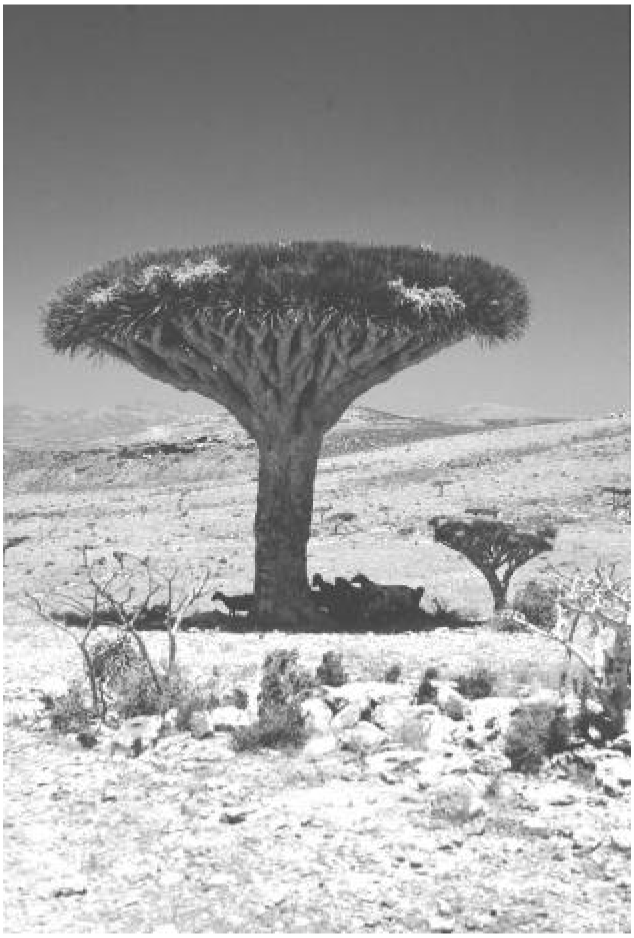

Fig. 1: Remnants of a formerly *Dracaena cinnabari* dominated woodland on the montain slopes of eastern Soqotra.

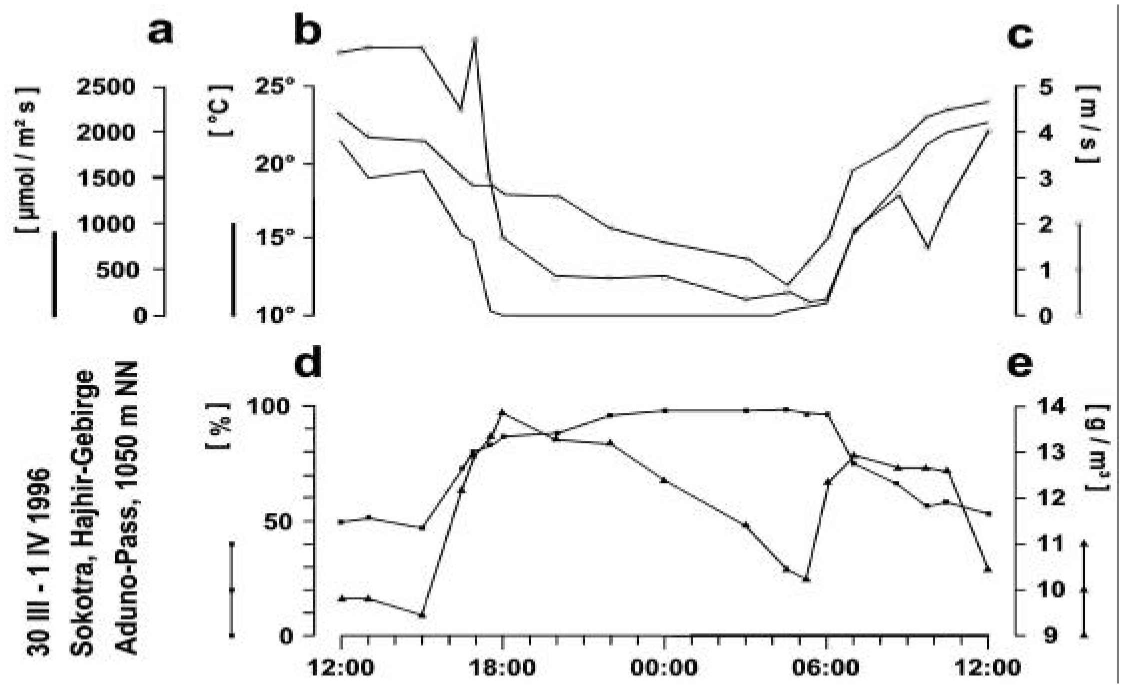

Fig. 2: Insolation, air temperature and humidity during a day course with nightly heavy cloud formation at the Aduno ridge on Hajhir Mountains (Soqotra).

Project ID: 01LC0025 (BIOTA East Africa, Yemen E15)
1.5.2001 –31.3.2004

PHYLOGEOGRAPHIC AND POPULATION GENETIC ASPECTS OF THE PHYTODIVERSITY IN PALAEO-AFRICAN REFUGIA OF THE COASTAL MOUNTAINS OF SOUTHERN YEMEN AND SOCOTRA (REPUBLIC OF YEMEN)

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Key words: Arabian peninsula, phylogeography, habitat fragmentation, genetic diversity, RFLP, AFLP

Abstract:

Using molecular genetic methods (PCR-RFLP analysis of the chloroplast genome, AFLP-fingerprinting) in five representative species or species groups of the palaeo-african refugia of Southern Yemen and Socotra, subproject E 15 aims at both the reconstruction of the temporal and spatial fragmentation processes which have led to the formation of these refugia and the effect of habitat fragmentation on the genetic diversity of the populations involved. While for the phylogeographical part of the project the assessment of chloroplast haplotype variation as revealed by PCR-RFLP analysis is planned, the genetic analyses of fragmented populations will be based on the AFLP fingerprint technique. A short overview of molecular genetic methods and plant groups involved in the analyses of subproject E 15 along with first results of the PCR-RFLP screening phase in Maytenus senegalensis (Celastraceae) is provided.

Subproject E15 of the Yemen-Project-Group within BIOTA-East uses molecular genetic methods to reconstruct the chronological fragmentation of the palaeo-african refugia under study. The elaboration of a hypothesis concerning the temporal and spatial development of these habitats will contribute to a discussion of aspects of taxonomic differentiation, floristic evolution (together with subproject E13), functional morphological adaptation (together with subproject E14) and will enable the comparison with comparable faunistic data (subproject E16). Additionally, population genetic analyses will be done to study the effects of fragmentation of populations on their genetic structure and diversity.

Molecular genetic methods involved:

- cpDNA PCR-RFLP: Using a set of universal primer pairs [1, 2, 3] non-coding regions of the chloroplast genome are amplified via polymerase chain reaction (PCR) and sequence and length polymorphisms are detected by digestion of the PCR-products with a set of restriction endonucleases followed by electrophoresis of resulting fragments. Phylogeographical interpretations are based on phylogenetic reconstructions of chloroplast haplotype evolution.
- AFLP-fingerprinting: The digestion of a total extract of genomic DNA with specific restriction endonucleases, followed by two selective amplifications of subsets of the population of restriction fragments and their electrophoretic analysis [4, 5] yields individual-specific band patterns (fingerprints) that are analysed in an population

genetic framework (e.g. Analysis of Molecular Variance, AMOVA [6]) to study genetic variation within and between populations.

Species and species groups under study:

- *Maytenus senegalensis, M. dhofariensis* (Celastraceae)
- *Gossypium stocksii, G. incanum, G. areysianum* (Malvaceae)
- *Launaea crassifolia* (Asteraceae)
- *Euryops arabicus* (Asteraceae)
- *Euclea schimperi* (Ebenaceae)
- *Justicia areysiana* (Acanthaceae)

Results:

Of the 16 pairs of cpDNA primers tested, different numbers were found to successfully amplify non-coding regions of the chloroplast genome in each of the species involved in the study. Starting the screening process with *Maytenus senegalensis*, the amplified fragments were digested with four restriction enzymes (*Alu*I, *BsuR*I, *Rsa*I, *Taq*I) and the resulting fragments separated by electrophoresis in agarose (2%) and PAA (8%) gels. While the screening is still in process presently with a small test population of 10 individuals from different Yemeni provenances, until now we found two polymorphisms and consequently three chloroplast haplotypes in this species: Digestion of PCR product *psb*C-*trn*S (c. 1650 bp long) with *Taq*I resulted in a fragment of 370 bp vs. 350 bp length in one N Yemen individual, while digestion of PCR product *trn*K1-*trn*K2 (c. 2580 bp long) with *Taq*I revealed a difference between plants from N and S Yemen populations (240 bp vs. 280 bp fragment; Figure 1).

The screening is presently continued for all other PCR products and the other species under study. Once established the relevant fragment/restriction enzyme combinations are used in analyses of whole populations.

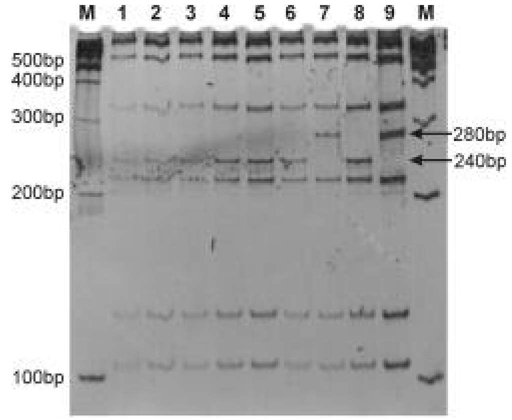

Fig. 1.: Screening of chloroplast DNA variation in *Maytenus senegalensis*. The figured gel photograph demonstrates the occurence of two different PCR-RFLP patterns of the non-coding region *trn*K1-*trn*K2 (c. 2580 bp long) when digested with restriction enzyme *Taq*I. M: 100-bp molecular weight marker; 1-6, 8: N Yemen populations; 7: Ras Fartak Mountains population; 9: Hadramaut population.

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Project ID: 01LC0025 (BIOTA East Africa, Yemen E16)
1.04.2001-31.03.2004

EVOLUTIONARY HISTORY AND PHYLOGEOGRAPHY OF SOUTH ARABIAN FAUNAL ELEMENTS

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Key words: South Arabia, biogeography, phylogeography, endemism, population genetics, evolutionary history, Lepidoptera, *Reissita simonyi*, *Lasiommata felix*, Amphibia, *Hyla savignyi*, Reptilia, *Varanus yemenensis*, DNA-microsatellites

Abstract:

South Arabia is inhabited by a highly specialized fauna and flora of peculiar interest to the biogeographer and evolutionary biologist. The rich biodiversity of the area is increasingly endangered by various hazards, most of which are related to human population growth and its consequences. Our project aims at analysing the origin of various endemic faunal elements, the amount of gene flow between partly highly separated populations and at identifiying viable populations that might be suited for population management and the establishment of permanently protected areas. During two periods of field work (June and September/October 2001) we have been able to 1. provide a clear picture of the present distribution of Reissita simonyi *and closing a considerable gap in the distribution of the two subspecies of the species (appr. 700 samples), 2. to document and sample about ten populations of* Lasiommata felix *(100 samples) and* Hyla savignyi *(200 samples) and 3. to collect first samples of* Varanus yemensis *and related taxa from other parts of the Afrotropical region. In addition we have been able to sample about twenty populations of the larval foodplant of* Reissita simonyi, *i.e.* Maytenus senegalensis *(Celestraceae) to be analyzed in subproject BIOTA E15. Genetic markers for population genetic analyses (DNA-microstaelliutes) of* Hyla savignyi *have been optimized and similar work has been started for* Reissita simonyi*.*

Results:

The South Arabian fauna consists mainly of Afrotropical elements and a few Palaearctic faunal elements. The amount of endemism is extremely high in the area (e.g. 13 endemic species of birds). Little is known on the temporal and spatial differentiation of these elements. Such questions therefore form the core part of our project. Of the four target species selected for the project two are of Afrotropical origin (*Reissita simonyi*, *Varanus yemensis*) and two of Palaearctic origin (*Lasiommata felix, Varanus yemensis*). Thus, our analysis includes a vertebrate and an invertebrate species of both categories.

Aims and Scopes

- to analyse the faunal history of southern Arabia, i.e. processes related to local colonization and subsequent differentiation of Afrotropical and Palaearctic faunal elements as a result of tectonic drift, post-glacial separation and subsequent habitat isolation due to regional desertification in the recent past.,

- to determine the duration of population isolation using genetic data and establishing a molecular clock for such events,
- to provide basic data for the establishment of priority and target areas for nature conservation in the south-western parts of the Arabian peninsula.

Reissita simonyi

So far, two distinct and disjunct subspecies of this ecologically highly specialized taxon have been identified: *R. s. simonyi* along the southern coast (Oman, eastern governorates of Yemen; large, dark blue sheen, both sexes monomorphic) and *R. s. yemenicola* (along western escarpment from the Hejjaz to Taiz; considerably smaller, forewing with greenish blue sheen, males dimorphic, females monomorphic). The disjunction (distributional gap) between these two subspecies amounted to about 700 kms so far. In 2001 we have been able to discover a population of *R. simonyi* near Korseban (Prov. Hadramaut) which fills the middle of the present gap. Larval samples for molecular analysis have been taken from here and about 18 further populations of both subspecies in Yemen (about 700 samples). The phenotype of the intermediate population is still unknown and will be the target of further analyses during forthcoming field work. We assume that further investigations will still narrow the gap between the populations enabling us to estimate whether or not there is still gene flow between the two populations. We have also been able to document in detail the range of *R. s. yemenicola* and its larval host-plant, *Maytenus senegalensis* (Celastraceae). Of the latter, population samples have been secured for project Biota E15 (Dr. Oberprieler, Berlin) enabling our two research teams to compare data on gene flow in this phytophagous insect and its respective larval food-plant. Population samples of *R. simonyi yemenicola* have now been documented from the border with Saudi Arabia in the north down to Jabal Sabr (near Taiz), with maximum distances of 10-50 kilometers between locations. A number of localities has been recorded for the first time.

Hyla savignyi, *Lasiommata felix*

Similarly, we have been able to document the range of these two taxa to a rather detailed scale, again from the north (Jabal Rhaza) to Jabal Sabr in the south. The number of population samples taken so far from both taxa is promissing and will allow further sampling during the next two years.

Molecular work

The development of DNA-microsatellites has been started for Reissita simonyi. In addition, DNA-microsatellitesd have een tested for Hyla savignyi and the conditions for PCR work have been optimized.

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1.1.2001-31.12.2003

BIODIVERSITY OF SELECTED MODEL GROUPS OF THE PHYTOPLANKTON IN STANDING INLAND WATERS OF KENYA

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Key words: biodiversity, phytoplankton, Kenya, Rift Valley lakes, reservoirs, small water bodies

Abstract:

The objective of the project is to investigate the biodiversity of phytoplankton communities in standing inland waters of Kenya with respect to the following items: (i) selection of priority waters representing model ecosystems of different phytoplankton biodiversity, trophic state and human use, (ii) investigation of the physico-chemical conditions of the waterbodies, (iii) detailed inventory of the species stock of model groups of phytoplankton with high ecosystemare relevance and (iv) conclusions concerning their functional role in these waters. During the field work various Rift Valley lakes, reservoirs and small standing waters were investigated. The chemistry of the water bodies showed a great variety. Significant differences were also found in the composition of the phytoplankton communities. The phytoplankton biodiversity in Kenyan standing waters is higher than expected, especially in the diversity of picoplanktic (< 3 µm) and nanoplanktic algae (< 20 µm).

Results:

East Africa suffers from a deficit of high quality and easily accessible water resources, due to long drought periods and increasing demographic pressures. Hence, there is an increasing need for the evaluation and formulation of management strategies for these water bodies. The water quality can be characterized by physico-chemical criteria and biological criteria like the phytoplankton community structure. The importance of the phytoplankton community structure and biodiversity can be explained by the following circumstances: (i) being the main pelagic primary producer the phytoplankton plays a key role in standing water bodies, (ii) the structure of the phytoplankton community, i.e. its biodiversity has a principal influence on many kinds of water utilization by man, (iii) as a consequence of its high reproduction rates, phytoplankton gives a rapid response to changes of environmental conditions, (iv) phytoplankton communities in general are more diverse than other eucaryotic populations in aquatic food webs.

Despite of the importance of phytoplankton biodiversity, the investigations in this area still suffer for various reasons: the lack of specialists of algal systematics, minor knowledge on phytoplankton diversity in different climatic regions of the world and the sometimes necessary expensive methods (electron microscopy and molecular biology) for correct determination. It is estimated that so far only 10-20 % of the algal taxa are known worldwide [1]. In East Africa, phytoplankton investigations have been going on for about 100 years [2]. However, the investigation of standing waters were mainly focused on large lakes like Lake Victoria or Rift Valley lakes [3,4,5]. About reservoirs and small water bodies only few data are available [6,7,8].

An extensive working program will be conducted in co-operation with: Kenyatta University Nairobi (KU); Kenya Wildlife Service (KWS); Kenyan Ministry of Education, Science & Technology (MEST); Tana & Athi Rivers Development Authority (TARDA); Kenya Electricity Generation Naivasha and Masinga (KenGen); Nairobi- Baringo- Koibatek City Councils (NCC, BCC, KCC); National Museum of Kenya (NMK); International Center for Research of Agroforestry (ICRAF). The approaches are to link with the activities of the BIOTA-projects in Africa and the BIOLOG-project AlgaTerra.

During our field work interesting water ecosystems will be selected. The selection includes undisturbed and anthropologically influenced waters. Each sampling site will be characterized by its (i) geomorphological features (geographic position, morphometry, catchment area, inflowing rivers, human impacts, macrophytes), (ii) physico-chemical parameters (water temperature, pH, conductivity, oxygen, ammonia, nitrate, total nitrogen, phospate, total phosphorus, iron) and (iii) biological characteristics. Water samples will be taken for quantitative and qualitative phytoplankton analyses, single cells or single colonies of interesting algae will be isolated for uni-algal cultures for algae systematics, ecophysiological and biotechnological purposes, a checklist of phytoplankton species and their abundance in the investigated waters will be established. The main focus is on cyanobacteria, coccoid green algae (Chlorophyta) and centric diatoms (Bacillariophyta) as remarkable producers of biomass and groups with the highest biodiversity. The preliminary investigations will also include Desmidiaceae, Euglenophyceae and Dinophyceae.

During the first sampling trip in June 2001 24 standing waters were investigated, e. g. Rift Valley lakes: including the freshwater lakes Naivasha, Ol Oiden, Baringo and Ol Bolossat and the saline lakes Nakuru, Elementeita, Bogoria and Sonachi; reservoirs: Kibutie-, Kirandich-, Ngewa-, Ruiru-, Athi- and Masinga-Reservoirs and small standing waters: Uhuru park pond (Nairobi), Nakuru final sewage pond, div. small standing waters in Nakuru National Park.

Table 1: Main results of the physico-chemical investigations in June 2001

Parameter	Rift Valley Lakes	Reservoirs	Small water bodies
pH	8.9 – 10.5	6.5-7.7	8.0 – 9.3
Conductivity (µS/cm)	355 – 60000	45 – 235	202 – 3620
Alkalinity (mg $CaCO_3$/l)	250 – 70000	24 – 144	136 – 2500
NH_4-N (mg/l)	< 0.04 – 1.1	< 0.04 – 0.05	< 0.04 – 0.5
NO_3-N (mg/l)	0.9 – 7.9	< 0.3 – 3.6	2.6 – 6.1
total-N (mg/l)	2.4 – 11.3	< 0.5 – 3.9	2.7 – 15.9
PO_4-P (mg/l)	< 0.01 – 4.5	< 0.01 – 0.08	0.5 – 2.3
total-P (mg/l)	0.2 – 18.0	0.05 – 0.8	0.5 – 4.4

The composition of the phytoplankton communities differed considerably, depending on the character of the lake ecosystem. The alkaline Rift Valley lakes were dominated by blue-green algae, e.g. *Arthrospira fusiformis*, *Anabaena* sp. and *Anabaenopsis abijatae*. The fresh water lakes showed like Lake Naivasha either a diverse phytoplankton community dominated by coccoid green algae e.g. *Pediastrum* div. sp., *Scenedesmus* div. sp. and *Oocystis* div. sp., blue-green algae like *Aphanocapsa* sp. and *Cyanocatena* sp., *Euglena* div. sp. and *various* diatoms or a variety of desmids (Lake Ol Bolossat). In the turbid Lake Baringo the blue-green alga *Microcystis aeruginosa* and the green alga *Thorakomonas* sp. were found in high amounts. Most of the investigated reservoirs were only recently filled due to the severe droughts of the last years and were highly turbid. In this case only a poor phytoplankton diversity was found. We expect that after settling of the silt a diverse phytoplankton community like in the clear Kibutie-Reservoir will develop. The turbid small and shallow standing waters in Nakuru National Park were extremely different in phytoplankton diversity: from mass developments of only one or few taxa to high diverse communities.

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Biodiversity Informatics

Project ID: 01LC9901 (SysTax)
1.4.2000 – 31.10.2003

SYSTAX - ELECTRONIC DATA PROCESSING FOR RECORDING AND ANALYSING BIODIVERSITY DATA WITH THE SYSTEMATIC AND TAXONOMIC DATABASE SYSTEM SYSTAX

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Key words: SysTax, ORACLE DBMS, biodiversity data, botanical systematics, zoological systematics, botanical garden, herbarium management, multimedia data, biological database system, biodiversity informatics

Abstract:
The SysTax system is a comprehensive biological database system which can be used for storing and retrieving biodiversity data from different sources. The data can be distributed over the World Wide Web. The system is available free of charge to all research institutions, botanical gardens, and herbaria for online use. It has been developed since 1989 [1, 2, 3] based on the ORACLE database management system. In this project the program modules "zoological systematics", "management of zoological collections", and "information on taxa" (IOT, incl. "ethnobiology" and "plant-animal-interactions") will be added to the system. The program will be used by several BIOLOG projects (esp. "EDIS" and "InfoComp-Types") for information storage to prove its usability as a common central database for biodiversity data.

Introduction. Within joint research biodiversity programs a large amount of primary and secondary data on the biodiversity of plants, animals, and micro-organisms are accumulated. This includes information relating to taxonomy and systematics, geography and geology, species distribution, ecology, paleontology, and ethnobiology. Reference material, e.g. data on or pictures of collection objects, text protocols and field notes, and sound or video recordings can enormously increase the amount of information to be stored and administered. The storage and retrieval of the data in a powerful system is indispensable to promote synergistic effects, to allow multidisciplinary evaluation, and to make the data generally available and usable for all project participants and the scientific community in general.

The concentration of computer resources and of database development at one site is - in our opinion - a prerequisite for effective work and collaboration within joint projects. The development of small local database applications often leads to systems incompatible with each other. Because of these incompatibilities and because of the cost involved in data exchange between different systems, such local solutions end up being much more expensive than the development of a small number of large and powerful systems.

The SysTax system has been developed at the University of Ulm and the Ruhr-University of Bochum since 1989 with the support of the DFG (Deutsche Forschungsgemeinschaft), the GTZ (Gesellschaft für Technische Zusammenarbeit), the University of Ulm, and the BMBF (within the " Federal Information System Genetic Resources - BIG; a project coordinated by Prof. Dr. Th. Stützel, Ruhr-University of Bochum). SysTax is based on the ORACLE database management system. From the very beginning, the entire system was implemented not only as a multi-user system but also as a "multi-institutional" system. Several scientific institutions can store e.g. their collection data separately but all the data can be queried together. Because of this feature the system can be used for the installation of comprehensive information systems on the World Wide

Web. A “security system” allows to hide sensitive data from being read by the public so that an abuse of data can be prevented to the greatest possible extent.

Results. In this project the program modules “zoological systematics”, “management of zoological collections”, and “information on taxa” (IOT, incl. “ethnobiology” and “plant-animal-interactions”) are being added to the system. SysTax is used by several projects in the BIOLOG-Biodiversity programme (esp. EDIS) for information storage to prove its usability as a common central database for biodiversity data.

Up to now, the program module zoological systematics has been developed. It follows the “potential taxa” concept [4] thus providing the possibility of storing several “alternative taxonomies” as well as the corresponding “alternative synonymies” and the so called “concept synonyms” for a taxon name. The program modules “ethnobiology” and “pictures” did already exist as prototypes. They were now combined to a new module “information on taxa” which is now used to store any additional (multimedia) information on animal and/or plants. Data of the EDIS project as well as of the InfoComp project have been imported.

SysTax –
Task Profile

Botanical and zoological systematics and taxonomy
hierachical storage of names and (potential) taxa; flexible synonymy; linkage of taxa with literature and specimens; linkage of taxa with characters and character states; taxonomical reports for direct use in revisions

Literature
storage and administration of references; cross referencing literature data and taxa; storage of literature scans (plant descriptions)

Botanical Garden
storage and administration of garden accession data; label printing; retrieval of accession lists; creation of seed catalogues; mailing lists for seed catalogues and seed material

Herbarium
storage and administration of herbarium label data; administration of loans; output: herbarium labels, revision labels, specimen lists, letters for loan, reminders, exchange, returns

Vernacular names

Addresses

Information on Taxa (IOT)
storage and retrieval of information on taxa (plants and/or animals): texts, pictures, movies, sound, and OLE-objects; thesaurus for ethnobioloy and plant-animal-interactions

Queries by WWW-Forms
taxonomic reports: taxonomy, synonymy, pictures, texts sound, movies, OLE-objects, collections (incl. pictures of specimens)

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Project ID: 01LC9902 (ARB)
1.4.2000 – 31.03.2003

AUTOMATED MAINTAINANCE OF INTEGRATED DATABASES FOR RRNA AND OTHER RELEVANT GENE SEQUENCES; SOFTWARE DEVELOPMENT, OPTIMIZATION, AND PARALLELIZATION FOR AUTOMATED SEARCHING OF SEQUENCE IDENTIFIERS FOR ANALYZING DIVERSITY

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Key words: databases, identification, rRNA, specific probes, software development

Abstract:

Within the scope of BIOLOG the ARB project provides periodic releases of integrated databases of processed sequence and other data for rRNA and other genes relevant in biodiversity studies. New ARB software tools are currently being developed, optimized or evaluated for automated database maintenance and evaluation. Further software developments focus on the automated design and permanent in silico evaluation of comprehensive sets of taxon specific probes or primers for biodiversity analyses according to the multiple probe concept. These probe sets will later be accessible via the Internet.

Introduction. Comparative sequence analysis of informative genes nowadays plays a central role in biodiversity studies for identification as well as phylogenetic and taxonomic analyses. Doubtless, the currently most important marker genes are those encoding ribosomal RNAs especially 16S/18S rRNAs. This is reflected by a dataset of about 30.000 primary structures available in public databases. Given that the vast majority (> 90%) of prokaryotes cannot be kept in pure culture thus far, comparative sequencing in combination with taxon specific probe and/or PCR approaches often represent the only methods for identification, detection and quantification in environmental samples [1]. These molecular methods are also getting more and more routine techniques for studying diversity, evaluating taxonomy, identification and detection of eukaryotic organisms.

The project. The most important prerequisites for diversity studies based upon these molecular tools are comprehensive sequence databases and powerful software for database maintaining, handling and analysis. Both aspects are in the focus of the ARB project initiated some years ago [2, 3]. The ARB program package provides a software environment for these tasks. Processed (with respect to alignment, quality, conservation, secondary structure and other criteria) sequence data are stored in a central database. Any additional information such as descriptive data, bibliography, user comments or links to external databases can be assigned to individual sequence entries and visualized along with a phylogenetic tree. Database access and navigation is possible via mouse click in that tree or by using search tools. A powerful editor for real or virtual primary structures includes versatile tools for string searching, automated alignment and secondary structure check as well as secondary structure visualization. Conservation profiles and column filters can be established according to user defined criteria. Phylogenetic treeing can be performed applying the respective integrated tools. A special maximum parsimony approach allows reconstruction and optimisation of comprehensive trees representing the full sequence data set (> 30.000 entries). The ARB PT server (positional tree) provides the basis for rapid searching of closest relatives or specific sequence signatures. Such signatures can be evaluated as taxon specific probes or primers against the background of the full database. The ARB package is available at www.arb-home.de and in use worldwide.

Results. Within the scope of the BIOLOG project ARB databases comprising processed sequences of small and large subunit rRNA, elongation and initiation factor, ATPase, RecA, HSP60, polymerases and other conserved gene sequences including additional information and analyses are maintained and permanently updated. Periodic releases are available at http://www.arb-home.de or upon request.

In order to reduce the need of manpower and expertise for processing the rapidly increasing amount of data, software for automation of database maintenance is being developed, evaluated, and/or optimised. The focus is on further automation of data retrieval, selection, update or correction, quality and higher order structure check, alignment, and phylogenetic analyses as well as automated database optimisation based upon iterative cyclic application of the former tools.

The concept of integrated databases giving access to any data (molecular, physiological, morphological, ecological and other) known for an organism has been followed from the beginnings of the ARB project. Concerning the integration of foreign data ARB tools for rapid access to external databases have been improved. Via mouse click and Internet browsers queries can be performed according to ARB data field entries such as accession numbers, DNATAX (project 01LC9904/2) numbers, organism names, or other identifiers on remote databases such as EBI, GenBank, Medline, and SysTax. (project 01LC9901).

Another important task in ARB biodiversity informatics is the design and evaluation of taxon specific probes or primers as tools for studies of diversity with the ultimate goal of automated design and permanent evaluation of all potential probes against the background of the full data set of available sequences. In the ARB version currently available, probe design is an interactive procedure and can be performed for selected organisms or groups only. The ARB-PT-(positional tree)-server which represents the central tool for probe design and in silico evaluation has been improved. A new tool for automated definition of specificity levels according the criteria of presence of potential target sites and phylogenetic relationship is currently being tested. Further tools for finding all minimal probe sets characterizing individual taxa as well as for automated designing comprehensive probe sets of hierarchical specificities according to the multiple probe concept are currently being developed.

Software and database support is provided to the DNATAX project. Parts of the existing databases (rRNA elongation factor) can be immediately used, others (Cytochrome oxidase) have to be established de novo. Collaboration with respect to data exchange and software development had already been established between the ARB group and the BIOTA S04 project.

In collaboration with the MPI for marine microbiology and the VAAM (Vereinigung für allgemeine und angewandte Mikrobiologie) four and two ARB courses for beginners (three days each) and advanced users (two days each) have been performed.

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Project ID: 01LC9903 (ZEFOD)
01.05.2000 – 30.04.2003

REGISTER FOR BIOLOGICAL RESEARCH COLLECTIONS IN GERMANY

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Key words: access system, biodiversity, biodiversity informatics, biodiversity information, biological collections, botanical gardens, botany, collection metadata, herbaria, zoological museums, zoological gardens, zoology

Abstract:

Only occasional overviews and analyses of botanical and zoological research collections in Germany exist at the moment, but individual collections are in various stages of self documentation. The existing data will be combined by ZEFOD, systematized and, together with new data, presented via the Internet as an expandable, interactive information network for a broad range of users in science, administration, and the general public. Apart from an overview of collections, the ZEFOD information system will provide a structural and content-orientated description of biological research collections in Germany based on metadata provided by collection holders. To record the metadata, questionnaires have been designed, mailed to the collection holders, and made available via the ZEFOD homepage [1]. Metadata areas covered include data on the institution or collection holder (address, contacts, staff), general information about the collection (taxonomic and geographical foci, state of documentation), and a description of the collection's contents (number of objects, degree of computer recording, number of nomenclatural types).

ZEFOD stands for "Zentralregister biologischer Forschungssammlungen in Deutschland".

Current state of the database of national zoological collections. The questionnaires for zoological collections in museums or universities were mailed in three batches (13.6., 3.8., 5.9.2001) to 214 institutions. The questionnaires for zoological gardens have been mailed in November, because these institutes usually have more time to do paper work in winter. By October 9, 2001, 20% of the institutions had answered the questionnaires (42 institutions with 102 collections), 13% announced that they want to participate, but need more time, and 10% do not hold the sort of collections required for participation in the ZEFOD database. In all 43% of the institutions responded to our initiative within the first four months. A further increase of coverage is expected, because the response rate for the first batch of questionnaires (mailed in June) has reached 82%.

Some of the museums were visited in order to clarify the aims of the project and to obtain the data. Similarly several scientific as well as other meetings within the community of collection holders, curators, etc. were visited. Representatives of Naturweb (Austria) and BIODIV (Belgium) were contacted in order to exchange experience with regard to online databases carrying meta information about biological collections. A representative of ISIS (International Species Information System), a database for zoological gardens, was contacted to check the possibility of using some of their data for ZEFOD.

Current state of the database of national botanic collections. Questionnaires were mailed to 70 herbaria. For Botanic Gardens data from 435 special collections in 71 gardens have already been collected in previous projects (see, e.g., [2]). The survey for living collections will be based on this information, so the gardens will obtain partly filled-in questionnaires to complete their data in a next step. An Access2000 database application is used for interim data collection and the data existing for Botanical Gardens have been transformed into the ZEFOD data format and integrated into the data bank. The database already accepts queries for different collection characteristics like taxonomy, geography, biotopes, and functional types. It also allows a detailed analysis and shows the amount, variety, and diversity of living plant collections in Germany and different spectra of the representation of diversity in nature and in collections.

To ensure support for the project and to achieve maximum data quality, the Association of Botanical Gardens (VBG) has been informed about the objectives and working plan of ZEFOD. 16 Botanic Gardens and 6 herbaria have already been visited to inform directors and staff about ZEFOD and to give practical support in answering the questionnaire. Moreover, the project has been presented in 4 meetings within the botanical collection community. Within this audience ZEFOD is now well known and the utility of its aims is widely accepted.

Information technique. The ZEFOD database itself is being implemented as a relational database, optimised to store the complex data resulting from the filled in questionnaires. Data input from these questionnaires is done by routines reading the word files and by off-line input, using interfaces containing 'classical' input fields (checkboxes, drop down lists, etc.). Tools for online-data input are also under development which will help to develop ZEFOD into a permanently sustainable information system. Acceptance of the Internet has to be improved, however, before these tools will be used by all collection holders. Scripts for checking correctness of links to homepages of the institutions are under development to guarantee that the provided information is up-to-date.

One important access path to the information in ZEFOD is the search for taxa by their name. Therefore a database structure to store scientific and common names is under development. The user will also be supported by a thesaurus for querying system.

While data capture will be done through the whole phase of the project, some of the results are already available by querying the online-database [1]. Technically this is realised by using ORACLE 8i and scripts for creating dynamic pages. Access to institution names and places is free but there is temporary a restricted area for accessing further details. This allows collection holders to check the data before they will be published.

Biological collection information may be provided on the collection metadata level and on the unit (specimen) level. ZEFOD provides metadata for all biological research collections in Germany and will make unit level information access possible. Seen in the international context ZEFOD is a direct contribution to international initiatives like the 'Global Taxonomic Initiative (GTI)', the Convention on Biological Diversity (CBD) and the 'Global Biodiversity Information Facility (GBIF)'. ZEFOD is the German national node in BioCASE [3].

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Project ID: 01LC9904 (EDIS)
1.4.2000 – 31.03.2003

EDIS – ENTOMOLOGICAL DATA INFORMATION SYSTEM

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Key words: biodiversity informatics, taxonomy, type specimens, world checklists, species identification, DNA sequencing, molecular systematics, image analysis, geographical information systems, bio-acoustics, interactive keys, insects, *Collembola, Saltatoria, Lepidoptera, Hymenoptera, Coleoptera, Acari, Araneae*

Abstract:

The Entomological Data Information System (EDIS) is a co-operative research project jointly undertaken by a number of leading German natural history museums and university institutions in the area of biodiversity informatics. The purpose of EDIS is to facilitate access to information about insects and other arthropods for biodiversity research and the general public by developing and linking relevant databases and information tools established by EDIS partner institutions. The information provided by EDIS includes scientific data about insects from a wide variety of sources ranging from global species inventories, molecular sequences, digital images and sounds to geographic distribution maps.

EDIS organisation:

The EDIS framework project is co-ordinated at the State Museum of Natural History, Stuttgart, Germany, and currently comprises six separate projects (ABIS, DNA-TAX with sub-project MOLART, DORSA, GART, INGE and OBIF) undertaken by different partner institutions. The databases and information systems developed by EDIS are in the public domain and will all be accessible via a central Internet gateway developed in co-operation with the Department of Systematic Botany and Ecology at the University of Ulm, Germany, making use of the SysTax database system. The individual EDIS projects are implemented independently by the respective research institutions, and focus on specific questions in selected insect groups (see following status reports of individual projects). The information provided by EDIS is primarily intended for use by research and development, but also for other users with a general interest in insects.

EDIS goals:

- establishing and extending scientific databases on insects using collection specimens, literature, multimedial and molecular data
- developing and improving new IT-tools for identification of - and information access on - insects
- linking separate databases containing insect biodiversity data of various kinds through a common access point
- providing a common public gateway to a variety of information sources about insects

Project ID: 01LC9904 (EDIS, Subproject ABIS)
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ABIS - AUTOMATED IDENTIFICATION OF BEE SPECIES

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Key words: species identification, taxonomy, image analysis, supervised learning, biodiversity informatics

Abstract:

Computer aided systems have become popular in zoological systematics in recent years. For insects, the difficult taxonomy and the lack of experts greatly hamper studies on conservation and ecology. Bees in particular, as the main pollinators of food crops, represent a critical ecological and economical resource which needs to be carefully exploited and managed. We have developed a system for the automated identification of species that employs knowledge-based image analysis of the bee forewings. The system has been successfully deployed in Germany, Brazil and the U.S.

Results:

The key idea of the Automated Bee Identification System ABIS is to identify bee species from images of their forewings. Using diffuse background illumination, the wings of the bees show a clear venation within a transparent skin. The structure of this venation is genetically fixed and therefore suited to species identification [1]. Analysing each wing image gives rise to a set of about 300 characteristic numerical features. These features are used in a new knowledge-based classification approach to identify the bees' species. The image analysis and classification are performed in a hierarchy of consecutive operations. First, ABIS identifies the genus. In the second step, ABIS identifies species groups – so-called species complexes. In the final step, ABIS employs a new non-linear discriminant analysis to perform the species identification [2]. Each step of this hierarchical approach is guided by the knowledge extracted at the previous step [3]. The result of this classification can be visualised in terms of cluster images or dendrograms. The equipment required is easily portable and suited for work in collections or in the field [4].

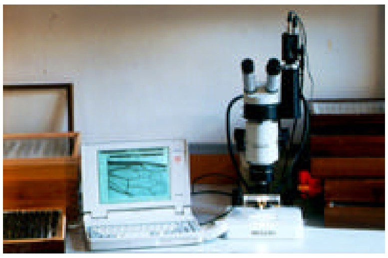

Fig. 1: Use of ABIS in collections

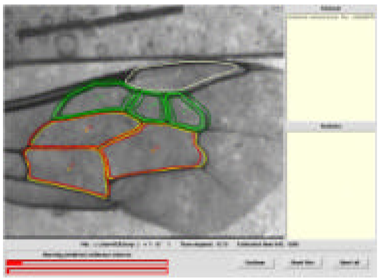

Fig. 2: Automatic image analysis

Fig. 3: Use of ABIS in the field

We give two representative results of our prototype system. Figures 4 and 5 show species identifications for the genera *Bombus* and *Colletes*. Figure 4 shows the genus identification with two clearly separated cluster centres (top: the *Bombus* species, bottom: the *Colletes* species). Figure 5 shows the identification of two species complexes of the genus *Bombus*. The seven *Bombus* species (*B. cryptarum* (Fabr. 1775), *B. lucorum* (L. 1761), *B. magnus* Vogt 1911, *B. terrestris*, *B. ruderarius*, *B. sylvarum* und *B. veteranus)* in the given example belong to two subgenera: *Bombus* (*Bombus*) and *Bombus* (*Thoracobombus*). The clustering in figure 5 and its visualisation in figure 6 clearly show the systematic difference in species membership. For the identification of the species, we employed a new nonlinear discriminant analysis technique and were able to identify even the very difficult to distinguish species *Bombus sylvarum* and *Bombus veteranus* with a correct classification rate of 99.3 % using a leave-one-out cross-validation procedure.

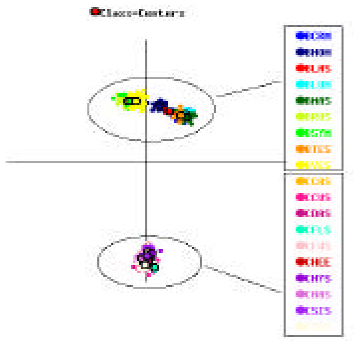

Fig. 4: Genus identification

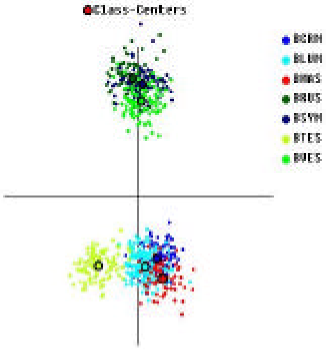

Fig. 5: Identification of species complexes

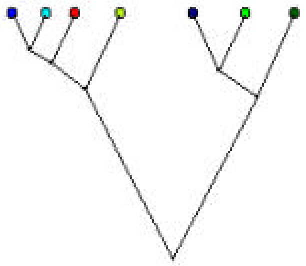

Fig. 6 Visualisation by means of a Dendrogram

ABIS has been successfully applied to species identification in Germany, Brazil and the U.S. Furthermore ABIS can be applied to other insects such as wasps or flies. The ABIS project is an important and innovative part of the joint EDIS project which aims to build and establish a national Entomological Data Information System in Germany. EDIS is funded by the Federal Ministry of Education and Research as a part of the programme Biodiversity and Global Change (BIOLOG). EDIS will permit Internet access and will comply with international standards. It should therefore play a role as a national centre for mapping and monitoring and as the basis for international exchange of information concerning the biodiversity of insects.

The important and crucial first step for each information system is the capture and classification of input data. ABIS offers an efficient solution of this task within the field of mapping and monitoring of insect species.

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Project ID: 01LC9904 (EDIS, Subproject DNATAX 1)
1.7.2000 – 31.3.2003

DNATAX – DNA TAXONOMY AS A TOOL IN BIODIVERSITY RESEARCH: RECORDING, ASSESSMENT, MONITORING AND UTILIZATION OF THE GENETIC DIVERSITY OF EUKARYONT SYSTEMS

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Key words: insects, DNA sequencing, taxonomy, molecular systematics, database, biodiversity informatics

Abstract:

The DNATAX project aims at compiling diagnostic DNA signatures for the main orders of insects. It focuses on the elaboration of phylogenetically informative DNA sequences (e. g. for Geometrid moths, INGE). Data are organized and streamlined in a database on the World Wide Web (SysTax, Ulm) for more efficient use in taxonomic and systematic basic research.

Introduction. In species-rich groups like the insects, which are represented in the environment and in collections by millions of specimens and tenthousands of species, accuracy of identification often is a serious problem for taxonomists and even more for the non-specialist scientists in applied zoology, especially dealing with very small species or immature stages of insects (eggs and various kinds of larvae). In addition, accurate phylogenetic trees provide a sound basis for many questions of evolutionary biology concerning species discrimination and speciation, biogeographic and ancestry-descendance relationships, but also concern important applied aspects like pest control and bio-indication. DNA-Taxonomy provides tools to cover both – identification and phylogeny.

In the initiation phase of the project a complete molecular lab including an ABI377 automated sequencer was established at the Zoologische Staatssammlung München (ZSM), an important institution holding natural history collections. The laboratory devices are intended for high-throughput sequencing which allows operating on different molecular markers such as mitochondrial (mt) or nuclear (c) DNA gene fragments. The broader relevance of molecular-aided taxonomy is to obtain clearly defined taxa. Extensive DNA surveys of species limits and geographic lineage distribution, e. g. delimiting taxonomic units in species complexes are targeted by dense taxon sampling of morphologically highly variable geographic populations. A second important aim is to solve long pending problems in taxonomic classification, systematics, and phylogeny.

Results. At the start of the project protocols for DNA extractions from fresh and archival biomaterials were tested and optimised for routine DNA typing. Genomic DNA (over 600 probes) was isolated from either single legs or plugs taken from the thorax of single dried insects, or from dead animals recovered from the field (pheromone traps, ethanol-fixed fresh specimens). To link an individual to a source (a voucher, frozen biomaterial like tissue) by DNA typing, the repository of extracted DNA and its sources are curated in a resource bank at the ZSM, which allows applications for studying genetic variation, phylogeny, and the processes underlying diversity, such as gene flow. Laser-scanned label data on these repositories and annotation information on the voucher specimen can simply be exported in tabular form to secondary composite databases like SysTax using controlled vocabulary.

Since recommendations made by Caterino et al. [1] outline that "the cytochrome oxidase I, 16S, 18S, and elongation factor -1∀.[...] are informative across a broad range of divergences in insects

[..]", PCR-amplified fragments of these genes (more than 1200 contigs) are also used in our sequence efforts to identify species and lineages. These genes provide potent discriminators of phylogenetic relationships for newly determined sequences for insects, and are a valuable asset to the prospect of a global comparability with the substantial database that already exists for these genes in the principal DNA sequence databases like NCBI-GenBank/EMBL-EBI. In order to exploit the folding structure of RNA molecules in an approach called "molecular morphometry", the 16S like mitochondrial ribosomal RNA is now also routinely sequenced for the studied taxa (100 alignable sequences). Sequences are stored in ARB (see this volume), and compared to its structural alignments preheld in the "pt_Server" to recognize sequence and fold patterns using one of the secondary structure models of the SSU rRNA. Several sequencing projects are elaborated so far focussing on taxon description [2], identification of critical species [3], test of conspecifity of allopatric populations [4], and molecular systematics [5]. Others are under way by cooperation with national (Museum Koenig, Bonn, *Lepidoptera*: genus *Zygaena*, [6]; ZSM, *Lepidoptera: Geometridae, Drepanidae, Diptera: Diopsidae, Hymenoptera:* genus *Euglossa;* University of Jena, [7], University of Bremen, MOLART) and international partners (Zoological Museum, Dep. Entomol., Copenhagen, *Diptera: Sepsidae*, and genus *Themira)*.

Submission of sequence data and associated biological information to the EMBL database at EBI using the WWW site WEBIN is a standard practice prior to publications [2-5]. The unique accession number assigned by the database which permanently identifies the sequence submitted, is cross linked by queries made by SysTax. This interoperability using compressed versions of GenBank's feature table flat-file format ensures availability and distribution of new sequence data.

Phylogenetic trees as graphical representations of the putative evolutionary relationship between groups of organisms, e.g. as calculated from multiple nucleic acid sequence alignment can be generated by the specialized treeing programme tools of ARB. Using its tree-building functions according to an optimised maximum parsimony criterion, homologies between novel query sequences (i. e. of a newly sequenced animal) and stored database alignments are identified by a searching strategy which finds similar alignment positions in local sub trees. Nearest neighbour terminals of localized sub trees may be interchanged during the optimisation fit, while the global tree topology is maintained.

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Project ID: 01LC9904 (EDIS, Subproject DNATAX 2 - MOLART)
1.4.2000 – 31.3.2003 [1]

MOLART (DNATAX 2): MOLECULAR IDENTIFICATION OF COLLEMBOLA: METHOD OPTIMISATION VERIFICATION - DOCUMENTATION

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Key words: Collembola, Nordic species, biogeography, *Protaphorura armata* group, *Isotoma viridis* group, DNA, molecular methods

Abstract:

MOLART deals with the development and standardisation of molecular methods for safe and efficient identification of species which cannot (or only with great effort and expertise) be distinguished by morphological analysis. Different molecular techniques (such as DNA sequencing, AFLP, RAPD, allozymes) are applied, refined and evaluated according to their diagnostic power, their efficiency for different taxa, the necessary effort of time and the required experience This is exemplified by two problematic species groups within the Collembola (Insecta, Apterygota), the Protaphorura armata *group and the* Isotoma viridis *group. To ensure precise identification, the project is conducted in close cooperation with an international expert in Collembola taxonomy - Arne Fjellberg - who will also provide specimens of further Collembola groups for DNA-Tax 1, a database of his collection on Nordic Collembola and volume 2 of his identification key for Collembola of Fennoscandia and Denmark. At present, 9 genera of the family Isotomidae have been finished. For molecular analyses, a number of sites have been sampled, the first laboratory cultures have been started, and the DNA techniques were established. First analyses revealed a) differences within three species of the* I. viridis *group, b) restriction enzymes that could be used for quick species distinction, and c) that the power of the methods used so far differs between the two species groups investigated.*

Results:

1. Identification

The first nine months of the project have mainly dealt with extending and updating the identification key (monograph "The Collembola of Fennoscandia and Denmark"), building up laboratory infrastructure, establishing cooperations, collecting animals and establishing cultures.

Concerning the identification key, 9 genera of the family Isotomidae have been finished (incl. one n.sp. of *Folsomia*). The rest of the family (incl. 3 n.sp.) will be finished by the end of next year, together with the family Entomobryidae. The work for the remaining families of the Entomobryomorpha and Symphypleona will be conducted in 2003. The final Vol. 2 of the monography is expected to contain a total number of 223 species.

Representatives of the genus *Protaphorura* and the *Isotoma viridis* group have been collected from 14 sites in Germany, Denmark and Norway. The live catches are now being used for establishing laboratory cultures to obtain sufficient animal numbers for molecular biological

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[1] The project started only in January 2001

analyses. Thus far, DNA has been extracted, amplified and purified mostly from *I. viridis* s.l. (whole individuals, except for the furca which has been preserved for taxonomic check). Studies with four primer pairs out of subunits of the mitochondrial cytochrome oxidase gene (CO1-fa, CO1-ru, CO2-ab, CO3-ab) revealed CO2-ab to be most appropriate for *I. viridis* s.l., CO3-ab for *Protaphorura* sp.. The first individuals have been sequenced; new results are produced continuously. Based on them, appropriate restriction sites have been selected which can be used for displaying haplotype-specific length polymorphisms on agarose gels: a first step towards easy, quick, affordable and safe molecular identification (Fig. 1)

Present technique	**Future technique: easy and quick identification**
1. Field collection	1. Field collection
2. Microscopic identification	
3. Establishment of laboratory cultures	
4. Separation of furca --> (2)	
5. DNA extraction, amplification, purification	5. DNA extraction, amplification, purification
6. Sequencing	
7. Identification of haplotype-specific restriction sites	
8. Design of specific restriction enzymes	
9. Specific fragment length polymorphism on agarose gels	9. Specific fragment length polymorphism on agarose gels

Fig. 1: An example for improving molecular identification of Collembola within MOLART

2. Interoperability and Linking of Databases

The "collection Fjellberg" comprises about 13,000 records of Nordic Collembola, all of them including locality, habitat, date, collector, literature source and synonyms. The data are ready for import to Systax.

3. Life in time and space: collections as biodiversity information resources

MOLART is specialised in Collembola (Insecta, Apterygota), with special respect to the Nordic fauna. Here, one of the most complete collections worldwide is the "collection Fjellberg" which will be provided as a database by this project.

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1.4.2000 – 31.3.2003

DORSA - GERMAN ORTHOPTERA COLLECTIONS

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Key words: specimen database, geographical information systems, bio-acoustics, automated song recognition, documentation of type specimens

Abstract:

The DORSA subproject (abbreviation for "Deutsche Orthopteren-Sammlungen" = German Orthoptera Collections) is a specimen based Internet database of the Orthoptera held in German museum collections including illustrations of type specimens, sound recordings, and geographic information on a world-wide basis ("virtual museum"). A rapid assessment tool is developed for automated song recognition.

Results:

The aim of DORSA is to provide web access to (i) specimen information of *Orthoptera* in German collections, (ii) a virtual *Orthoptera* collection with link to the *Orthoptera* Species File Online [1], (iii) a photographic documentation of type specimens and other important specimens, and (iv) the wealth of acoustic data of *Orthoptera* in German institutions and private collections. Geo-referencing and combining the locality data with a geographical information system will be tackled further on.

Specimens databased up to now include type specimens (holo-, syn- and paratypes; see table 1), a selection of specimens on which important monographs were based, and voucher specimens for which sound recordings are available. The project covers collections held in the following museums: Berlin (ZMHB), Bonn (ZFMK), Dresden (SMTD), Eberswalde (DEI), Frankfurt (SMFD), Halle (MLUH), Hamburg (ZSMH), München (ZSM), and Stuttgart (SMNS). The private collections of Heller, Ingrisch, Riede and G.H. Schmidt will also be included. Databasing of specimens has been completed in the museums of Dresden, Eberswalde, and Hamburg, started but not yet completed in the other collections. The current state is documented in table 1. To trace the current locality for a given type specimen is often difficult due to incompletely published information, insufficient labelling of specimens, exchange between museums, destruction of specimens (i.e. in war), or "prolonged" loans. DORSA helps to improve the knowledge of the current type depositories. Information on the primary types of 424 species could so far be updated as compared with the *Orthoptera* Species File (OSF). From the taxonomic point of view, the focus was so far on the *Tetrigoidea* (354 species, 1014 specimens), *Gryllacridoidea* (257 [331 with Halle, Stuttgart and Munich included] species, 467 [593] specimens), and *Grylloidea* (323 [341 with Stuttgart and Munich included] species, 619 [655] specimens). The inventory data for those three groups are ready for import into the all-biology database SysTax.

12,000 photographs have so far been taken to document the specimens and the labelling of the specimens; about half of the photographs are already processed for web publishing.

For all specimens with reliable locality information, collection sites are geo-referenced by latitude/longitude co-ordinates. This allows mapping by any geographical information system (GIS) and many additional applications, such as intersection with environmental data. A first prototype for a Java-based graphical user interface can be found at www.groms.de. It allows geographic queries, retrieval and mapping of species data. Modern collections may be reliably geo-referenced in the field by means of a GPS. However, for information stored on historic specimen labels co-ordinates have to be looked up, using atlases or gazetteers. So far more than 2,000 localities have been reliably geo-referenced with latitude/longitude co-ordinates.

Tab. 1: Recorded (roman font) and estimated (italics) type specimens of *Orthoptera* in German museum collections.

museum	taxa with primary types in OSF	taxa with primary types checked	taxa with types including paratypes	number of type specimens	total recorded species	total recorded specimens	type data in OSF not confirmed in museum	primary types lost (taxa)	primary types not listed in OSF	no taxon entry found in OSF	unlabelled, newly recognised prim. types
Berlin	1115	*1546*	*2061*	*4915*	888	2004	15		141	68	11
Eberswalde	47	72	141	410	164	447		1	25		
Dresden	66	118	168	521	294	905	6		57	9	
Hamburg	144	130	200	367	253	478	5	57	47		
Halle	39	*54*	*72*	*172*			1		8		
Bonn	6	*8*	*11*	*26*							
Frankfurt	82	135	183	330	173	364			39	30	2
Stuttgart	47	*65*	*87*	*207*							
München	27	42	68	199				1			
Sum	1573	*2171*	*2991*	*7148*	1772	4198	27	59	317	107	13

The sound library comprises so far 4,000 sound recordings. The species-specific songs are used as a knowledge base for song recognition algorithms based on neural networks. First results indicate that reliable automated classification is possible for songs of *Grylloidea* from South East Asia and Amazonia. Automatic song recognition in crickets *(Grylloidea)* and katydids *(Tettigonioidea)* is a 4-step process: (1) pre-processing of the raw time signals, (2) segmentation of the filtered signals into single pulses, (3) extraction of typical characters (called features in the pattern recognition literature) of pulses or pulse series, (4) automated fusion and classification. In the pre-processing stage sound recordings are filtered to lessen environmental noise, making them better suited for the segmentation task. During signal segmentation single pulses are extracted from the filtered time series based on short-time energy analysis. In the feature extraction global and local features are extracted from the signal. Global features are characterising complete songs of an individual, local features are characteristic for single pulses or short segments of the signal.

Characters most suitable for classification of crickets are the distance between pulses, the duration of pulses, and the frequency course within pulses. The feature vectors are classified individually and the results of the single classifiers are combined through classifier fusion. This leads to local class decisions which are based on the whole feature set. These local class decisions are combined through temporal fusion over the whole time series. The classification uses artificial neuronal networks and statistical procedures, e.g. Radial Basisfunction Networks (RBF), Multi-Layer-Perceptrons (MLP), and Fuzzy-K-Nearest-Neighbour (Fuzzy-K-NN). The feature extraction and analysis tools are written in Matlab. Feature evaluation of single characters and sets of characters is important to find the optimal feature combination. The importance of single characters depends on species and individuals. For successfully training the neural networks we need a dataset from known taxa that allows to adapt the neuronal architecture. For that we need sound recordings from as many as possible different individuals of the same species. At present, the tool for the automatic sound recognition runs properly with a set of 215 songs from 137 individuals and 30 cricket species.

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Project ID: 01LC9904 (EDIS, Subproject GART)
1.4.2000 – 31.03.2003

GART – GLOBAL SPECIES REGISTER BUTTERFLIES

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Key words: biodiversity informatics, taxonomic databases, type specimens, world checklist, *Lepidoptera, Papilionoidea, Papilionidae, Pieridae*

Abstract:

The GART project's aim is to provide general access to information about the world's butterflies based on global taxonomic catalogues. In a first step, global species registers were developed for two families of butterflies, Swallowtails (Papilionidae) and Whites (Pieridae), based on comprehensive taxonomic databases. In addition to extending the taxonomic database, all butterfly primary type specimens housed in the collections of the co-operating GART partner institutions will be recorded, photographed, and databased. For selected taxa within the Papilionidae and Pieridae, a comprehensive species information system will be developed offering data about distribution, ecology, and morphology of individual species as well as links to other existing data sources. The species register and the underlying taxonomic and type specimen databases will be made publicly available through a central user interface on the Internet via the EDIS framework project.

Results:

The GART project is developing a worldwide information system for butterflies *(Papilionoidea)*. It is based on taxonomic and bibliographic databases, which will contain information on all described butterfly taxa, including scans of the original descriptions, illustrations, and on photographs of the primary type specimens in institutional collections.

GART is jointly undertaken by partners from eight major German natural history museums: Staatliches Museum für Naturkunde (SMNK), Karlsruhe; Deutsches Entomologisches Institut (DEI), Eberswalde; Zoologische Staatssammlung München (ZSM); Museum für Naturkunde der Humboldt Universität (MNHU), Berlin; Forschungsinstitut und Naturmuseum Senckenberg (FIS), Frankfurt; Staatliche Naturhistorische Sammlungen Dresden, Museum für Tierkunde (SMTD); Zoologisches Forschungsinstitut und Museum Alexander Koenig (ZFMK), Bonn, and is co-ordinated at the State Museum of Natural History, Stuttgart (SMNS). The project is also intended to provide a distinct contribution to the international 'Global Butterfly Information System' (GloBIS) initiative, to be developed jointly by SMNS and several international research collections [1-2].

In collaboration with leading butterfly taxonomists GART has developed annotated global checklists of the families *Papilionidae* and *Pieridae,* which include all currently recognized species names and important synonyms. These lists are already available via the WWW and will be periodically updated and maintained by a group of international specialists [3].

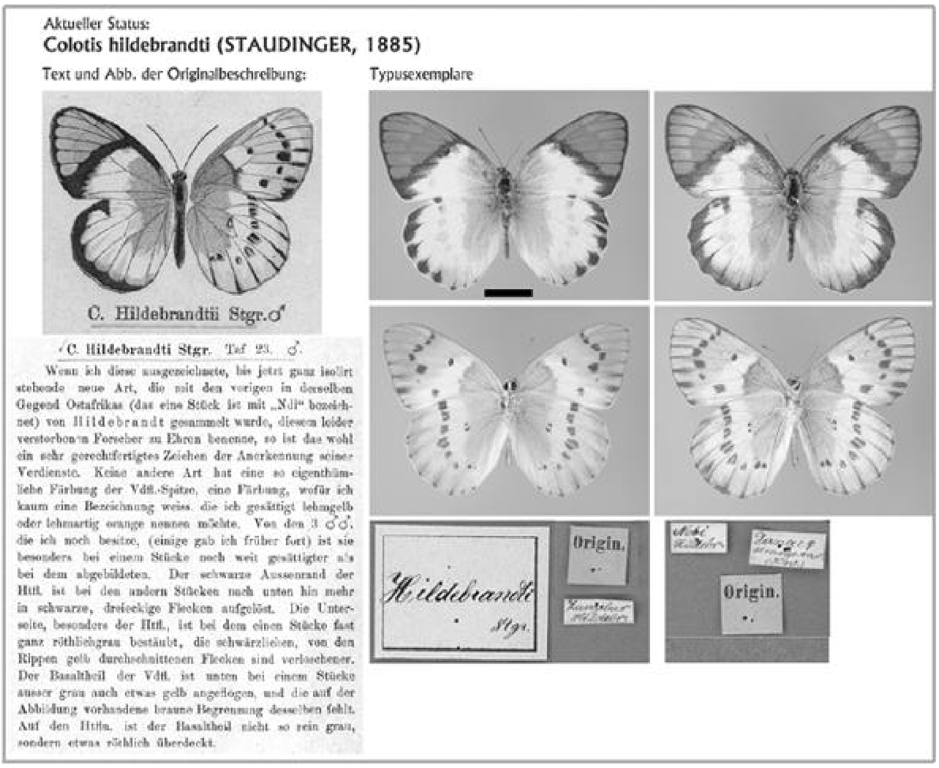
The GART taxonomic database includes information on the original description, primary and recent taxonomic status, taxonomic history, type locality (both original and subsequent information), type status as well as primary type material (including condition and current depository). Each record is linked to a literature database and to specimen and label photographs.

To date, the databases contain more than 1,000 taxon records, more than 20,100 literature references, and over 2,500 digital specimen images.

These data will regularly be transferred to the SysTax-database system at the University of Ulm [4], where they will be made publicly accessible via the Internet in combination with data from other EDIS projects.

Prior to the establishment of the GART databases, general standards for recording taxonomic data were formulated and agreed, which have also been adopted by other EDIS projects (INGE, OBIF). For the digital documentation of type specimens, special equipment (lighting devices) and procedures have been developed to ensure uniform and durable results.

For the difficult and time-consuming task of identifying previously unrecognised type specimens from historic collections, GART is being supported by several renowned butterfly specialists (Drs. Y. Nekrutenko, G. Lamas, and V. Lukhtanov) who have been working in the museums of Berlin, Dresden, and Stuttgart.



C. Hildebrandti Stgr. Taf 23. ♂.

Wenn ich diese ausgezeichnete, bis jetzt ganz isolirt stehende neue Art, die mit den vorigen in derselben Gegend Ostafrikas (das eine Stück ist mit „Ndi" bezeichnet) von Hildebrandt gesammelt wurde, diesem leider verstorbenen Forscher zu Ehren benenne, so ist das wohl ein sehr gerechtfertigtes Zeichen der Anerkennung seiner Verdienste. Keine andere Art hat eine so eigenthümliche Färbung der Vdfl.-Spitze, eine Färbung, wofür ich kaum eine Bezeichnung weiss, die ich gesättigt lehmgelb oder lehmartig orange nennen möchte. Von den 3 ♂♂, die ich noch besitze, (einige gab ich früher fort) ist sie besonders bei einem Stücke noch weit gesättigter als bei dem abgebildeten. Der schwarze Aussenrand der Htfl. ist bei den andern Stücken nach unten hin mehr in schwarze, dreieckige Flecken aufgelöst. Die Unterseite, besonders der Htfl., ist bei dem einen Stücke fast ganz röthlichgrau bestäubt, die schwärzlichen, von den Rippen gelb durchschnittenen Flecken sind verloschener. Der Basaltheil der Vdfl. ist unten bei einem Stücke ausser grün auch etwas gelb angeflogen, und die auf der Abbildung vorhandene braune Begrenzung desselben fehlt. Auf den Htfln. ist der Basaltheil nicht so rein grau, sondern etwas röthlich überdeckt.

Fig. 1: An example for a GART database entry: Comparison between original description (with illustration), and preserved type specimens (with labels).

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Project ID: 01LC9904 (EDIS, Subproject INGE)
1.4.2000 – 31.3.2003

INGE – INVENTORY OF GEOMETRID MOTHS OF EUROPE (INSECTA, LEPIDOPTERA): PROVIDING MULTIMEDIAL DATA ON SYSTEMATICS, ZOOGEOGRAPHY AND ECOLOGY

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Key words: *Geometridae,* Europe, systematics, zoogeography, ecology, multimedial publication

Abstract:

The main purposes of the INGE project are the critical examination and the coordinated compilation of available information on systematics, zoogeography, and ecology of the European Geometrid Moth species (Lepidoptera). The data are published using different media, such as a book series (Apollo Books, Stenstrup, Vol. 1 published in 3/2001), CD-ROM (Expert-center for Taxonomic Identification, ETI, Amsterdam, data partially submitted) and the Internet (SysTax, Ulm, data partially submitted). The results will offer easily accessible identification tools and biodiversity databases which include a virtual type collection and will greatly reduce the need of searching for material scattered widely in many institutions. Geometrids being one of the largest and worldwide distributed insect groups, INGE can serve as a model for modern methods and achievements in measuring and conserving biodiversity.

Results:

In the first half of the project period collection-based biodiversity data have been compiled to gain the information needed on morphology, distribution patterns and bionomics of European *Geometridae (Archiearinae-Sterrhinae).* The Zoologische Staatssammlung München (ZSM) houses one of the world's largest collections of moths including about 200,000 specimens of the subfamilies focused on by the project. Almost half of them have been investigated so far. Microscopic slides of about 3,000 dissected specimens served as the base for morphological studies and for 130 line drawings. Additionally, material from most major European collections was examined (about 100,000 specimens). Distribution maps reflecting collection data have been created for 120 species (of 240).

Quality control of all taxonomic information is one of the crucial aims of this monographic project. In this respect it overlaps with the EDIS–GART project, which established high standards in data-collecting and data-processing. Applying those standards, original descriptions of more than 1,000 taxa have been checked and largely databased. Interdisciplinary interaction with the DNA-TAX projects helps to evaluate the status of taxa at the species level (e.g. validity at species rank of *Timandra comae* has been confirmed), as well as on generic level (e.g. verification of sistergroup-relationship of the tribes *Cosymbiini* and *Timandrini*; synonymy of *Glossotrophia* and *Scopula*) [1]. To date, DNA-information has been provided for about 200 specimens of *Geometridae.*

The first volume of the series „The Geometrid Moths of Europe" [2] has already been published (282 pp.). The project is proceeding regularly and both Vol. 2 and the interactive CD-ROMs (by ETI) will be published in 2003, as planned.

Taxon-based data (checklists) from these publications are transferred via the GART-database into SysTax, where they will be made accessible via the Internet. Basic taxonomic information on the species under focus has already been submitted to SysTax. Furthermore, an object-database contains photos and object (label) data of primary type specimens and other characteristic individuals of all 240 European species of the subfamilies *Geometrinae* and *Sterrhinae*. 340 specimens are databased this way (partially submitted to SysTax).

Interactions and co-operations: The INGE project is a core activity crucial for other research. Alterations of feeding behaviour of certain *Lepidoptera* (e.g. *Cameraria ohridella*, *Gracillariidae*) can cause dramatic problems. DNA analysis of populations or subspecies with regional host-plant preferences may provide a basis for the prevention and biological control of pests [3]. Prerequisites are exact knowledge of regional host-plant utilisation linked with a secure taxonomy, combined with molecular genetic characterisation of properly determined specimens. In this respect INGE can benefit from the international project Geometrid Moths of Europe, the Research Initiative Herbulot [4], and the facilities of the Molecular Research Laboratory at the ZSM, a rather unique constellation in Germany.

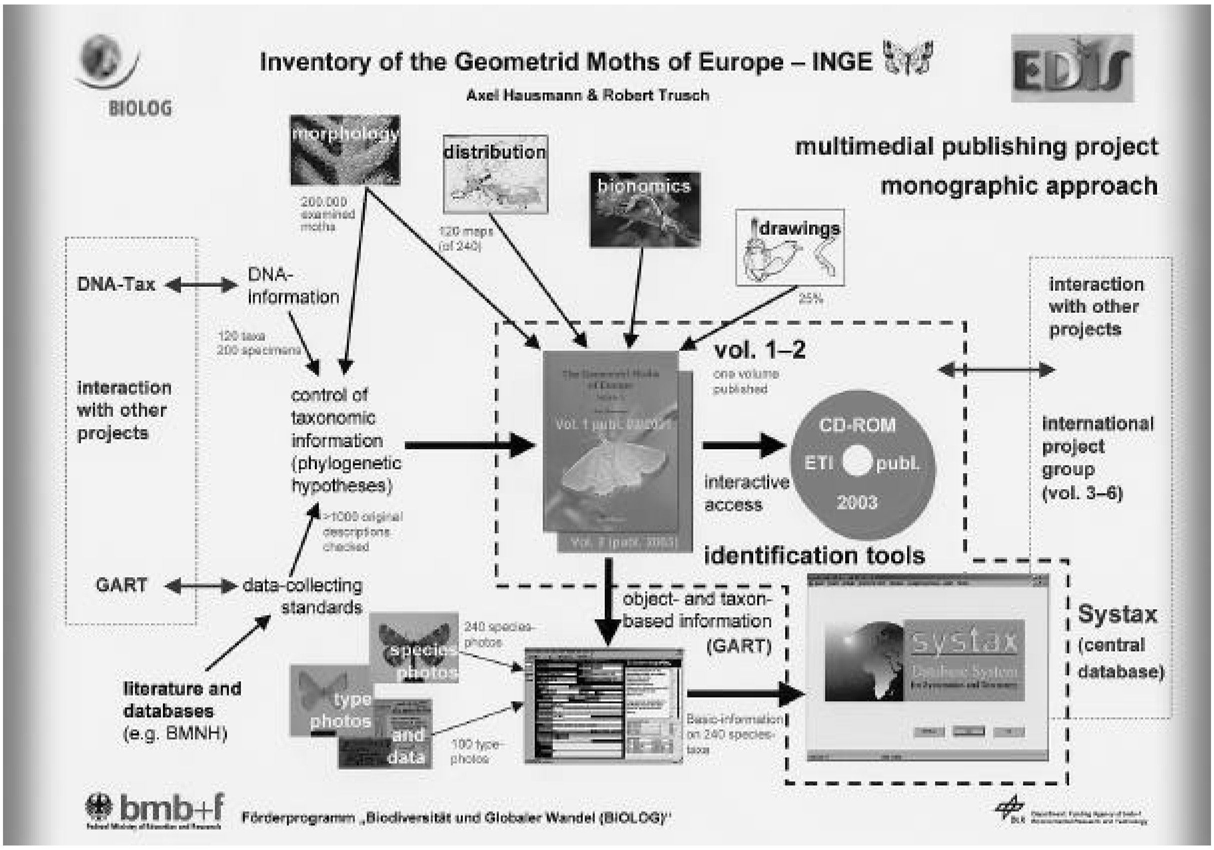

Fig. 1: Information flow and publication activities in the INGE project

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Project ID: 01LC9904 (EDIS, Subproject OBIF)
1.4.2000 – 31.03.2003

OBIF - OPTIMIZATION OF BIODIVERSITY INFORMATION FACILITIES ON APPLICATION-ORIENTED RESEARCH

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Key words: biodiversity information, natural history museum collections, digitalisation, interactive key, *Oribatida, Araneae, Formicidae, Buprestidae*

Abstract:

The OBIF project aims at optimising the input of - and access to - biodiversity data from research projects and collections at the State Museum of Natural History Karlsruhe. It combines electronic identification keys and morphological characters, information on collections sites and distribution of species, ecological data, text information, references with line drawings, digital light microscopy and REM-photos, as well as video sequences into an easy-to-use information system for the scientific and public user on the Internet and in the museum.

Introduction

Natural History Museums are traditionally devoted to recording and describing, i.e. inventorying, the biological diversity on earth. Therefore, they store and administer extensive scientific collections and distribute knowledge on natural history to the public.

OBIF has the objective to optimise the in- and output of biodiversity data at the State Museum of Natural History Karlsruhe. Scientists and technical assistants need the data internally for research and for the administration of the collection. On the other hand, biodiversity data is also to be distributed to external users such as scientists in other fields, NGOs, consultants, or the interested public. To that end, the project improves access to existing databases in the museum. It also cooperates in the construction of an extensive internet-accessible information system (SysTax) with contributions on several soil and wood inhabiting groups of animals. The geographical focus was set on the Palearctic and Neotropical regions, and the taxa chosen (Oribatid mites, spiders, ants, and jewel beetles) are those where years of study have already generated a broad base of information at the SMNK. The system will include information on collection sites and the distribution of species as well as on morphological characters and data of their natural history and ecology. Information will be provided as text, literature references, line drawings, digital light microscopy and REM-photos, and also as video sequences where convenient. As a service to the non-specialist user we combine the databased information with easy-to-use digital interactive keys in DELTA-format [1-4].

Acari: Oribatida

The *Oribatida* are a group of soil mites. Worldwide about 5,000 species have been described, with 500 of them occurring in Central Europe. Due to their detritivorous habits, they play an important functional role in many natural ecosystems. Though of great ecological interest, identification is currently not possible without the help of a specialist. Descriptions and ecological information are scattered over a large number of publications, which are often difficult to obtain. Most of the descriptions available are not suitable for re-identification. Furthermore, the highly specialized terminology for their external morphology deters students from getting familiar with this group.

For this reason, we provide non-verbose interactive keys based on the DELTA-System. The features of our identification system are:

1. digital images on light microscopy instead of alienating scans made by electron microscopy
2. colour markings of diagnostic characters in figures
3. easy-to-use terminology

In addition, taxonomic, bio-geographical, and ecological information will be provided by databases connecting literature data to species names. This enables an economic evaluation of data.

Hymenoptera: Formicidae

In a pilot-project a database will be combined with an interactive DELTA-key to carpenter ant species of the genus *Camponotus* with present and/or historical distributions in Baden-Württemberg (BW, South-West Germany). The key will be illustrated by line-drawings, REM- and light microscopy photos, and in some cases video sequences of living animals, and thus be of easy use for specialists as well as non-specialists. The database (SysTax) will include information on the specimens from the collection of the SMNK (date, sex, locality, habitat, etc.); general information on the ant species like its distribution in BW; literature references for the species; and data on individual morphological characters, which can be compared with the species' standard descriptors used in the interactive key.

Coleoptera: Buprestidae

The metallic wood-boring or jewel beetles are a group of insects with worldwide distribution, mainly in the tropics, but at least 80 species can be found in Central Europe. Some of the more frequent species may cause harm to timber, as they feed on wood during their larval period, like many species of the family. Others, however, are threatened species protected by law. Consequently, there is a high demand from foresters and conservationists for identifications of adult beetles and their larvae.

The latter can be identified with the help of their pronounced traces, i.e. characteristic courses of tunnels they originate while feeding: some species undermine the cambial layers of branches and twigs, some bore deeply into the wood. Furthermore, the imago's hatching hole is of characteristic outline and enables identification on generic level. Especially if one knows about the feeding plant, its age and climatic exposition, identification even to species level is possible with the help of these traces. However, the information about these features is scattered in the literature, and so specialists with much field experience are needed.

We present a DELTA-based key exemplifying different ways of identification in combining information on feeding plants, features of larval tunnels and of hatching holes, and characters of the beetles themselves, thus creating a tool operable by users without expert knowledge.

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Project ID: 01LC9905 (GLOPP)
1.4.2000-31.3.2003

GLOPP - GLOBAL INFORMATION SYSTEM FOR THE BIODIVERSITY OF PLANT PATHOGENIC FUNGI

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Key words: GLOPP, information systems, fungi, plant pathogens, biodiversity, DiversityWorkbench, biodiversity informatics

Abstract:

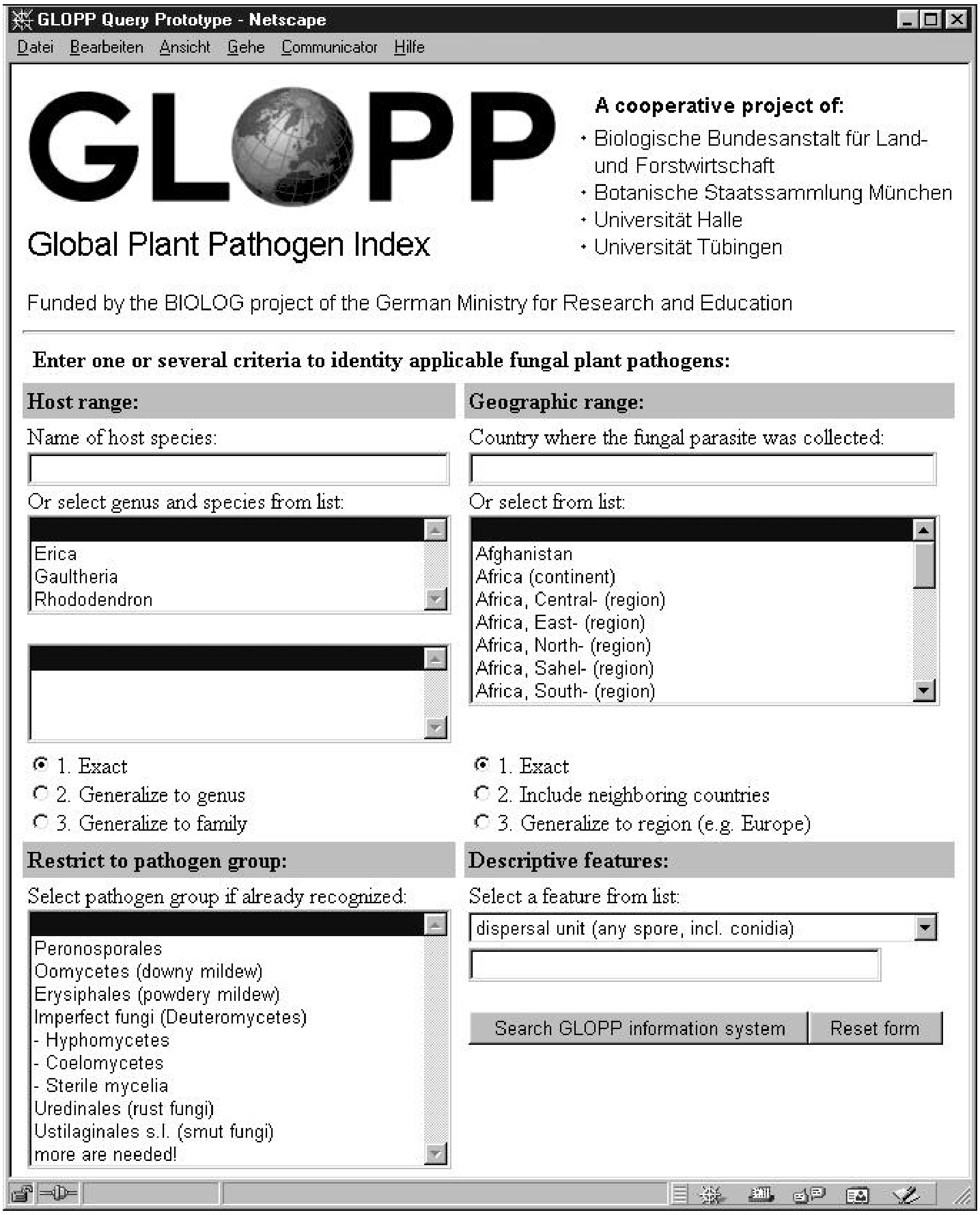
The biodiversity research of several generations of scientists has produced a huge treasure of biological specimen collections, as well as descriptions and reports of new or known organisms. Today, this knowledge should be made readily available in the form of digital media. An integrated information system will greatly improve the efficiency of the work of both the scientists and the applied users in agriculture and forestry.

Introduction:

The GLOPP project ("Global Information System for the Biodiversity of Plant Pathogenic Fungi") aims to provide a unified view of data about fungi parasitizing higher plants. The information system integrates data on host plant specificity, geographical distribution, and a core set of descriptive characters that allow an interactive online identification. Since our resources are limited, European pathogens will be treated with priority, to guarantee high data quality and a certain completeness, but it is planned to continue to extend the scope within a framework of international, collaborative projects in the future.

The information system that is currently being developed goes beyond a simple compilation. It is planned as a critical scientific revision of the available data. Uncritical acceptance of misidentifications and degeneration of data quality will thus be avoided. Original information is kept strictly separate from assessments and interpretations. It will be possible to document the (possibly contradictory) assessments of multiple scientists. The system allows the online interactive identification of plant pathogenic fungi and a retrieval of relevant information, as well as analyses that increase our understanding of biodiversity. Examples are the diversity of major taxonomic groups, the specificity of host-pathogen relations, co-evolutionary processes, or temporal and spatial dynamics in the distribution of pathogens. The project also has a considerable socio-economic impact due to the large number of economically important pathogens.

The system is designed to enable farmers or the general public to identify fungal pathogens without having to study the complete list of characters and without access to the scientific literature. For example, a query might be: "Show all parasites that belong to imperfect fungi, which have been found on Rhododendron in Germany, and which have oblong, aseptate spores, 4 x 10 µm large" (fig. 1). The information system would try to find all fungi that fulfil the given criteria based on past experience (i.e. information published in the literature or in herbaria). The system could provide error tolerant usage, by adding a second result list, which includes all records from the entire region (i.e. Europe), which have been found on a species in the *Ericaceae*, and includes fungi that fulfil the descriptive criteria only approximately. At the end of the project the information system will be available on the Internet free of charge.



Global Plant Pathogen Index

A cooperative project of:
- Biologische Bundesanstalt für Land- und Forstwirtschaft
- Botanische Staatssammlung München
- Universität Halle
- Universität Tübingen

Funded by the BIOLOG project of the German Ministry for Research and Education

Enter one or several criteria to identity applicable fungal plant pathogens:

Host range:

Name of host species:

Or select genus and species from list:

Erica
Gaultheria
Rhododendron

● 1. Exact
○ 2. Generalize to genus
○ 3. Generalize to family

Geographic range:

Country where the fungal parasite was collected:

Or select from list:

Afghanistan
Africa (continent)
Africa, Central- (region)
Africa, East- (region)
Africa, North- (region)
Africa, Sahel- (region)
Africa, South- (region)

● 1. Exact
○ 2. Include neighboring countries
○ 3. Generalize to region (e.g. Europe)

Restrict to pathogen group:

Select pathogen group if already recognized:

Peronosporales
Oomycetes (downy mildew)
Erysiphales (powdery mildew)
Imperfect fungi (Deuteromycetes)
- Hyphomycetes
- Coelomycetes
- Sterile mycelia
Uredinales (rust fungi)
Ustilaginales s.l. (smut fungi)
more are needed!

Descriptive features:

Select a feature from list: dispersal unit (any spore, incl. conidia)

Fig. 1: Prototype for a web interface to use the GLOPP integrated information system for the identification of plant pathogenic fungi

Project ID: 01LC9905 (GLOPP, Subproject IT)
1.4.2000 - 31.3.2003

GLOPP-IT - BIOINFORMATICS AND DEVELOPMENT OF THE INFORMATION SYSTEM

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Key words: GLOPP, information systems, fungi, plant pathogens, identification, bioinformatics, biodiversity, xml-schema, DiversityWorkbench, DiversityCollection, DiversityReferences, DeltaAccess, biodiversity informatics

Abstract:

GLOPP-IT is creating an integrated information system on the biodiversity of plant pathogenic fungi and their hosts by gathering descriptive and collection data, literature references, resource information and taxonomic names. The project provides a set of application modules to other projects within GLOPP and develops the public access system on the Internet.

Results:

Many current solutions to manage biodiversity data (e.g. SysTax, Specify, BioLink) are based on a highly complex, monolithic information model with different tasks tightly connected. These models are difficult to analyse and implement. The GLOPP IT project has therefore invested considerable time and effort to design a modular information model, where the various modules can be implemented separately and are exchangeable with 3rd party modules. Interface definitions allow to define associations between the central biological objects of the modules. This modular structure (see fig. 1) provides the basis for a customisable system that can be configured to suit the demands of scientists and other users. A data exchange format based on XML-schemata is currently under development. Preliminary versions can be downloaded from the Internet [5-8].

DiversityCollection was designed to capture label data from specimens of plant pathogens in the herbaria of Munich and Halle/S. (GLOPP-Erysiphales). DiversityReferences manages scientific literature citations; DiversityTaxonomy records the nomenclature and synonymy of scientific names and organizes them into (potentially multiple) taxonomic hierarchies.

The information from these three central modules is used in the two modules collecting the data for the identification process. DiversityDescriptions (derived from DeltaAccess version 1.7) represents a complete tool to manage descriptive, especially morphological and chemical data. The SpecialIndexing module records the project specific information on host-pathogen-interactions from literature and specimen data. The identification tool (DiversityIdentify) will use morphological data as well as geographical and host-parasite-interactions. A web interface will be implemented during the remaining time of the project to access the identification system from the Internet.

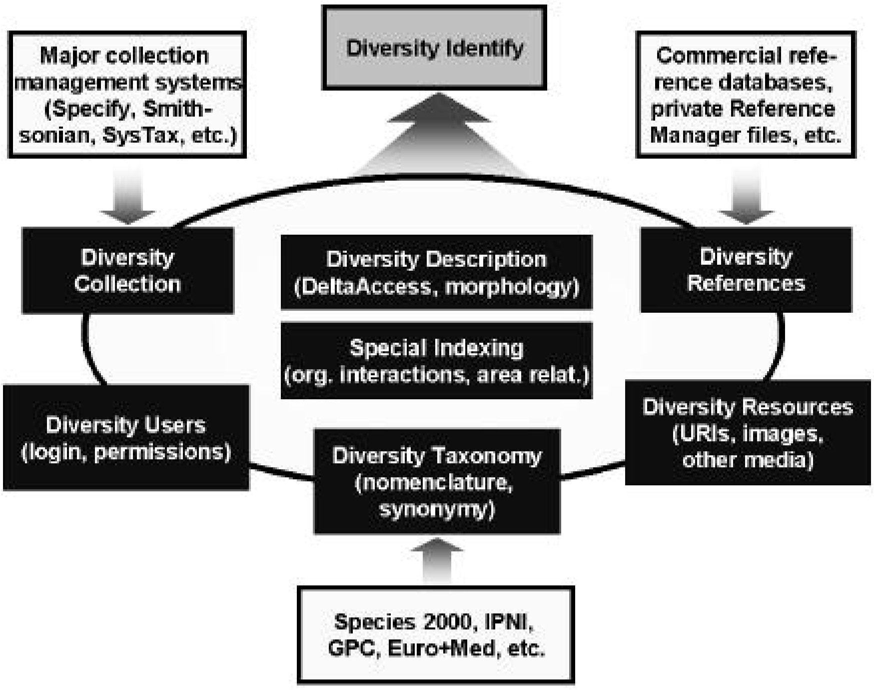

Fig. 1: Overview of the modular design of the DiversityWorkbench

Support modules are: DiversityUsers for user administration and documentation, a geographic names index (DiversityGazetteer, at present including the world-wide Getty TGN and the German GN250) used for geo-referencing; DiversityResources, to manage hyperlinks, images, and other media used to support the identification of organisms. DiversityResources indexes resources by keywords and organism names, addresses the problem of changing URLs, and documents intellectual property rights.

All modules and information models of the DiversityWorkbench system are open source and available from http://www.DiversityCampus.net.

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* References 5-8: All information models, including SQL DDL and xml-schemata documents can be found under http://www.DiversityCampus.net/Workbench/download.html

Project ID: 01LC9905 (GLOPP, Subproject LIT)
1.4.2000 - 31.3.2003

GLOPP-LIT - DIGITIZATION OF IMPORTANT EUROPEAN HOST-PATHOGEN INDICES FOR FUNGI

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Key words: GLOPP, fungi, plant pathogens, identification, host-parasite index, *Erysiphales*, powdery mildews, *Peronosporales*, downy mildews, Brandenburger, literature capture, biodiversity informatics

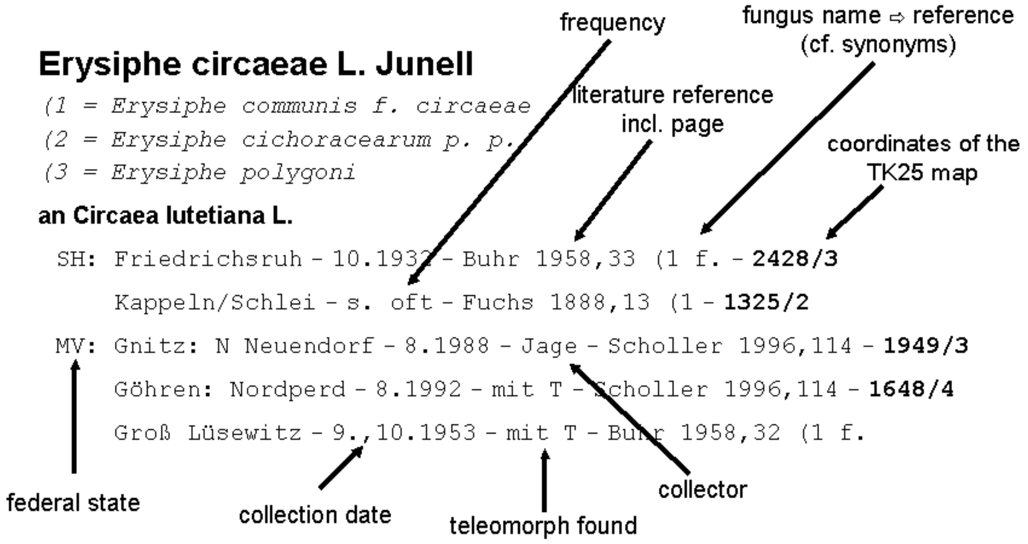
Abstract:

The GLOPP-LIT project focuses on capturing published or unpublished scientific information on plant pathogenic fungi. Scientists working in the particular fields of biodiversity will guarantee the high quality standard of the database. In the framework of the collaborative GLOPP project the literature project provides a base layer of information for the identification of plant pathogenic fungi that is supplemented with more detailed information from the projects working on specific groups. Eventually, scientists will not only be able to search for specific parasite-host-interactions, also a literature reference and geographic relations are given.

Results:

The most important publication on plant pathogenic fungi for Europe, Brandenburger [1], has been fully captured in a database of more than 11,200 records. Unfortunately, this publication does not provide any information on literature references or other resources used in its compilation. It thus has to be supplemented from index cards and manuscripts provided to the project by Dr. Brandenburger. The original references on index cards have been scanned, partly transcribed, and indexed in a networked database (7,600 references). The manuscript (comprising 12 binders) and personal communications are currently ran through to connect the references with the host-parasite observations. Approximately half of the work has been finished up to now.

In addition two unpublished manuscripts (fig. 1) on the *Erysiphales* (powdery mildews) and the *Peronosporales* (downy mildews) are currently edited in cooperation with Dr. Brandenburger and converted to structured documents. Based on an XML-like mark-up, they will ultimately be converted to a relational database and integrated into the GLOPP information system.



Erysiphe circaeae L. Junell

(1 = Erysiphe communis f. circaeae
(2 = Erysiphe cichoracearum p. p.
(3 = Erysiphe polygoni

an Circaea lutetiana L.

SH: Friedrichsruh - 10.1932 - Buhr 1958,33 (1 f. - **2428/3**
Kappeln/Schlei - s. oft - Fuchs 1888,13 (1 - **1325/2**
MV: Gnitz: N Neuendorf - 8.1988 - Jage - Scholler 1996,114 - **1949/3**
Göhren: Nordperd - 8.1992 - mit T - Scholler 1996,114 - **1648/4**
Groß Lüsewitz - 9.,10.1953 - mit T - Buhr 1958,32 (1 f.

Fig. 1: Plant parasite record from an unpublished manuscript by Dr. Brandenburger. The information is identified using named style tags, which are displayed in different colours, allowing the correction of mark-up mistakes.

Other publications [2-9] have been prepared for conversion into a database. The remaining time of the project will be necessary to finish the conversion and integration of these sources. Subsequently specialists of the fungal groups will improve the quality level of the data.

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Project ID: 01LC9905 (GLOPP, Subproject Oomycetes)
1.4.2000-31.3.2003

GLOPP-OOMYCETES

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Key words: GLOPP, data base, biodiversity, *Oomycetes*, *Peronosporales*, molecular evolution

Abstract:

A combination of classical morphology and modern molecular methods allows to achieve high quality of taxonomic data in a biodiversity information system for plant parasitic Oomycetes.

Results:

The *Oomycetes* are a monophyletic group including obligatory parasitic and saprophytic species. Members of the *Saprolegniales*, *Sclerosporales*, *Pythiales* and *Peronosporales* may cause considerable economic damage on crop plants, e.g. *Aphanomyces raphani*, causing the radish black dye, *Phytophthora infestans*, causing the late blight of potato and *Plasmopara viticola*, causing the downy mildew of grapevine.

The GLOPP project does not aim at a simple compilation of data, so critical appraisal of the data found in taxonomic literature is necessary. As a rule, this entails experimental re-examination of the published data. Current systematics of plant parasitic *Oomycetes*, at least above species level, are based mainly on morphological characters, so extensive light microscopical studies are required. As optical microscopy is the customary tool in applied phytopathology, quality data achieved with this technique are of highest practical value.

Unfortunately, the morphological data so far used for Oomycete taxonomy are often ambiguous. This is especially important where only few morphological characters are available, as it is the case in species delimitation in most parasitic Oomycete genera. Even the total number of species in *Peronosporales* and *Sclerosporales* stated in the literature can vary very much depending on the underlying species concept used by different authors [1]. Where species circumscriptions are based mainly on the taxonomy of the respective hosts [2] and no additional infection experiments have been carried out, a vicious circle arises with respect to conclusions on cospeciation. The same is true when practical questions concerning host specificity are considered.

To cope with the mentioned uncertainties, the combination of morphological with modern molecular methods is required. Application of the latter has been exemplified already in earlier work from Tübingen [3] with emphasis on the systematics of aquatic *Oomycetes*. Our recent publication [4] presenting results from sequence analyses of LSU rDNA focuses on taxonomic problems in the field of plant parasitic *Oomycetes* or downy mildews. Below, we will give some examples from these results and how they influenced our light microscopical analyses and the arrangement of the Oomycete database.

Important parts of the current classification of the *Peronosporomycetidae* [5, 6] proved to be unsatisfactory. With regard to family concepts, we posited that *Lagenidium* should be placed within the *Pythiaceae*, *Phytophthora* and *Peronophythora* within the *Peronosporaceae*.

It could also be shown that the genera *Bremiella* and *Peronophythora* should be dismissed and transferred to *Plasmopara* and *Phytophthora*, respectively. Therefore, the character “swollen conidiophore tips” used so far for the delimitation of *Bremiella*, is probably of minor taxonomic value. Instead, *Bremiella baudysii*, a species that parasitizes a member of the *Apiaceae*, seems to be most closely related to the *Plasmopara* species infesting this plant family, a result that gives an example of the meaning of cospeciation in plant parasitic *Oomycetes.*

Following the work of Fraymouth [7], we had already erected a morphological typology of the haustoria in *Peronosporales* to be used in the database that was clearly supported by the molecular results. Haustoria seem to be of major importance for the characterization of groups of genera in *Peronosporales*. So the *Peronospora* species possessing haustoria of our type D are genetically highly diverging from the ones with type C haustoria. Additionally, the former contain all *Peronospora* spp. infesting *Brassicaceae*. Therefore, we focussed microscopical research on this group. Indeed, we could find some other morphological characters that separate it from the *Peronospora* spp. not specialized on *Brassicaceae* (unpublished data). Likewise, many of the groups Gäumann [2] called “Formenkreise” were preliminarily supported. However, oospore characters of *Peronospora* turned out to be of negligible value for infrageneric taxonomy.

If data quality of an information system about biodiversity is to be guaranteed, three main interdependent questions arise: (1) Which taxa represent natural groups? (2) Which characters possess taxonomic significance? (3) How should the character states be defined to achieve a clear-cut separation of taxa? Obviously, the content of the database will depend to a high degree on how these questions are answered. In our opinion, a dual strategy employing morphological and molecular methods not only facilitates finding the correct answer, but is the only possible way to proceed. This justifies the often time-consuming search for fresh material of Oomycete-infested plants and for molecular methods adjusted to this material and the taxonomic problems that have to be solved. We hope that the examples from our recent molecular and morphological results given here may support our view.

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Project ID: 01LC9905 (GLOPP, Subproject Erysiphales)
1.4.2000 – 31.3.2003

GLOPP-ERYSIPHALES - A GLOBAL INFORMATION SYSTEM FOR THE BIODIVERSITY OF POWDERY MILDEWS (ERYSIPHALES, ASCOMYCOTA)

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Key words: GLOPP, ColdFusion modules, DiversityCollection, *Erysiphales*, LabelScan, LIAS, molecular phylogeny, biodiversity informatics

Abstract:

The labels of 8500 specimens of Erysiphales stored at the state-run herbaria in München and Halle were digitised using LabelScan. Approximately 20–25 % of the label data have already been transcribed to the database DiversityCollection. Three ColdFusion modules were developed for making the data available via the Internet. The molecular studies resulted in 40 complete sequences of the rDNA ITS region and partial sequences of the rDNA 28S region. An ITS sequence alignment including 50 Genbank sequences was built up for performing cladistic analyses. Published descriptive data of all taxa of the Erysiphales have been included in the LIAS information system and are provided as natural language descriptions. In addition, data can be queried for interactive identification by the DeltaAccess Perl interface. All data will be evaluated and presented in a global information system.

Results:

The project *Erysiphales* uses a number of joined database modules mainly developed within the GLOPP project (DALI, DiversityCollection, DiversityExsiccatae, DiversityDescriptions). The biodiversity data were collected from herbarium labels, from original literature and images and – especially within molecular studies – derived from primary research activities. All types of data and databases are stored in a modularised database system.

Recording and evaluation of herbarium label data based on the *Erysiphales* collections in Halle (HAL) and München (M). In order to solve the problems of recording large amounts of herbarium data, a concept for a standardized and user-oriented data recording in collections was developed. In a first stage the material is labelled with barcodes. These labels are scanned together with the original historical labels showing all information provided by the collector such as locality data, as well as later revisions. For this purpose the scan-software LabelScan v. 2.0 was developed to provide an automatic recording of the barcode-labels and a simplified administration of image files [1]. In another stage the digital label images are imported into DiversityCollection in order to establish a comfortable and structured way of transcribing the label data into this MS Access database. The herbarium material is only needed for the scanning of the labels, all succeeding work can be done within the database, either locally or over the Internet. Due to the great amount of material (8500 specimens in M and HAL) the transcription process had to be divided into a number of stages, some of which could be carried out even by untrained persons. Actually a selective entry of data is performed in three parallel and independent procedures, namely the entry of collection data (2500 data records already completed), of host data (1200 data records already completed), and of location data via Getty TGM (600 data records already completed). The data input into DiversityExsiccatae, a database module with bibliographic specifications and abbreviations of 220 exsiccata series, is now complete. A pull-up list, containing the basic information of DiversityExsiccatae, was integrated into DiversityCollection in order to facilitate data entry of the exsiccata series.

Online access to collection data, images and literature of *Erysiphales*. Several ColdFusion modules have been developed to give public access to the data via the Internet: "Search Exsiccatae" is a tool for searching and remote editing the entries in DiversityExsiccatae [2], "Search Collections" allows a search for host-parasite relationships and collectors in DiversityCollection [3] and the module "Search Drawings Braun 1987" [4] gives online access to more than 300 plates with ink drawings originally published by Braun [5]. The literature database DALI (A Database of Ascomycete Literature) has been extended by the category *Erysiphales* and contains 400 pertinent data sets [6].

Data recording for molecular phylogenies (18S, ITS, 28S). The molecular studies on the phylogeny of *Erysiphales* resulted in 40 complete sequences of the internal spacer region (ITS) of the rDNA and partial sequences of the 18S and 28S rDNA. The sequences were aligned with 50 sequences received from GenBank. Alignments of all sequences and several subgroups have been made. On the basis of these alignments cladistic calculations were performed to get new insights into the relationships of European taxa of powdery mildews. The analyses of the *Uncinula adunca* group are especially promising. Currently the molecular studies are extended to non-ribosomal genes such as the beta-tubuline coding gene. After successful primer selection the first beta-tubuline sequences were obtained. The relevancy of this gene for phylogenetic studies on various systematic levels has still to be tested.

Build-up of a LIAS associated online-system for interactive identification and character analysis. The descriptive data of Braun [5] were partly transferred to LIAS (A Global Information System for Lichenized and Non-Lichenized Ascomycetes [7]. For this purpose the LIAS character list had to be extended to *Erysiphales*-specific characters, and a list with all species names and their basionyms including author abbreviations checked for correctness had to be compiled. The data are now accessible as natural language descriptions [8]. In order to complete the descriptive data sets with digital illustrations of the organisms (see "Search Drawings Braun 1987") an interface for cross linking is under construction. The interface DeltaAccess Perl [9] is used for establishing an online identification tool for *Erysiphales* within LIAS [10].

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Project ID: 01LC9905 (GLOPP, Subproject Smut Fungi)
1.4.2000-31.3 2003

GLOPP – SMUT FUNGI

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Key words: GLOPP, smut fungi, *Tilletiales, Ustilaginales*, China, DiversityDescriptions, biodiversity informatics

Abstract:

Data on the morphology of smut fungi are integrated into the GLOPP information system using the module DiversityDescriptions. Up to now, 460 different species of smut fungi have been documented. Field research conducted in the Neotropics and in Yunnan, China, provided collections of fresh material of smut fungi, which was used to study the morphology and alpha-taxonomy. These primary data significantly improved the quality of species information in the database.

Results:

The software DiversityDescriptions (see GLOPP-IT) presently offers 169 characters with numerous character states for the description of species of smut fungi. These characters and character states (descriptors) are based on those observed in detail by M. Piepenbring on neotropical smut fungi for which a monograph for Flora Neotropica is prepared. The monograph includes 227 species in 34 genera, or ca. 17.5 % of the about 1,300 species of smut fungi known world-wide. With more species of smut fungi added to the database, further characters and/or character states have to be added. The database allows this at any time, without affecting existing data sets.

As many as possible species will be studied by us personally before including them into the database. Further species are included based on descriptions in literature we consider reliable. European smut fungi, for example, are relatively well known by a monograph written by Vánky [1], descriptions of North American smut fungi can be found in the book of Fischer [2]. The character states of species descriptions in literature are transferred into the characters and character states available in GLOPP-DiversityDescriptions. In some cases like size and colour characters, this is a relatively straightforward task, but e.g. for soral morphology and for spore ornamentation, different authors use different terminology. Illustrations like detailed drawings and SEM photographs of teliospores can help, but a broad knowledge of the diversity of morphological features of smut fungi is indispensable to avoid transcription errors.

By now 460 more or less complete and revised species descriptor sets are present in the DiversityDescriptions database. We intend to include descriptions of most of the known species of smut fungi until the end of the project, however, present knowledge on many species of smut fungi is limited in several ways:

- Details of soral morphology are only evident in good material including young states of development.

- Some species are known by only one or few poor collections which do not always allow a detailed study of morphology nor the identification of the host plant.
- The identification of host plants documented in literature is not always reliable.
- For many species we do not know the morphology of the basidia, which can only be observed with recently collected teliospores placed on water agar.
- There are many taxonomic problems including unresolved synonymy, problematic generic placements, and unclear delimitation of species.

In addition to these problems, we are far from knowing the really existing diversity of smut fungi, especially in large countries where few mycologists looked for this group.

In order to improve the quality of data for poorly known species, field work is a constant part of our investigations. In Bolivia, with only five weeks of field work and study of herbarium specimens, four new species were found [3].

For China the diversity of *Ustilaginales* is documented by Guo Lin [4]. She described 140 species of this order for China, which has regions with very high diversity of higher plants. This can only be a small proportion of the existing diversity of smut fungi, because for Europe, with less diversity of higher plants, we know ca. 400 species of *Ustilaginales* and *Tilletiales*, with the *Ustilaginales* being the larger group [1]. Fieldwork and study of herbarium specimens in Yunnan during the summer of 2001 led to 50 collections representing 25 species. These can now be examined in detail and the respective descriptor sets can be completed in the database, including e.g. the morphology of basidia. Among the species are new ones, new records for the region, and some of them occur on species hitherto unknown as host. More field work of this kind, however, is necessary to come to a more realistic assessment of the diversity present in China.

Recently collected specimens of smut fungi can be used for molecular analyses. Phylogenetic hypotheses based on LSU rDNA provide important arguments for systematic and taxonomic conclusions. They directly improve the quality of the data in the database by indicating generic placements of the species. The delimitation of characters and character states is also affected because molecular phylogenies allow to distinguish similar character states based on homologies from those based on analogies. This has recently been demonstrated for species of *Cintractia* by Piepenbring et al. [5].

While field research on smut fungi is going on, we complete the database hoping to encourage more mycologists and taxonomists of higher plants to look for this group of plant parasitic fungi, which is not only of economic importance but also a fascinating example on how parasitic fungi coexist with their host plants in a natural balance.

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Project ID: 01LC9905 (GLOPP, Subproject *Uredinales*)
1.4.2000-31.3.2003

GLOPP-UREDINALES - REGISTRATION OF TROPICAL AND SUBTROPICAL RUST FUNGI

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Key words: biodiversity-database, Costa Rica, *Prospodium*, *Uredinales*

Abstract:

Rust fungi are economically important but still insufficiently studied in tropical regions. In our approach we ascertain data on taxonomy, distribution and ecology of tropical rust fungi and complement them by basic systematic and field research. This combination yields high quality data that are essential for the applied research and utilization of taxonomic knowledge e.g. in agriculture as well as to solve elementary questions of rust fungal biology.

Introduction and research plan:

With about 7.000 species, rust fungi are the biggest and economically most important group of obligate plant parasites. Beside their economic importance, rust fungi have a uniquely complicated life cycle and offer excellent opportunities for the study of plant-parasite co-evolution. The knowledge about biodiversity, distribution and host relationship of rust fungi from the tropics and subtropics is still restricted and difficult to access as summarising floras and monographs are widely lacking.

Our work aims to contribute to the investigation of tropical and subtropical rust *mycota*

(1) by providing data on the taxonomy, distribution and host selection of the parasites

(2) and by ascertaining own field and systematic data.

Only the permanent control of literature data by accompanying critical elementary studies can guarantee a reliable data quality.

In our approach we concentrate on three subjects:

- a study of the rust fungus *mycota* of Costa Rica
- a monographic study of the neotropical rust genus *Prospodium*
- the building of a database/checklist of tropical and subtropical rust fungi containing data on nomenclature, distribution and host spectra.

Results:

Rust fungus *mycota* of Costa Rica. During our exploratory trips to Costa Rica we secured approx. 300 rust specimens, of which 250 are determined and registered in the database. Among the collected specimens we found seven species that were new for science. Several species represented new reports for Costa Rica or were found on hosts that had not been recognised before. In the next step the important Döbbeler-collection of Costa Rican rusts will be evaluated.

So far, 220 species of rust fungi have been ascertained for Costa Rica from literature.

***Prospodium*, a neotropical genus of rust fungi.** We selected the genus *Prospodium* for a case study for several reasons: with approx. 70 species the genus is exclusively neotropical and shows a strict host restriction on *Bignoniaceae* and *Verbenaceae*. Its tropical distribution, species number and morphological diversity makes *Prospodium* an ideal example to combine a monographic study with processing the data in a character and biodiversity database. Up to now, a species- and synonym list have been built up. Two new species, *Prospodium manabii* and *P. kisimovae,* were collected in Ecuador and Costa Rica.

Database/checklist of tropical and subtropical rust fungi. We are working on a database that contains nomenclatural information as well as data on distribution and host spectra of rusts. At the present stage, mainly literature data on tropical and subtropical species are included and is being critically evaluated. The database presently contains information on approx. 13.000 parasite-host combinations that are represented by ca 21.000 geographical reports.

Project ID: 01LC9906 (INFOBOT)
1.4.2000 – 31.3.2003

INFOBOT - DEVELOPMENT AND TESTING OF INFORMATION SYSTEMS COVERING DIFFERENT ASPECTS OF BOTANICAL COLLECTIONS

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Keywords: information systems, botany, vascular plants, *Compositae*, living collection, natural history collection, botanical garden, natural substances, biodiversity informatics

Abstract:

INFOBOT demonstrates the application of information technology on different aspects of botanical collections: the management of living collections, the linking of factual information (chemical compounds) important in applied research, and access to type specimen information as one of the keys to basic taxonomic research. The resulting information systems are to be published on the WWW and will be integrated into information networks.

Introduction. INFOBOT is a collaborative project creating information systems about different aspects of plant collections. Two of the three partial projects focus on the world's largest vascular plant family, the *Compositae*. Although they lack the urgently needed central taxonomic component (a global species database of the family), the two projects demonstrate different approaches towards the mobilization of taxon information in electronic databases. The third project incorporates the aspect of living collections. The potential of botanic gardens as a source of information and materials for education and research will not be fully realized until their information is available on-line. At the same time, information technology greatly assists in the internal management and quality control of the information held and produced by such collections.

INFOCOMP/TYPES uses digital photography (see fig. 1 and following article) in combination with textual input to provide access to nomenclatural type specimens (vouchers on which the species' description was based and which fix the application of the scientific name). The types of the *Compositae* present in the most important German herbaria are being recorded and will be made accessible to scientists on the WWW.

INFOCOMP/CHEM, the “Bohlmann Files”, is a database of all natural substances in the *Compositae*. A former card index which was transferred to an ISIS/PC database is now converted to a relational database format and will be accessible on the WWW. In this database chemical and botanical expertise is united, providing combined information which is of great potential for a wide range of users, e.g. in pharmaceutic industry and biotechnology. The project pinpoints the diversity of natural substances and will contribute to the taxonomic research attempting to elucidate the relationships and evolution within this important group of plants.

INFOBOT-BoGART, the Garden Accessions Database of the Botanic Garden Berlin-Dahlem, is a model project for a complete accession and administration of the living collection of a botanic garden. This system provides effective access to the actual living stock of vascular plants of one of the largest living collections world-wide. It is a program for the data management of a botanic garden and acts as a basis for further scientific research. With the linking of the database to the WWW, the information will be accessible to a wide range of users and can also be connected to other databases and information systems dealing with biodiversity information.

Fig. 1: A botanical type specimen (INFOCOMP/TYPES). The rules of botanical nomenclature prescribe that any taxonomic group named like this specimen (or carrying a name based on this name) will have to include this specimen. Type specimens thus form the essential base of the process of naming taxonomic concepts.

Project ID: 01LC9906 (INFOBOT, Subproject INFOCOMP/TYPES)
1.4.2000 – 31.3.2003

COMPOSITAE TYPES IN GERMAN HERBARIA

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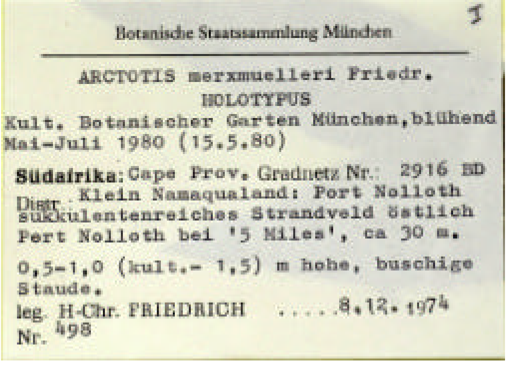
Key words: types, *Compositae*, specimen images, German herbaria, biodiversity informatics

Abstract. *Of the estimated 2,700 Compositae types held in Munich, 1,533 have been photographed, resulting in approximately 7,600 high-resolution images. All the bibliographic information has been checked and linked to the images. The completed data is gradually being made available on the Internet, using the software "Filemaker Pro".*

Introduction. The Compositae are the largest family of seed plants with an estimated 25,000 species [1]. They are found in all places colonised by higher plants on all continents and often form significant parts of the most diverse ecosystems [2]. They are not only scientifically interesting but also have economically important representatives. Nomenclatural types are the reference sheets of pressed plants laid down in herbaria. These are directly and permanently connected to their plant names and allow species to be unambiguously identified. They thus underpin even the most modern research techniques (see [3]). The more traditional and larger a herbarium, the richer it will be in types. For historical reasons, many types originate from developing countries and have attained value through European botanical research. With this project it is now possible to contribute to data repatriation by making this information globally available to scientists.

The project was established primarily as a pilot scheme for the digital recording of essential components of German herbaria. The project is supported by three graduate scientists and, from time to time, a Database/Network administrator and the current excellent co-ordination of the staff has greatly increased the speed of progress in recent months. With the experience gained, digital imaging in targeted spheres can now be rapidly and successfully completed.



Botanische Staatssammlung München

ARCTOTIS merxmuelleri Friedr.
HOLOTYPUS
Kult. Botanischer Garten München, blühend
Mai-Juli 1980 (15.5.80)

Südafrika: Cape Prov. Gradnetz Nr.: 2916 BD
Distr.: Klein Namaqualand: Port Nolloth
sukkulentenreiches Strandveld östlich
Port Nolloth bei '5 Miles', ca 30 m.

0,5-1,0 (kult.- 1,5) m hohe, buschige
Staude.
leg. H-Chr. FRIEDRICH 8.12.1974
Nr. 498

Fig. 7: Original label

Fig. 8: Capitulum

Results. Initial teething problems have now been resolved and image format and quality standardised. On average, five images per type are taken: the original label(s) (fig. 1) [necessary when determining provenance and authorship of older sheets, as well as for subsequent data capture from the images], the entire sheet (see previous page), relevant habit detail, and macro images of taxonomically important features - usually the capitulum(a) (fig. 2, 3). Special emphasis is placed upon the correct and accurate citation of the protologue.

Figure 9: Detail of capitulum necessary for species identification

Types from all seventeen of the *Compositae* tribes have been recorded (fig. 4). In total 350 genera and 1,533 types have been photographed, forming a database of over 7,600 images. Awaiting a fully functional interface for image storage and retrieval in the database system SYSTAX, the software "iView MediaPro" has been used to organize image and text data, retaining flexibility for other software options. The database software used to capture data, "Filemaker Pro", provides an integrated web interface allowing direct access to the database via the World Wide Web. It is anticipated that the work in Munich, including the preparation of the information for Internet access, will be completed during the next year.

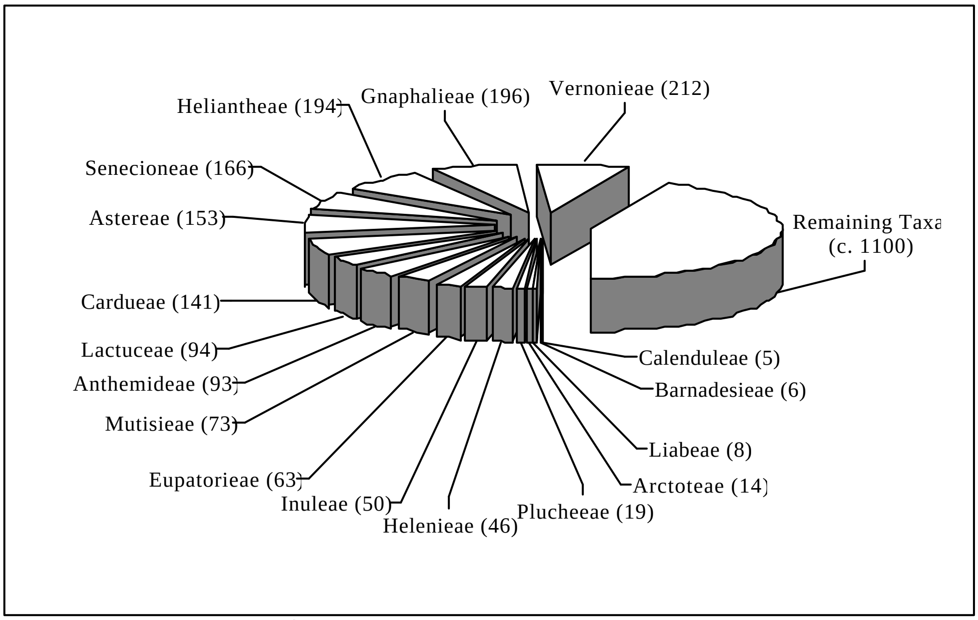


Fig. 4: Number of *Compositae* Types in Munich (M) photographed
(as of Sept. 2001) arranged by Tribe (after [4])

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Project ID: 01LC9906 (INFOBOT, Subproject INFOCOMP/BOHLMANN)
1.8.2000 – 31.05.2002

THE BOHLMANN-FILES – A DATABASE OF NATURAL SUBSTANCES IN THE COMPOSITAE

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Key words: Compositae, Asteraceae, natural substances, chemotaxonomy, chemical database, taxonomic database, secondary metabolites, biodiversity informatics

Abstract:

The Compositae (Asteraceae) contain numerous chemical compounds, many of them with a high potential in, e.g., pharmaceutical utilisation. A relational database was designed holding almost 20,000 chemical structures from about 5000 taxa. The revision of plant names and chemical data is almost concluded, reviewing of synonymy is under way, and publication on the World Wide Web will follow in the near future.

Introduction. Members of the *Compositae* are renown for their contents of a variety of physiologically active compounds [1], for example, they are used as remedies such as chamomile, insecticides such as pyrethrinoids, or pharmaceuticals such as the antimalarial agent Artemisinin from *Artemisia annua*. The late Ferdinand Bohlmann, professor at the Technical University of Berlin, dedicated much of his life to the investigation of these substances [2]. Together with his technical assistant C. Zdero he started in the beginning of the 1960ies to compile a card index on natural substances and taxa of the *Compositae*, encompassing both data from original research and from literature. About 95% of the data are published. In 1994, Zdero and one of Bohlmann's pupils, J. Jakupovic, started to transfer the data to an ISISBase chemical database, constantly adding data from more recent publications.

The project. At the outset of the present project, the database held data on about 5000 taxa, with a total of 19,351 chemical structures. In addition, (trivial) name of the compound, molecular weight and formula, literature references, and various revision notes were on record. The ISISBase program allows searching on structures and partial structures as well as on the contents of the text fields. However, ISISBase is not designed for the publication of small datasets on the World Wide Web, and it cannot easily be linked to other data sources. The Bohlmann Files project was thus proposed to meet three main objectives: (i) Convert the database into a relational system and transfer all data, (ii) revise the chemical and nomenclatural data and fill in remaining gaps from literature, and (iii) make the database accessible via the WWW, including the search features of a chemical database (see fig. 1).

Results. The data is considered reasonably complete for secondary metabolites found up to now in the *Compositae*. Providing free access to this wealth of information will not only serve applied sciences (e.g. to identify potential sources for substances), but also enhance basic research, e.g. by providing additional clues to the taxonomy of groups considered to be paraphyletic (e.g. the tribe *Lactuceae*) or not yet assigned to a tribe (e.g. the genera *Corymbium* and *Centipeda*) and to elucidate end-products of gene expression and biosynthetic pathways.

The project database has been set up under MS Access 2000, adapting the taxonomic module of the BoGART-database system (see next project) for the treatment of identification and nomenclature. Data from the flat-file format ISIS database were parsed to separate and atomise plant names, synonyms, and literature data. Chemical structures are stored using the add-in

"Accord" software. Its structural search capabilities allow searches via the WWW and thus form the core of the web publishing component which will be released before long.

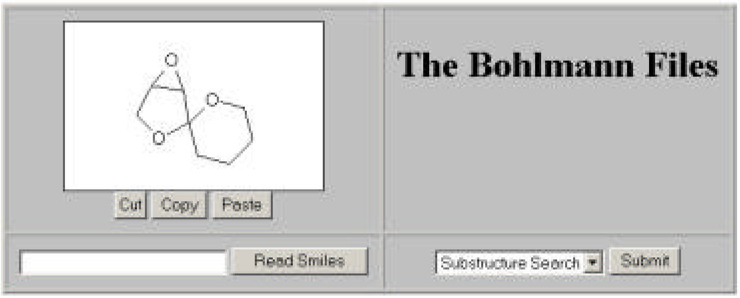
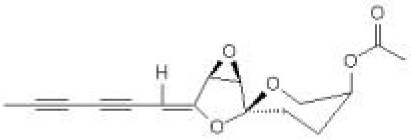
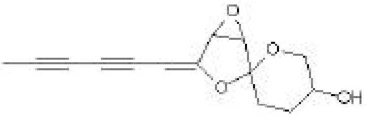
Query: A (sub-)structure can be drawn or input in textual form in the WWW query form can be made	
Result: The result consists of secondary metabolites containing the structure and (among other data) the taxa they were isolated from	 *Artemisia douglasiana* Besser *Dendranthema maximowiczii* (Komar.) Tzvelev *Athanasia dregeana* Harv.
	 *Dendranthema maximowiczii* (Komar.) Tzvelev

Fig. 1: Searching for a substructure in the database

Plant names have undergone a revision process including spell checking, standardisation (including author citations), and a check against major web-based databases on plant names [3, 4]. They now reflect the recent classification of the *Compositae* [5]. The data conform to the TDWG standard on names [6] complete with source citations for taxonomic data. Literature citations are kept in a separate reference list. Further taxonomic and bibliographic information and data on the bioactivity or use of compounds or the plant itself can be linked at a later date. Taxa from about 755 genera represent all tribes within the 3 subfamilies.

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Project ID: 01LC9906 (INFOBOT, Subproject BoGART)
1.4.2000 – 30.06.2002

BOGART - THE INFORMATION SYSTEM OF THE BERLIN BOTANIC GARDEN

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Key words: biological collection, botanical garden, living collection, botany, taxonomy, information system, biodiversity informatics, accessions

Abstract: *The "BoGART" database system of the BGBM demonstrates system development in a large living collection. The original system has been converted to a client server environment. Existing data (electronic or in writing) were transferred to the new system and the user interface adapted to specific tasks in the management of the garden's collection. A prototype XML wrapper provides access for networks and local or remote query interfaces.*

Introduction. With more than 20,000 taxa and 35,000 accessions on 43 ha, the Botanic Garden Berlin-Dahlem is one of the world's largest gardens. It is a scientific research collection, an educational exposition, and at the same time a recreational site for the public. Collections of this size not only demand constant physical care but also require an elaborate system to administer the information flow for scientific as well as practical work (see fig. 1). Detailed tracking of information on provenance and handling of accessions is an obligation with regard to the CBD's (Convention on Biological Diversity) demand for benefit sharing with countries of origin. Adequate documentation is also a pre-requisite for the botanical garden's role in species conservation [1].

INFOBOT-BoGART will complete the last phase in the process of transferring this system from the labour intensive index card system of the past to a networked electronic information system. It upgrades the internal prototype system to a scalable and publicly available multi-user application, based on widely used technology (SQL-Server, MS Access, WWW). It builds on several prior projects, starting in the 1980ies, which provided a sound foundation of evaluation, modelling, and implementation (see [2] for further historical details).

Results regarding data import, input, control and standardization. The import of static electronic data files from existing isolated applications within the garden has been finished. Data input of taxonomic information was completed and the data content has been checked against the card files. The system now contains information on more than 38,000 taxon names. Likewise, almost 37,000 accession datasets from imports have been checked, supplemented and partially reworked, achieving a high level of detail e.g. on the original provenance of the plants. Data standardization was a major focal point, concentrating on the areas of literature data (ca. 1450 citations), geography, and names and authors of plant taxa.

Technical results. The complex data model, as well as the increased data content had severely limited the performance of the system. True multi-user functionality was achieved with the conversion of the Access97 database into an Access2000 project. The backend resides in an MS SQL-Server2000 client-server database, and the Access-frontend's client connection has been converted from ODBC to OLE DB. The new system provides efficient parallel access from workstations distributed throughout the Botanic Garden area. Work in progress includes further performance optimisation, transferring functionality from Visual Basic code in the front end to server-sided stored procedures and triggers.

Networking. An XML-DTD was prepared which covers all data items provided by the BoGART system as well as concatenated or converted items demanded by exchange standards such as the ITF format [3]. Based on the DTD, a prototype XML wrapper has been programmed, which will be used to connect the database to national and international networks.

Integration in the work process. The ongoing final period of the project is focussed on the implementation of specific functionalities, supporting e.g. inventory processes, the scientific scrutiny of taxon names and linked data (synonyms, common names, species distribution, poisonous, medicinal, and protected plants, literature), the identification process, the collection and documentation of herbarium specimens, etc. The functions are developed in close cooperation with the respective user groups.

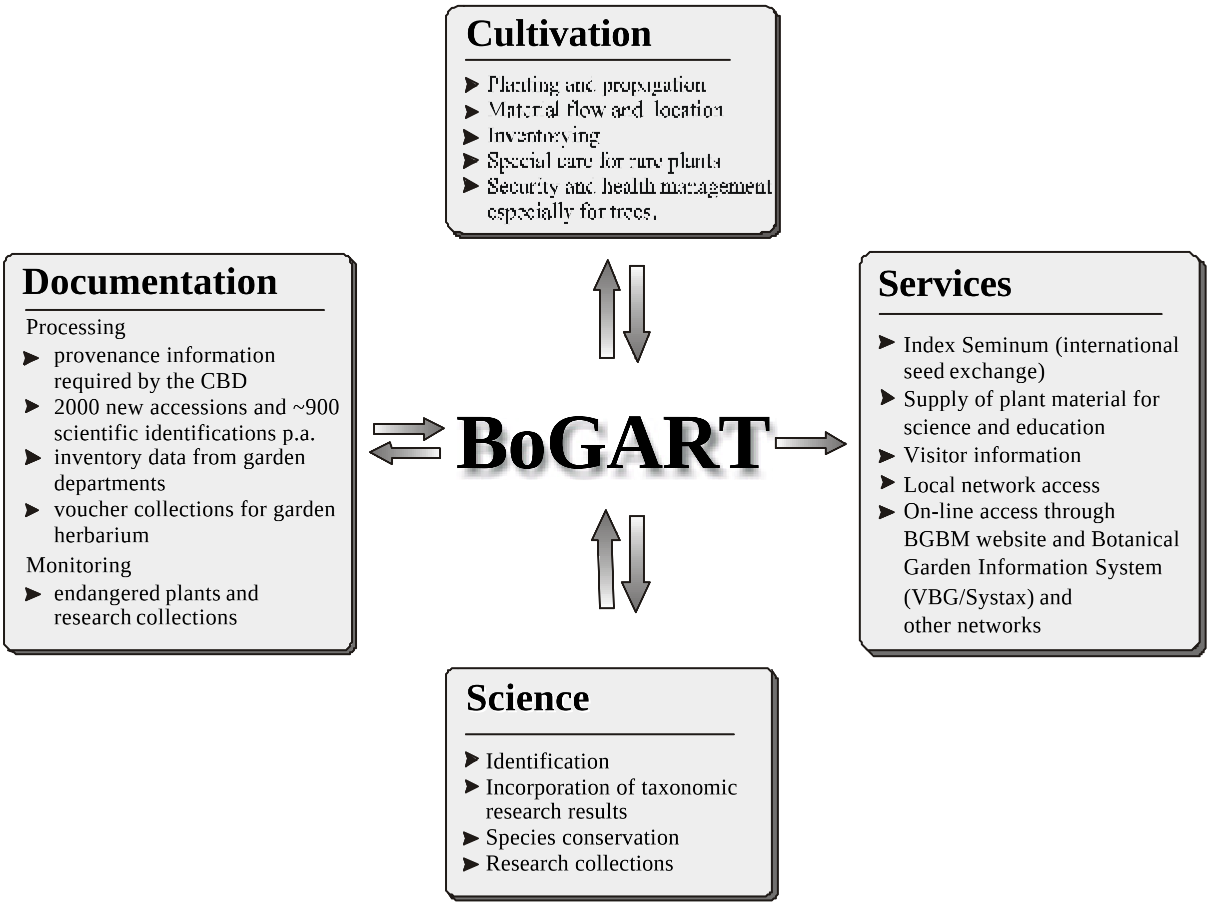

Fig. 1: Information domain of the BoGART program

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Project ID: 01LC0026 (AlgaTerra)
1.10.2001-30.09.2004

ALGATERRA – AN INFORMATION SYSTEM FOR TERRESTRIAL ALGAL BIODIVERSITY: A SYNTHESIS OF TAXONOMIC, MOLECULAR AND ECOLOGICAL INFORMATION

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Key words: information system, Internet accessibility, biodiversity, algae, diatoms, green algae, cyanobacteria, types, taxonomy, nomenclature, Ehrenberg, Hustedt, collection data, literature data, identification, morphology, culture strains, rDNA, sequence analyses, phylogeny, ecological data, biodiversity informatics

Abstract:

Aim of this recently started project is to build a comprehensive information system on terrestrial micro-algae, integrating taxon, type, name and collection data as well as ecological and molecular information. The main target groups will be scientists pursuing basic research, such as taxonomy and biodiversity studies, as well as applied researchers, such as ecologists, limnologists [1], and public agencies, engaged in biomonitoring for public health and environmental conservation. The system will be made available on the Internet (World Wide Web).

Background:

Microscopic algae have been recognized as useful tools in global change research, e.g. for monitoring water quality indicating trophic status, acidification, and salinization, for reconstruction of paleoclimates through sediments, and for the assessment of biodiversity of diverse ecosystems. The taxonomy and in particular the nomenclature used to record these observations is often ambiguous, leading to incoherent data sets published by different researchers that need to be synthesized for global studies. The available ecological information for these taxa is thus doubtful and modern molecular information cannot be assessed correctly. The problems are frequently due to poorly documented nomenclatural types as well as to divergent secondary interpretations of the taxon concept behind the name.

The network:

The BGBM Berlin-Dahlem (see AlgaTerra – AT1) will be responsible for the development of the comprehensive information system, and for data evaluation and typification of selected taxa housed at the Ehrenberg Collection. The other participants of the AlgaTerra network are the Museum für Naturkunde Berlin (Ehrenberg Collection, see AT2), the Alfred Wegener Institute, Foundation for Polar and Marine Research (type data of the Hustedt Collection, molecular, morphological and ecological data of diatoms, see AT3), the Culture Collection of Algae at the University of Göttingen (morphological and molecular data of green and bluegreen algae, see AT4), and the University of Leipzig (ecological and applied data of aero-terrestrial algae, see AT5). This cooperation (see fig. 1) will synthesize taxonomic, molecular and ecological information from all subprojects for worldwide accessibility.

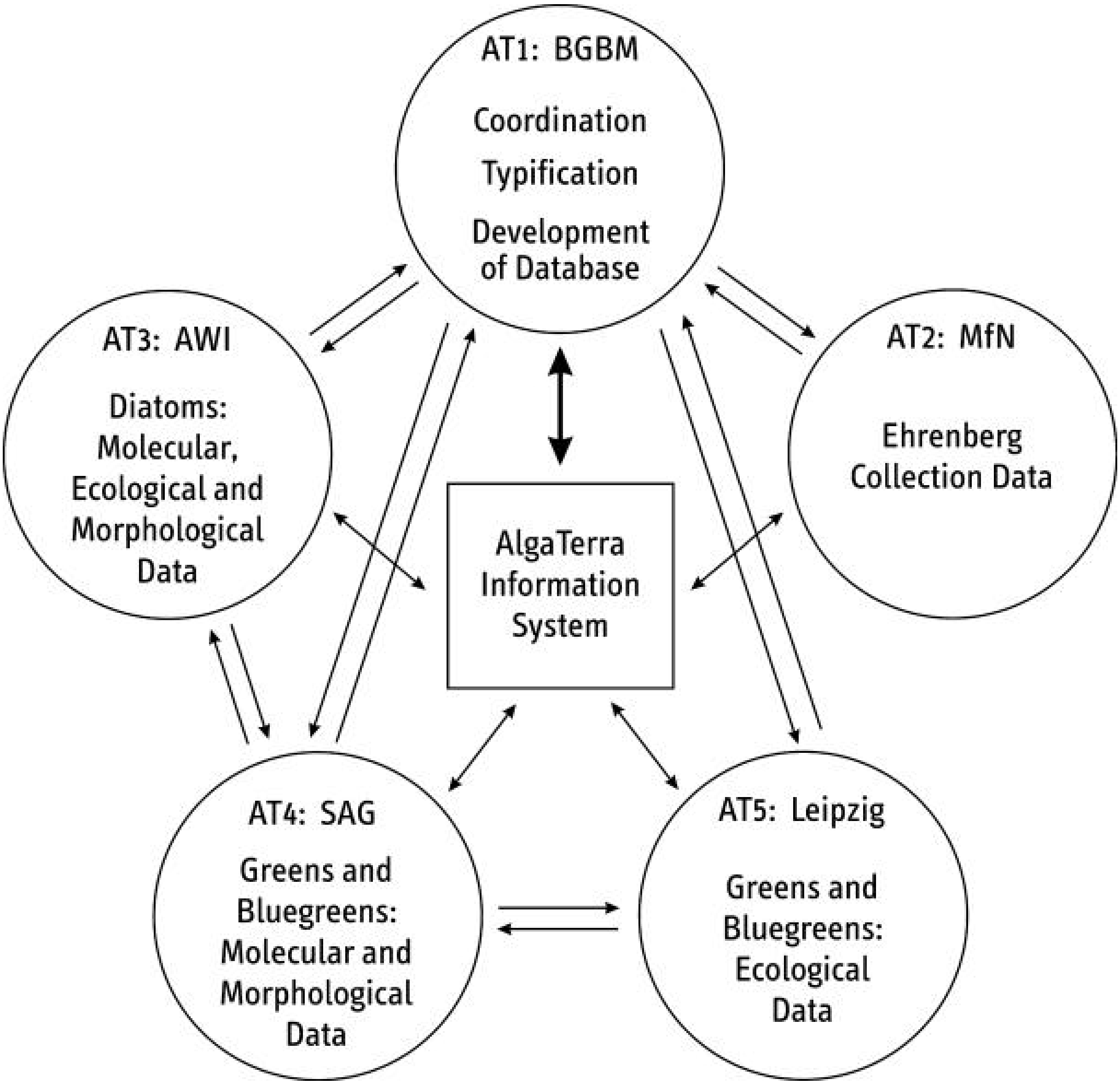

Fig. 1: The AlgaTerra network: Subprojects, topics and information flow

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Project ID: 01LC0026 (AlgaTerra Subproject 1)
1.10.2001-30.09.2004

THE ALGATERRA INFORMATION SYSTEM INCLUDING THE IDEAL-MODULE

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Key words: types, taxonomy, nomenclature, identification, morphology, algae, diatoms, biodiversity, Ehrenberg, database, internet accessibility, biodiversity informatics

Abstract:

A comprehensive Internet Information System for terrestrial algal biodiversity as a synthesis of taxonomic, molecular and ecological information (AlgaTerra) will be developed and implemented. The IDEAL-Module (Internet Database of Ehrenberg's Algae Lectotypes) will supply original data on algal types as a calibration tool for the identification of micro-algae. The Information System will be managed and supported over the long-term by the Botanic Garden and Botanical Museum Berlin-Dahlem as part of its scientific information services.

Results and research plan:

The BGBM Berlin-Dahlem will be responsible for the information system and for data evaluation.

The IDEAL-Module will give access to original data of selected taxa described by C.G. Ehrenberg (1795-1876). The relational database will include the validated name of the type, the original diagnosis, type locality information, a digital photograph of the selected type, and, where possible, a SEM-analysis of the original material (for Ehrenberg's scientific life and taxonomic concept, see [1, 2]). The database will also supply possible synonyms, notes of experts plus links to updated nomenclature, modern taxonomic interpretations as well as biogeographic, ecologic and molecular data.

Typification of Ehrenberg-taxa, housed in the Ehrenberg-Collection ([3], see AT2) was established and published for a small number of genera [4, 5] and species [6, 7, 8], but no data is accessible via Internet.

The main steps of data preparation for the IDEAL-Module are:

- digitalization of the algal name and description
- translation of the original description
- validity check according to the rules of nomenclature
- digitalization of the published picture
- digital photograph of the chosen (lecto)-type

Quality evaluation of data will include:

- taxon concept of the data source (fig. 1)
- type data versus interpreted data (observation data, applied data)

The development of the information system [9] will include:

- elaboration of an appropriate data model and database design
- programming and implementation of the database
- development of a user-oriented web-interface

- establishment of the connection between database and Internet

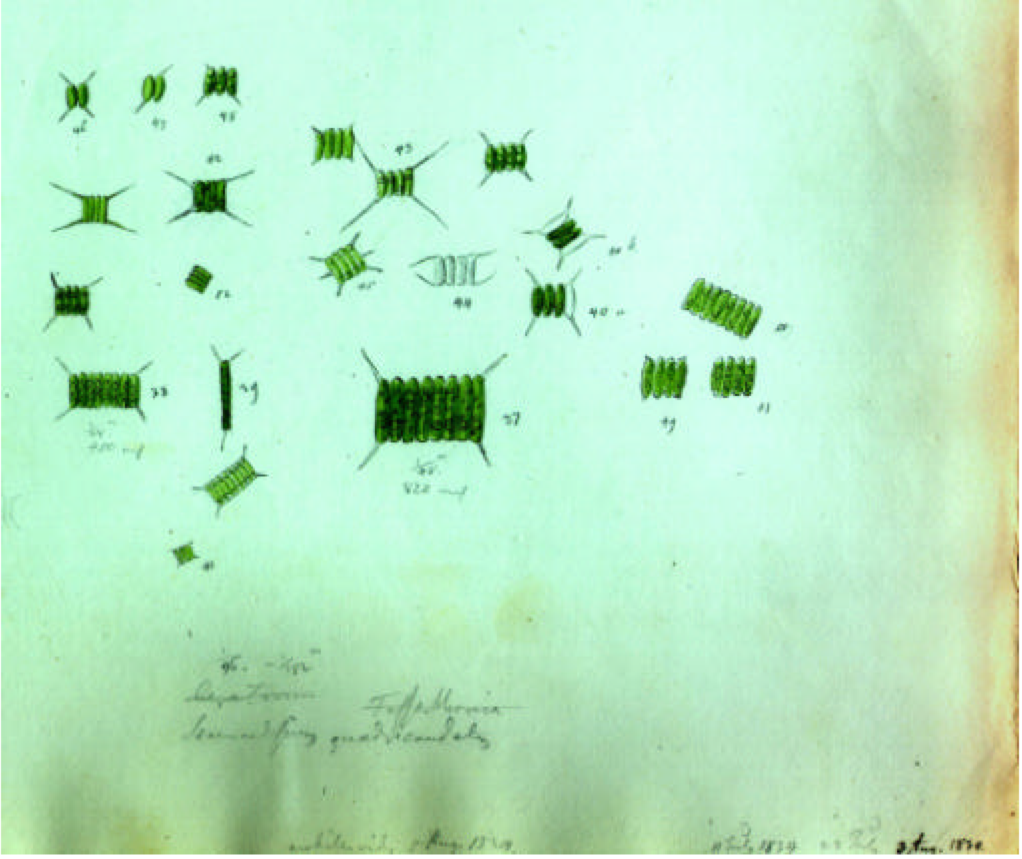

Fig. 1: Example of an unpublished drawing by C.G. Ehrenberg. This drawing sheet of 1834 shows his taxonomic concept, representing at least five taxa in our current understanding. It includes manuscript names, data on collecting dates as well as size measurements which are to be compared to his published data (fig. provided by AT2).

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Project ID: 01LC0026 (AlgaTerra Subproject 2)
1.10.2001-30.09.2004

ACCESSIBILITY OF THE EHRENBERG COLLECTION

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Key words: Ehrenberg, algae, diatoms, collection data, types, original materials, internet accessibility, biodiversity informatics

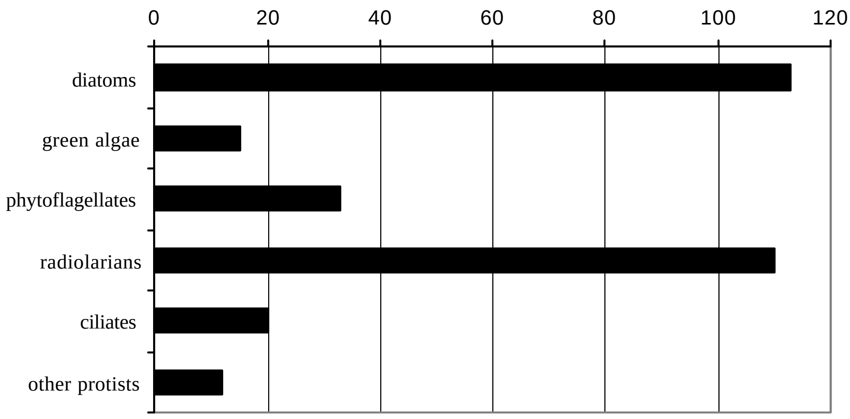
Abstract:

The Ehrenberg Collection holds the scientific legacy of Christian Gottfried Ehrenberg (1795-1876), generally considered to be one of the founders of both microbiology and micro-paleontology. Ehrenberg was one of the most taxonomically prolific of all scientists, and the type specimens for several thousand algal species and several hundred algal genera are present in the collection. These include many of the most common species and genera names now in use, and the collection includes the types and original material for many of the species and genera (diatoms and also other algae) that will be examined in the AlgaTerra project.

Introduction:

The collection was deposited with the Museum für Naturkunde in Berlin upon Ehrenberg's death, and has been preserved through the years in good physical condition. Experience in working with the collection has shown that the majority of all type material is indeed present in the collection (fig. 1). However, locating these type materials in the Ehrenberg Collection is currently very difficult, as the collection has not been adequately curated since it was deposited with the Museum more than 100 years ago, and the original collection structure is not well suited to modern research needs [1, 2, 3].

Fig. 1: Number of types for genera in Ehrenberg Collection



The project. The goal of this subproject is to carry out the minimum amount of basic inventory, labelling, archiving and database work (fig. 2) needed to allow other subprojects to use the Ehrenberg Collection efficiently in their own work. The work will result in a database of the Ehrenberg Collection; properly labelled, sorted collection objects; working image copies of fragile original documents (see AT1, fig. 1); and, for those taxa selected for study by the project as a whole, data extracts from the Ehrenberg Collection database that will be imported into the main project database (see AlgaTerra – AT1). The Ehrenberg Collection database will be maintained at the Museum für Naturkunde and will be accessible online via standard Internet protocols.

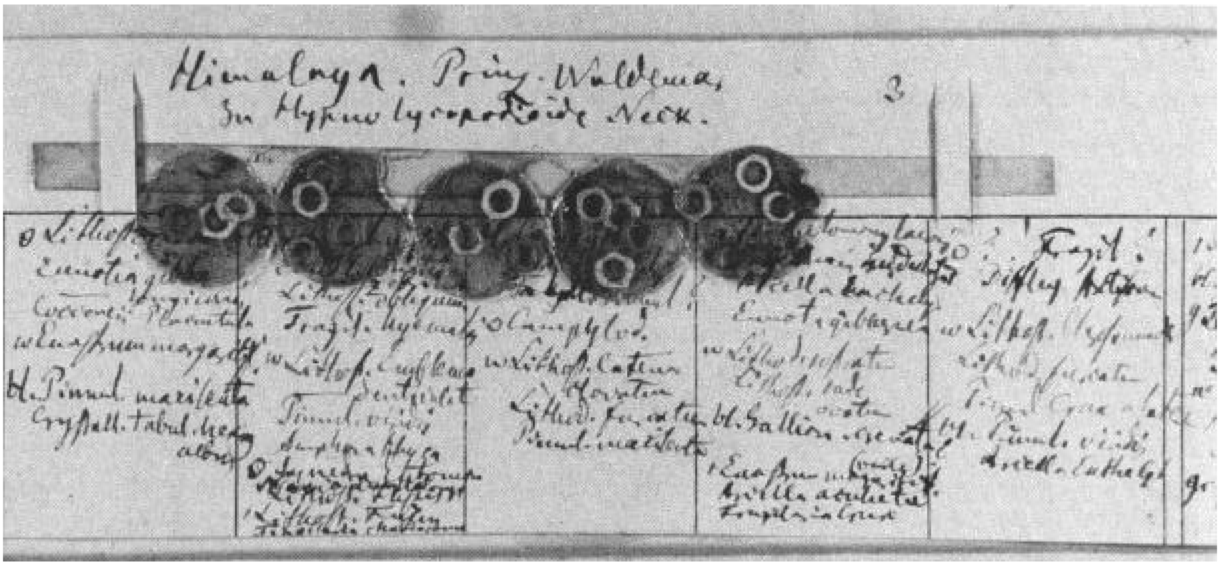


Fig. 2: Mica strip holding five mica preparations with original material and information; to be catalogued in this subproject

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Project ID: 01LC0026 (AlgaTerra Subproject 3)
1.10.2001-30.09.2004

MOLECULAR AND ECOLOGICAL DATA OF TERRESTRIAL DIATOMS

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Key words: diatoms, Hustedt, rRNA, phylogeny, ecological data, culture strains, *Nitzschia*, biodiversity informatics

Abstract:

Type localities of the species described by F. Hustedt from terrestrial habitats in Germany and Northern Europe will be established and re-visited to generate living cultures for deposition as epitypes in culture collections. Phylogenetic analysis of these epitype cultures will be performed using molecular techniques. In collaboration with AlgaTerra AT1 a database will be created including image-based keys to facilitate the identification of terrestrial diatoms.

Introduction. The diatoms (Bacillariophyta) are one of the most successful and ecologically important groups of microalgae, occurring in both aquatic and terrestrial habitats with over 10,000 described species and potentially many more cryptic species. They are distinctly well known for their architecturally complex siliceous cell walls (valves and girdle bands) and their unusual pattern of reduction in cell size of one of the daughter cells following mitosis, among other features. The intricate designs of their cell wall have been the basis for their classification system for more than two centuries. In the last fifty years, the diatoms have been routinely used to provide estimates of ecological perturbation, specifically eutrophication and acid rain. Currently they are being exploited as proxies for climate change in paleo-environments by looking at salt tolerances and the changes in the diatom communities in saline lakes and some terrestrial habitats influenced by salinity.

Germany has had at least three renowned diatomists from the last two centuries – Kützing, Ehrenberg and Hustedt – who described many hundred new species. Kützing's material was distributed to several contemporary scientists and has found its way into museums worldwide. The Ehrenberg and Hustedt collections remain more or less intact, the former at the Museum für Naturkunde, Humboldt Universität zu Berlin (see AT2), and the latter at the Friedrich Hustedt Arbeitsplatz at the Alfred-Wegener-Institute in Bremerhaven, Germany. The Hustedt Collection will be the basis of this subproject concerning names, types, ecological and molecular data.

Research plan. The Hustedt collection is fully curated [1, 2]. It is currently being catalogued into an Internet database [2] and will be the focus of our project. The research objectives of subproject AT3 are:

- To establish the type localities of the type species described by F. Hustedt from terrestrial habitats from Germany and Northern Europe.
- To return to these localities at the same time of the year to re-establish living cultures of these earlier described species for deposition in modern culture collections, such as the SAG (AT4). These new cultures will be designated as epitypes and epitype permanent preparations will be prepared and deposited in the Hustedt Herbarium.
- To perform phylogenetic analysis of these epitype cultures using an analysis of their rRNA genes or ITS regions if they are varieties of the same species.

- To create a database, from which an image-based key will be made to facilitate the identification of these diatoms from both living and fixed, cleaned material using the epitype culture and the original material in cooperation with AT1. These will be supplemented with database entries for other important terrestrial diatoms in these collections that were not described by Kützing, Ehrenberg and Hustedt so that a meaningful assemblage of terrestrial diatoms will be compiled for identification purposes using our database.

Accordingly, the project is divided into 4 workpackages:

- Databasing of names, pictures and type localities of terrestrial diatoms described by F. Hustedt.
- The establishment of epitype cultures based on the types and localities from work package 1 and the documentation of dominant feature of each species using both fresh and cleaned material.
- The reconstruction of the phylogeny (see [3]) of dominant species of terrestrial diatoms from Germany and Northern Europe based on 18S rRNA sequences derived from the epitype cultures established in work package 2 and from other cultures of representative diatoms dominant in our collection from type localities re-sampled throughout Germany and Northern Europe.
- Construction of an identification key using our database of the photographs of terrestrial diatoms.

Results. B. Beszteri came to the AWI in July 2001 on a DAAD scholarship. He began immediately to collect diatoms from one site on the estuary of the Geeste river near the AWI where Hustedt had made many collections and had described 4 species. B. Beszteri made about 19 collections (16 benthic from different substrates and 3 planktonic) from this site from which he established 40 cultures. Among the species recovered at the time of the collection he searched for *Nitzschia hoehnkii, N. aestuarii, N. tryblionella* f. *subconstricta* and *Diploneis dimorpha* which were described by Hustedt from this site. We are currently awaiting the grow up of existing cultures to see if we have obtained either of these species in our rough cultures. Preliminary indications are that we likely have *Nitzschia hoehnkii* and *N. aestuarii* in culture collected exactly at the same location from where they were originally described. We are growing the algae both in liquid and solid culture to facilitate their manipulation.

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1.10.2001-30.09.2004

DOCUMENTATION OF CHARACTERS OF TERRESTRIAL ALGAE IN CULTURE: R-DNA SEQUENCE ANALYSES, MORPHOLOGY AND CRYO-PRESERVATION OF REFERENCE STRAINS

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Key words: algae, cyanobacteria, rDNA, sequence analyses, phylogeny, morphology, cryopreservation, culture strains

Abstract:

The project will primarily analyse molecular characters of terrestrial microalgae from cultures, and will also gather morphological data for those strains that have been sequenced. The results will be integrated into the comprehensive information system for the unambiguous identification of these algae and they will be used to explore phylogenetic relationships. In addition, all strains used in this project will be preserved by cryotechniques and thus made available for further comparisons and investigations. The project is closely connected with one of the largest culture collections of algae (SAG, Sammlung von Algenkulturen Göttingen).

Research plan:

Phylogeny research in terrestrial algae, in particular green algae and cyanobacteria from aero-terrestrial habitats:

Molecular characters of terrestrial microalgae (excl. diatoms) will be examined by means of DNA sequence analyses of ribosomal genes (rDNA) using reference strains. This will help to clarify the phylogenetic relationships of these algae [1, 2, 3, 4]. A regularly updated gene tree will guide the user to the sequence data as well as to all other relevant information. The DNA sequence data will be provided as secondary structure-model based alignments ([5], e.g., in ARB format). The sequence database will help in identifying algae even from uncultured material (e.g., soil crusts) or environmental DNA extractions, a feature which is essential for applied research.

Authentic culture and other reference strains form the basis for the documentation of molecular and morphological characters.

This brings a large culture collection into the focus of modern research. The main source for culture strains is the “Sammlung von Algenkulturen Göttingen (SAG)” which is one of the world’s largest living collection of algae [6]. Of the ca. 2100 strains currently in the SAG, 419 are authentic strains (i.e. represent subcultures of the culture material used for the original taxonomic description of algal species) of which 369 were isolated from terrestrial habitats. These strains will be supplemented by additional authentic culture strains, particularly from the culture collection at Innsbruck, Austria (ASIB, Dr. G. Gärtner), which mainly holds stocks of soil and airborne algae [7, 8]. Other reference strains used by the project will be carefully selected in collaboration with the other subprojects of AlgaTerra i.e. AT1 (taxonomic identity, Ehrenberg type) and AT5 (ecological importance as currently known), as well as from other culture collections needed to represent the diversity of genera of microalgae from aero-terrestrial habitats as best as possible.

Further strains may be provided by the projects AlgaTerra AT5, and the BIOTA projects TP05-1 and S05-1.

Preservation of reference strains by cryotechniques

All the information as gathered by the project will be referenced to genetically stable cryo-preserved culture material which will be available to the public for further comparisons and investigations. Although cryopreservation is routinely used in other culture collections, new protocols for the cryopreservation of microalgae will be developed. The establishment of cryocultures will ensure the prolonged survival of important reference strains.

Documentation of morphological characters and culture data

All relevant information that is available for the culture strains used in this project (e.g., origin, optimal culture conditions) will be collected and integrated into the information system. Morphological features of the strains will be documented, and a collection of image data (with attached comments that explain morphological characters) will be provided with the information system.

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Project ID: 01LC0026 (AlgaTerra Subproject 5)
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CHARACTERISTIC DATA OF GREEN AND BLUEGREEN AERO-TERRESTRIAL ALGAE (CHLOROPHYTINA AND CYANOBACTERIA)

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Key words: cyanobacteria, green algae, literature data, culture strains

Abstract:

Whereas information on marine and freshwater algae is one of the standard topics of phycological textbooks, comparably few data are available for aero-terrestrial taxa, i. e. those algae which live on and in soil [1, 2], cover surfaces such as rocks and tree barks or which are part of the aero-plankton. The reasons for this information gap are manifold, but one clear obstacle for a better understanding of these algae is the difficult access to published information. Important data are scattered among journals of low citation impact or grey literature and is often not available in English. This subproject will contribute to overcome this impediment by assembling available information and making it accessible worldwide.

Research plan:

In order to create the basis for an intensified research on aero-terrestrial algae this project will focus on:

- the search for, assembly, and processing of data on aero-terrestrial algae (blue-green and eukaryotic algae excluding diatoms), including translation into English
- axenic cultures of aero-terrestrial algae including their description and taxonomic identification by classical standard methods and
- the development of an image-based web-interface to chlorophycean aero-terrestrial algae

Progress made:

Currently we are engaged in data mining (morphology, taxonomy, ecology, original descriptions) of predominantly Russian and Ukrainian sources, translation and processing of data into a compatible structure. Parallel to this, we are completing data sheets of axenic isolates of aero-terrestrial algae of our algal collection (literature data such as original descriptions, ecophysiological data, morphological documentation by drawings and photographs).

References:

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Appendix

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