

IFZ Interdisziplinäres
Forschungszentrum
Giessen Research Centre for
BioSystems, Land Use and Nutrition



**Crosstalk between
basic and applied sciences**

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Editorial



The development of ideas for sustainable exploitation of natural resources is a major challenge for science. Securing biological resources using basic research into complex biological systems is the vision of the Justus Liebig University Giessen Interdisciplinary Research Centre for BioSystems, Land Use and Nutrition (IFZ).

The main objective of the IFZ concept is to ally ideas, concepts and people from both basic and applied sciences to address problems at all relevant scales of our environment. The interaction of scientists from different disciplines shall encourage pioneering research at the frontiers of agricultural science, ecology, environmental science, nutritional sciences and biotechnology.

Shared technology platforms offer a wide range of tools for both research and teaching. Given the great variety of disciplines at the IFZ, researchers are enabled to tackle complex real world problems spanning from bio- and geo-scientific basics to the development and testing of methods for sustainable use of natural resources at the landscape scale.

Our mission is to both keep up with state-of-the-art international research and to support industry and decision makers requiring scientific input to solve critical problems.

A handwritten signature in black ink, appearing to read 'U. Wenzel'.

Prof. Dr. Uwe Wenzel, IFZ Spokesman

IFZ – on 1 page

IFZ Members and Associates	26 Professorships from the Faculties of Biology and Chemistry (08) as well as Agricultural Sciences, Nutritional Sciences and Environmental Management (09)
Scientific Staff (2010)	State: 66 Research Grants: 184
Technical and Administrative Staff (2010)	State: 127 Research Grants: 13
Bachelor Student Projects (2010)	Biology: 22 Agriculture, Nutrition, and Environment: 126
Master Student projects (2010)	Biology: 12 Agriculture, Nutrition, and Environment: 98
PhD Students (2010)	Biology: 32 Agriculture, Nutrition, and Environment: 124
Research Grants (2009 / 2010)	4.5 / 5.3 Mio. €
Board	
Executive Spokesman 2009/2010:	Prof. Dr. Thomas Wilke
Executive Spokesman 2010/2011:	Prof. Dr. Uwe Wenzel
Executive Spokeswoman 2011/2012:	Prof. Dr. Dr. Annette Otte
Manager:	Dr. Edwin Weber



Crosstalk between basic and applied sciences

The loss of biodiversity, the need for food and energy, the battle against pests and diseases, all require a sustainable approach to future planning. However, none of them can be tackled by a single scientific discipline with its limited toolbox. A way to get a grip on these complex topics is the combination of model-oriented basic research with system-oriented applied research. This is the underlying concept of the IFZ, the Research Centre for BioSystems, Land Use and Nutrition at Justus Liebig University.

From molecule to ecosystem

A prerequisite for this approach is the possibility to conduct experimental studies from molecule to ecosystem scales. IFZ facilities and a number of national and international research stations closely linked to the centre provide the necessary scientific infrastructure.

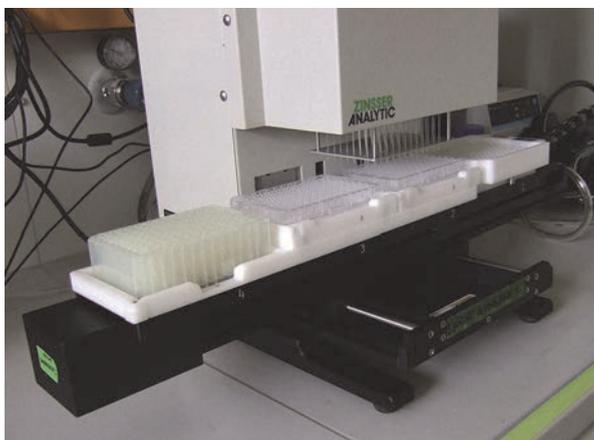
“Insect Biotechnology”, “Land Use and Biodiversity”, “Stress Resistance and Adaptation”: the three focus areas of the centre bundle valuable resources thereby enabling a high level of competition within the international research community. Making use of these resources, problems brought to science by practitioners and decision makers can also be addressed. Both

ways, the profiles of both IFZ and the faculties involved are sharpened.

At present, thirteen institutes with 26 professorships out of the Faculty of Biology and Chemistry (08) and the Faculty of Agricultural Sciences, Nutritional Sciences and Environmental Management (09) of Justus Liebig University form the IFZ.

Research is conducted in an interdisciplinary research environment supporting the exchange of methods and technologies and the transfer of scientific concepts. Common facilities, joint use of equipment and cross-disciplinary courses form scientific networks fostering new approaches to scientific questions and real world problems. Several international collaborative projects were initiated by IFZ institutes. The IFZ is strongly interlinked with Justus Liebig University Centre for International Development and Environmental Research (ZEU), where a number of projects are coordinated by IFZ investigators.

Numerous international research students and guest scientists profit from this constellation. Furthermore, substantial scientific knowledge is transferred to decision makers, pupils and the public, environmental issues and efficient use of natural resources being the key issues.





IFZ Research Focus “Insect Biotechnology”

Insects represent the group of organisms with the highest biodiversity. The development of this diversity coincides with the acquisition of a huge arsenal of molecules securing their nutrition and enabling their defence against diseases. Using insects as resources for new molecules to be applied in medicine, in plant protection or industrial biotechnology is the core objective of insect biotechnology.

The key to success is a result of knowledge-based search: knowledge on evolution and ecology of insects

helps focusing research on species, which are resistant against microbes or which can survive in remarkable niches.

This top technology shall be developed in cooperation with Fraunhofer for the first time in Germany and integrated in the Justus Liebig University Life Sciences concept. Thinking of the enormous potential of the new research area, the state of Hessen has granted 4.5 Mio. € for the LOEWE Focus Group Insect Biotechnology.

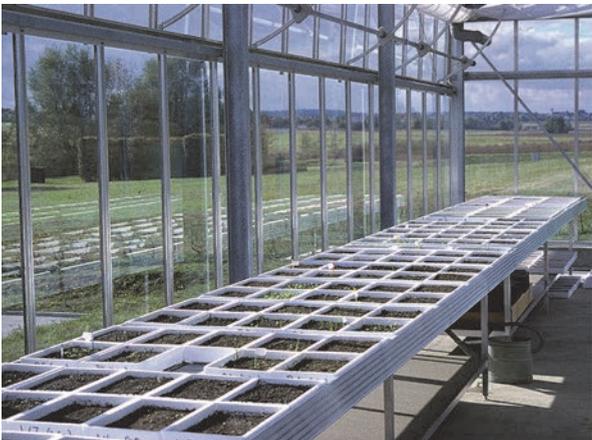




IFZ Research Focus “Land Use and Biodiversity”

Any form of land use is coupled with specific costs and benefits. The many facets of this insight are reflected in the term “multi-functionality”. When it comes to organizing land use systems and establishing sustainable agrarian production, it is essential to understand the various landscape functions and their interactions, particularly with regard to biodiversity. There is an urgent need for integrated methods for the development of economically and ecologically reasonable, regionally adapted, sustainable land use concepts.

Another major challenge in the near future is the change in the composition of the earth’s atmosphere, probably coupled with dramatic changes in ecosystem functions and biodiversity. Essential "ecosystem services" might be impaired, putting at risk vital functions of man’s natural life support system. Knowledge derived from climate change research must be put into a practical context, on appropriate space and time scales, to create realistic scenarios for decision makers.

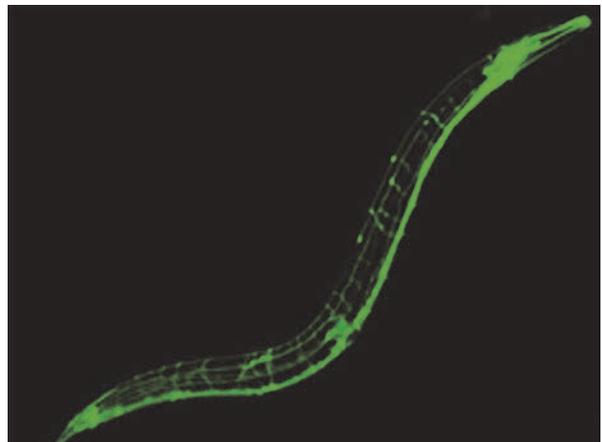
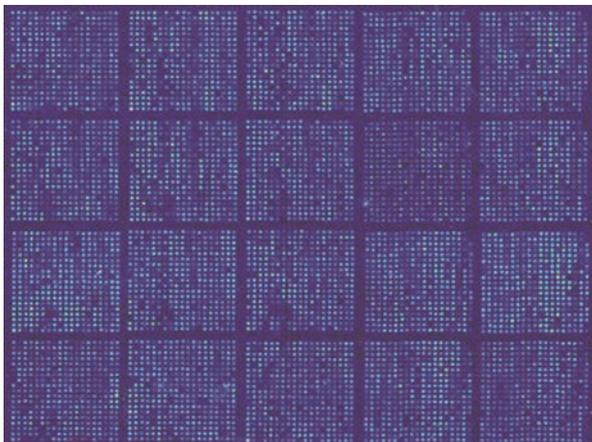




IFZ Research Focus “Stress Resistance and Adaptation”

During evolution, organisms had to cope with a plethora of environmental cues. This “stress” required a multiplicity of new adaptation processes that evolved on the basis of complex molecular signaling networks and changing metabolic activities. Today, organisms have to adapt very quickly to manmade environmental changes such as eutrophication of natural ecosystems, reduced biodiversity and global temperature rise. IFZ researches these complex mutual effects between organisms and their environment, and ex-

plores concepts to manage the detrimental events like desertification of arable land and progression of pathogens. The interdisciplinary approach is exemplified by special research topics where IFZ scientists analyze response of microbes to environment, look at distribution and functional relations of microorganisms in diverse environmental niches, explore the mechanisms by which microbial parasites or symbionts interact with their hosts or search into the biochemistry of salt and drought stress tolerance in plants.



IFZ Technology and Research Facilities

State of the Art Technology in IFZ Labs

- ⊗ Proteome and transcription analysis of stress responses (Crystallization robot and 3-D-visualization, real time PCR, 2-D-Gel electrophoresis, microarray, ...)
- ⊗ Fluorescence and laser scanning microscopy
- ⊗ Biochemical and molecular taxonomy and phylogeny
- ⊗ Stress physiology (Model organisms, model environment systems, patch clamp, ...)
- ⊗ Environmental analytics (ICP-MS, GC-MS, HPLC-MC, AAS, CNS, ...)
- ⊗ Food and quality analysis (GC-MS, HPLC-MS, AAS, CNS, ...)
- ⊗ Land use and biodiversity modelling (GIS-Cluster, model regions, ...)

Plant-Environment Research Facilities

- ⊗ *More than 50 growth chambers*
More than 30 walk-in growth chambers are located at walking distance to IFZ laboratories. In close vicinity, further 14 growth cabinets are available to IFZ researchers. Additional growth chambers and cabinets are located at the research stations of IFZ institutes.

- ⊗ *Research hangar*

A research hangar directly connected to the growth chamber facilities provides the space for experimental equipment at technical scale, like lysimeters or an experimental sewage treatment unit.

- ⊗ *Greenhouse facilities*

The IFZ teams profit from a climatized, common greenhouse facility close to the labs. Further greenhouses are available at various research stations.

- ⊗ Environmental Monitoring and Climate Impact Research Station Linden with Free Air Carbon dioxide Enrichment (FACE Linden) since 1998.

Research Stations

- ⊗ Animal Nutrition Research Station Giessen
- ⊗ Phytopathology Research Station Giessen
- ⊗ Plant Nutrition Research Station Giessen
- ⊗ Landscape Ecology Research Station Linden
- ⊗ Plant Breeding Research Stations Rauischholzhausen and Gross-Gerau
- ⊗ Animal Ecology Station Hoherodskopf
- ⊗ Center of Excellence in Marine Sciences Research facilities in Giessen and Santa Marta (Colombia)





Animal Ecology

Institute of Animal Ecology and Systematic Zoology

Faculty 08 — Biology and Chemistry

Prof. Dr. Volkmar Wolters

Structure and function of animal communities

The animal ecology group conducts research on the ecology of many different taxa - ranging from spiders and insects to birds and rodents. Research topics are manifold encompassing landscape ecology, landscape genetics, functional ecology, limnology, modeling and soil ecology. Yet, often transitions among these scientific focuses are smooth. The overarching research question is: which factors drive community structure and function at various spatio-temporal scales?

Our research focus “**landscape ecology**” studies the effects of landscape pattern on the biodiversity of the fauna. We quantify, for example, the relation between biodiversity, spatial complexity and socio-economy in agricultural landscapes. An important aspect is to share scientific ecological knowledge not only among researchers, but also with stakeholders involved in land use planning and with the general public. Further projects deal with germination ecology of aquatic macrophytes and wetland ecosystem diversity; the latter two are directly related to methods and policies for ecosystem restoration.

Landscape genetics integrates landscape ecology with population genetics. Our research focuses on microevolutionary processes related to the influence of land use change on the population genetic structure of selected insect species. We do not only assess the effects of present but also of past landscape structure. Moreover, studying the effects of increasing isolation over a continuously sampled area enables us to detect

genetic discontinuities and isolation thresholds. Selection and comparison of species differing in habitat requirements and mobility allows us to model landscape effects for a wide range of species traits.

Functional ecology identifies the importance of biota for ecosystems processes. Within this context we apply correlative and manipulative approaches to study the impact of habitat complexity, resource availability, land-use intensity and landscape structure on processes such as pollination, herbivory, predation or decomposition. Predator-prey relationships are evaluated by using spatial analysis techniques. Pollination efficiency of hover fly and wild bee species is determined by means of flight cages. The pollination service at large spatial scales is estimated by investigating differences in the distribution patterns of pollinators in agricultural landscapes.

Limnology studies the ecology of lakes, running waters and groundwater. Limnological research in our group focuses on the role of microorganisms in the



flow of matter and energy in streams and rivers, but we are also working on groundwater environments. The development of molecular biology methods now allows us to determine the composition of microbial communities in natural environments. Concerning the function of microbial communities, research is directed especially to the degradation of macromolecular organic substances. Major scientific topics include the consequences of increasing desiccation of headwater streambeds as a result of both climate change and water withdrawal, the special food chains of groundwater ecosystems and their dependence on organic matter inputs from the earth's surface as well as the mineralizing microbial communities associated to the roots of *Eichhornia*.

Models help us to understand the environment, since they are simplified abstract views of the complex reality. The growing need for information on the geographical distribution of biodiversity has stimulated interest in and research on species distribution modeling (SDM) techniques. We use high-resolution SDMs to model the population size of 10 indicator bird species for farmland to evaluate farmland sustainability in Ger-

many. Moreover, we have projected distribution and abundance of 46 bird species under present climatic conditions and under an IPCC scenario for the year 2050 to predict the impact of climate change on bird species distribution.

Our **soil ecological studies** mainly concentrate on topics related to belowground biodiversity. The number of species in soil by far exceeds aboveground diversity, but the complex community living below our feet is still a widely neglected field of research. This is a serious shortcoming, since soil biota carry out an enormous range of functions and is pivotal for delivering food, fiber and biofuels and carbon storage. Moreover, soil biodiversity affects the organisms living on the other side of the soil interface in a multitude of ways, either through nutrient supply or as herbivores, pathogens, and symbionts.

Ecological consequences of future changes in rice production in SE Asia

The DFG research unit ICON, which is coordinated by Prof. Wolters, aims at exploring and quantifying the



ecological consequences of future changes in rice production in SE Asia. A particular focus is on the consequences of altered flooding regimes, crop diversification and different crop management strategies on the biogeochemical cycling of C and N, associated green-house gas emissions, water balance, and other important ecosystem services of rice cropping systems. The overarching goal is to provide the basic process understanding necessary for balancing the revenues and environmental impacts of high-yield rice cropping systems while maintaining their vital ecosystem services. Within this framework our group investigates the effect of shifting from continuously flooded rice cropping to crop rotation and diversified crops on the soil fauna communities and associated ecosystem functions.

Changes of soil biodiversity and ecosystem services

We are partners of the EU FP7 project SOILSERVICE, which combines interdisciplinary empirical studies and soil biodiversity surveys to construct soil food web models and to determine effects of changing biodiversity in agricultural soils on stability and resilience of C-, N- and P- cycling, as well as to assess consequences for outbreaks of pests or invasive species. Major objectives are to value soil ecosystem services during different pressure of land use and changes in soil biodiversity, to establish methods for determining and predicting sustainability of ecosystem services at different types of land use, and to build scenarios for identifying economic and social drivers of how land use such as biofuels production and land abandon-



ment can influence soil biodiversity and ecosystem services over European scale.

Biodiversity and functioning of soil food webs

Within the context of the DFG projects SOILFOODWEB and SOILFUN, which are part of the Priority Program “Biodiversity Exploratories”, we study the impact of land-use intensity and landscape structure on the biodiversity and functioning of soil food webs. The community structure of soil biota in terms of species diversity, functional diversity, body size and abundance distributions is compared between the three Exploratories, two contrasting ecosystems and two opposite land-use intensities under consideration of landscape structure.

Land-use sustainability and species diversity

The DFG transfer project “Land-use Sustainability and Species Diversity” explores options for sustainable farmland management by generating land-use scenarios at a national scale. We use SDMs to model population sizes of 10 indicator bird species for farmland to evaluate sustainability of farmland in Germany. To facilitate nation-wide SDMs on a high resolution we developed the GIS tools GEPARD and SLICER.

Volkmar Wolters

phone ++49-641-99-35701

mail Volkmar.Wolters@allzool.bio.uni-giessen.de

www.uni-giessen.de/cms/fbz/fb08/biologie/tsz/tieroekologie



Ecology, physiology and genetics of small mammals and bats

The Mammalian Ecology Group covers various research areas like foraging ecology of insectivores, habitat use and species diversity of forest-dwelling mammals, reproductive biology of bats, as well as metabolic and digestive physiology of small mammals with field and laboratory methods. On top of basic principles of mammalian biology we convey recent research results in our teaching.

The “foraging ecology” research focuses on energy requirements and food acquisition of insectivores. For this we study bats and small mammals in the wild and in the laboratory. We characterized, for example, foraging strategies and determined insect capture rates of bats in a flight tent. As part of the research focus “reproductive biology” we compare the reproductive success of different male bat groups by paternity analysis using molecular markers. With the aid of these markers we also clarify the effects of reproductive isolation and low migration rates on mammal populations. To this end we collect many DNA samples of various mammalian species and analyze them. To support the results of molecular analysis reproductive strategies of different species are investigated in the field. We conduct digestion research to determine energy utilization by mammals. For these studies bats and small mammals are captured in the wild and feeding experiments take place in the laboratory. We expect differences between species depending on vari-

ous factors like food spectrum, foraging strategy and life history. Within the “landscape ecology” research we carry out GIS-based habitat analyses of mammals in order to generate habitat models. The questions are related to habitat usage, isolation, and migration of populations and the relationship of species diversity with habitat structure. For this approach we resort to existing databases but also acquire new data by catching and marking further species in the field.

Basal metabolic rate of bats

The aim of this project is to relate differences of the basal metabolic rate (BMR) to differences in behaviour and habitat utilisation of bats. BMR is the energetic cost an individual has to expend in order to stay alive and it is a valid indicator to objectively compare energy demand between individuals and species. It is measured via indirect calorimetry where we determine the consumption of O₂ and the production of CO₂ in



animals which allows us an accurate determination of their BMR. We investigate if BMR of bats is related to climate, food availability or sociality. It has been pointed out that a reduced environmental temperature leads to a clearly elevated O_2 consumption which might lead to an elevated BMR in bats of the same species living in suboptimal regions. Individuals living in habitats with low food availability should show several strategies to save energy like lowering their BMR. Sociality could also influence BMR where bats roosting in bigger groups should have a lower BMR than solitary roosting individuals since they have lower costs of thermoregulation.

Genetic diversity of Common Hamster populations

The Common Hamster is a highly endangered species in Europe. Populations of this species suffered from dramatic declines in the last decades, resulting in low population densities and declining genetic diversity. As habitat loss and landscape fragmentation are considered as the major threats, we investigated how land-

scape structure and isolation affect genetic distances and diversity of hamster populations. Since hamsters are endangered, rare and elusive we used a self-made hair-trap for non-invasive genetic sampling. The application of strict guidelines for non-invasive genetics allowed us to analyze Common Hamster populations with microsatellite markers. We compared genetic diversity between three distinct local hamster populations in Hesse.

Results showed that independently from short geographic distances hamster populations were genetically highly isolated. Detected genetic diversity differed significantly ranging from moderate to very low diversity. These results were consistent with landscape configuration. The population with lowest genetic diversity was found in the smallest and the population with the highest diversity was located in the largest unfragmented area. These results demonstrate that fragmentation affects genetic diversity of hamsters and that future conservation is only possible when considering these effects.



Diversity and community structure of forest inhabiting bats and small mammals

Deciduous forests play a very important role as habitats for many bat species and small mammals. However, little is known about how the mammalian community composition and species abundance is influenced by specific forest characteristics. These include relative prey abundance, proportion of dead wood, composition and density of vegetation or stand age. We investigated the influence of forest structure on diversity and community composition of small mammals and bats in standardized survey plots. To assess prey abundance and diversity we used pitfall, sticky, and cross window traps. For faunistic assemblage small mammals were captured with live-traps. Presence of bat species was recorded by mist netting and ultrasound detection. Microclimatic conditions were

recorded by data loggers in each plot. In addition to site-specific data we analyzed landscape metrics as well as topographic and climate conditions in GIS. All variables and their contribution to species occurrence were analyzed using ordination techniques as well as regression analysis. This approach allowed us to identify site characteristics which had the highest explanatory values (e.g. forest) for observed species richness patterns. The results of our study contribute to the understanding of species richness patterns and may also help to create predictions for larger spatial scales.

Jorge A. Encarnação

phone ++49-641-99-35760

mail Jorge.A.Encarnacao@allzool.bio.uni-giessen.de

www.uni-giessen.de/cms/fbz/fb08/biologie/tsz/st





Systematic Zoology and Biodiversity Research

Institute of Animal Ecology and Systematic Zoology

Faculty 08 — Biology and Chemistry

Prof. Dr. Thomas Wilke

Tracking the evolution of biodiversity in space and time

What are the processes driving the enormous diversity of animal species on earth? When and how do new species emerge? How is biodiversity distributed on regional and global scales, and how are changes in biodiversity related to local, regional, and global environmental changes? These questions are being studied by the Systematic Zoology and Biodiversity group in various parts of the world, ranging from the heights of the Tibetan plateau, the glaciers of Patagonia, river plains in China, and lakes in the African Rift Valley to the coral reefs in the Caribbean.

Understanding the processes generating biodiversity and the factors responsible for changes in biodiversity in space and time are of fundamental importance for evolutionary biologists, ecologists and biogeographers. These are also questions of main interest for the Systematic Zoology and Biodiversity group. The group uses a set of model groups, mainly invertebrate taxa such as mollusks, leeches and corals, but also vertebrate groups such as fish and birds to study evolutionary changes in various places on earth. Based on a research strategy that explicitly addresses spatial and temporal aspects of evolution on various scales, the group studies evolutionary events ranging from Miocene to Holocene times, from continent-wide to local scales.

Ongoing research projects address questions such as:

What are the factors driving adaptive and non-adaptive radiations?

Why do species differentiate and how do environmental events affect rates of speciation?

How did Pleistocene refugia contribute to the genesis of biodiversity?

What are the factors causing an unequal distribution of taxonomic and genetic biodiversity?

How does human impact affect the distribution of disease-causing vectors?

What makes species invasive?

SCOPSCO: Drilling for biodiversity in Europe's oldest lake

Within the framework of the *International Continental Scientific Drilling Program* (ICDP) an international team of scientists aims at conducting a scientific drilling campaign in the oldest European lake, the Balkan Lake Ohrid. The SCOPSCO-Program (*Scientific Collaboration on Past Speciation Conditions in Lake*



Ohrid) is coordinated from the geological side by Bernd Wagner (University of Cologne) and from the biological side by Thomas Wilke.

Lake Ohrid is the most outstanding European ancient lake with the highest degree of endemic biodiversity of any worldwide ancient lake when taking lake size into account. The limnological history and age of Lake Ohrid are largely unknown. The SCOPSCO program aims at drilling several sites in Lake Ohrid, with the deepest one having a depth of some 700 m. Major goals of the campaign are to study age and geological evolution of Lake Ohrid and to reconstruct changes over the past 2 to 3 Mio. years in order to unravel processes that have led to the extraordinary degree of endemic biodiversity in the lake.

The SCOPSCO program is the first ICDP project worldwide that is primarily conducted for evolutionary purposes. At the same time, supplementary projects aim at utilizing DNA data and molecular clock approaches in order to reconstruct the evolutionary history of selected groups of endemic species. The combination of both approaches, deep drilling and DNA analyses, allows for testing specific hypotheses relative to

the effect of environmental changes on speciation processes.

CEMarin: Biodiversity and environmental change in Columbian coral reefs

The DAAD funded *Center of Excellence in Marine Sciences* (CEMarin) is a Colombian-German consortium. The mission of the CEMarin aims at providing primarily Ph.D. level education in marine sciences, promoting marine sciences in northern South America, and conducting cutting-edge research under the main topic "Coastal Colombian resources and environmental changes". The main scientific goals of the CEMarin-related research conducted by the Systematic Zoology and Biodiversity group at the IFZ are to unravel the consequences of environmental changes on coral reef biodiversity in space and time, study the interactions of abiotic factors on the population dynamics of selected coral and fish species, and investigate patterns and processes of biological invasions in the southern Caribbean. In addition, the group in Giessen is interested in maintaining genetic resources of critically endan-



gered invertebrates by raising genetically distinct strains of selected coral species together with associated protists and algae in aquaculture. These populations will potentially enable a future re-colonization of damaged or destroyed coral reefs in Colombia.

Speciation and extinction processes in the East African Rift System

The DFG Research Unit “Rift dynamics, uplift and climate change in Equatorial Africa- RiftLink” is an interdisciplinary research group that addresses the causes of rift-flank uplift in the East African Rift since the Late Miocene, its impact on climate changes in Equatorial Africa, and the possible consequences for faunal evolution.

The Systematic Zoology and Biodiversity group studies the impact of environmental change since the Plio-

Pleistocene on the evolution of aquatic mollusks using genetic methods and the fossil record. Speciation and extinction events of rift-wide distributed taxa are unraveled and evolutionary assumptions are tested.

Within this project, it is investigated whether and to what extent large scale environmental and evolutionary changes correlate using phylogeographic methodology and molecular clock approaches. The results will help to better understand evolutionary and biogeographic consequences of the rifting processes in the East African Rift on aquatic organisms.

Thomas Wilke

phone ++49-641-35720

mail Tom.Wilke@allzool.bio.uni-giessen.de

www.uni-giessen.de/wilke





Microbiology

Institute of Microbiology and Molecular Biology
Faculty 08 — Biology and Chemistry

Prof. Dr. Annegret Wilde

Molecular biology and genetics of cyanobacteria

Cyanobacteria are photosynthetic bacteria that populate extremely diverse environments like soil crusts, open oceans, deserts, hot springs, permafrost and glacial regions, or have adopted a symbiotic lifestyle. They have produced the oxygenic atmosphere on Earth and are the ancestors of chloroplasts. The group of Annegret Wilde investigates regulatory systems and adaptation strategies of cyanobacteria on a molecular level.

Cyanobacteria are increasingly relevant for basic and applied research because they are able to fix CO₂ and N₂ and can simply be grown in seawater with light as the sole energy source. They contribute substantially to the global carbon cycle and primary production in aquatic ecosystems and serve as a major model for the analysis of oxygenic photosynthesis of higher plants. We intend to focus our work on a model cyanobacterium (*Synechocystis* sp. PCC 6803) with a well-annotated genome and simple genetic manipulation systems in order to characterize specific cyanobacterial functions that might be relevant for future biotechnological applications like the production of high value bioactive compounds as well as biofuels.

A major limitation of algal productivity is absorption of sunlight by specific photosynthetic antennae systems. On the other hand, absorption of high-intensity light is also very harmful in terms of oxidative stress. During the previous years, our group obtained comprehensive data sets on changes in the transcriptome and identi-

fied new enzymes and proteins that are components of pigment biosynthetic pathways and of the assembly machinery of photosynthetic complexes. In addition, we have shown that cyanobacteria harbor a high amount of non-coding RNA molecules as sequence specific regulators of gene expression.

The main focus of this research group is on the use of cyanobacteria as model organisms for the investigation of general problems in photosynthesis, light perception, stress response and RNA metabolism.

Identification and function of regulatory RNA in bacteria

Recent data from pro- and eukaryotic organisms show the extremely high potential of non-coding RNAs (ncRNAs) as sequence-specific regulators of gene expression, thereby mediating a plethora of cellular responses to changing environmental conditions. Systematic searches for ncRNAs are still lacking for most



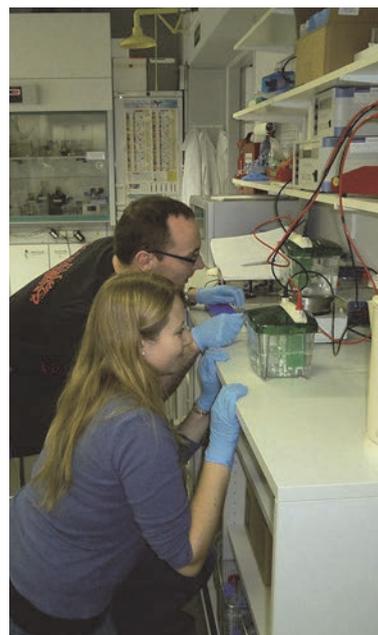
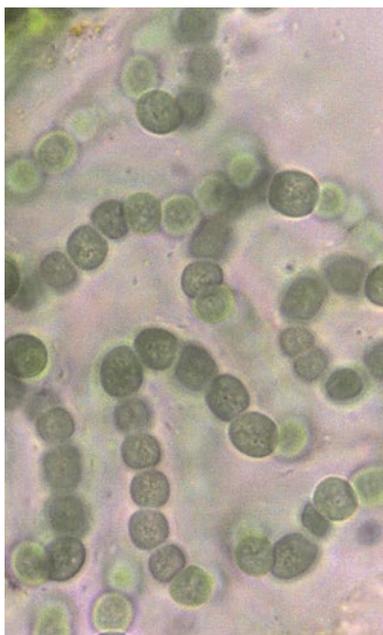
eubacterial phyla outside the Enterobacteria mostly because genes encoding ncRNAs are not annotated during standard genome analysis procedures. Therefore, additional efforts have to be taken to accomplish their identification. In collaboration with the group of Prof. Wolfgang Hess from University of Freiburg we have started a project on the systematic search for small regulatory RNA molecules in the cyanobacterium *Synechocystis* sp. PCC 6803 using bioinformatics and molecular methods. Based on this research we verified the existence of a large number of yet unknown functional regulatory RNAs. We intend to unravel the molecular function of RNA regulators as reversible switches to respond to environmental changes.

One practical result of our studies is the construction of a full transcriptome microarray for *Synechocystis* with probes covering all annotated genes, as well as asRNAs and ncRNAs found in the course of our studies, hence providing a comprehensive way of measuring any change in the total transcriptome.

Systems biology of cyanobacterial biofuel production

Cyanobacteria have the potential to become one of the future sources of biofuel. They can be used as effective producers of biomass, hydrogen and ethanol because they have the distinct advantage of being able to use carbon dioxide as their primary carbon and sunlight as the sole energy source.

The project (FORSYS Collaboration) is part of the efforts to efficiently and economically produce biofuels. Our approach is to combine photosynthesis with the synthesis of ethanol in a cyanobacterial cell. Together with our partners, we want to establish a systemic understanding of a photosynthetic prokaryote by experimental analysis of relevant metabolic pathways combined with data-based mathematical modeling. Well-established genetic tools together with an accumulating body of information from transcriptomic, proteomic and metabolomic data provide an excellent background for systems biology-based modeling, analytical prediction and simulation of cellular processes. The understanding of several cyanobacterial regulator



systems will be a milestone on the way of developing industrial relevant expression strains for biofuels.

phototrophic model bacteria that encode non-standard sets of the basic clock components.

Cyanobacterial circadian clock

Circadian rhythm, the coordination of cellular activities into daily cycles by an internal clock occurs in a wide spectrum of organisms. Among prokaryotes only the cyanobacteria harbour a robust circadian rhythm of gene expression. Experiments showed that three cyanobacterial Kai proteins, which share no sequence similarity to any known eukaryotic clock component, are sufficient to generate temperature-compensated circadian oscillations of protein phosphorylation in a test tube. The basic timing mechanism in eukaryotic circadian systems is based on transcription/translation feedback loops. Thus, the cyanobacterial core oscillator is a highly fascinating system as it is able to operate independently of transcription and translation processes. KaiC as the major clock component functions as an autokinase, autophosphatase and ATPase. KaiA enhances the kinase and KaiB the autophosphatase activity, respectively. Our analyses revealed that complex formation between Kai proteins and, therefore, their stoichiometry is essential in maintaining robust circadian oscillations. Our research (in collaboration with Humboldt University Berlin) aims at the elucidation of the functioning of the circadian oscillator systems with special emphasis on systems in different

Annegret Wilde

phone ++49-641-99-35545

mail Annegret.Wilde@mikro.bio.uni-giessen.de

www.uni-giessen.de/cms/fbz/fb08/biologie/mbio/Forschung/Agwilde





Microbiology and Molecular Biology

Institute of Microbiology and Molecular Biology
Faculty 08 — Biology and Chemistry

Prof. Dr. Gabriele Klug

Mechanisms of gene regulation in bacteria and archaea

Small unicellular organisms have to rapidly adapt to changing conditions in their environment. We study gene regulation in prokaryotes at the levels of transcription, RNA processing and translation. Regulatory proteins as well as RNA-dependent regulation are investigated with main focus on responses to redox- and light signals.

Microorganisms are continuously exposed to changing environments and have to cope with many stress factors in order to survive. One of our model organisms is the photosynthetic bacterium *Rhodobacter sphaeroides* that is found in freshwater habitats. It is able to perform aerobic or anaerobic respiration or anoxygenic photosynthesis. The formation of photosynthetic complexes is inhibited by high oxygen concentrations and at intermediate oxygen concentrations by light. This reaction diminishes the risk to form the harmful singlet oxygen, which destroys many cellular components. We also study the response to reactive oxygen species in members of the aerobic anoxygenic phototrophic bacteria, which form photosynthetic complexes under high oxygen concentration, and try to understand how these organisms cope with the related stress.

Response of phototrophic bacteria to oxidative stress

The ability to perform photosynthesis allows facultatively

phototrophic bacteria like *Rhodobacter* to use sunlight for ATP production when low oxygen concentrations do not allow aerobic respiration. However, the simultaneous presence of oxygen, light and pigments leads to the generation of the harmful singlet oxygen. *Rhodobacter* can also be exposed to high levels of other reactive oxygen species, which are generated in its natural environment, especially at high oxygen concentrations due to oxygenic photosynthesis of algae or cyanobacteria. We aim to understand how bacteria can sense reactive oxygen species and which mechanisms trigger the response leading to stress defense. One focus of the studies is on the role of alternative sigma factors that target the RNA polymerase to specific genes. Another focus is on the role of regulatory RNAs in the response to oxidative stress. We have identified a number of RNAs which change in level in response to stress and will now elucidate the mechanisms of regulation. Special emphasis is also given to the regulatory link between oxidative stress and the regulation of iron metabolism. The metabolic versatility



of *R. sphaeroides* allows discrimination between direct effects or iron availability and indirect effects which are caused by oxidative stress.

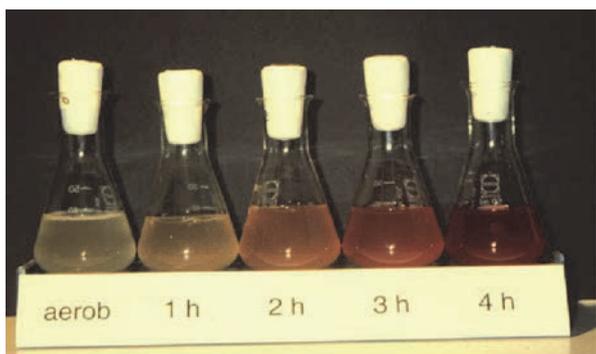
Photoreceptors in bacteria

Light is an important environmental stimulus for phototrophic bacteria. On the one hand it can serve as an energy source, on the other hand it can be harmful by generating reactive oxygen species. It was anticipated for a long time that only higher eukaryotes have developed photoreceptors that recognize light signals. It is now well established that also prokaryotes have evolved photoreceptors. *Rhodobacter sphaeroides* harbours at least three different types of blue light photoreceptors which all affect the formation of photosynthetic complexes. We identified the AppA protein with its new BLUF photoreceptor domain. AppA is the only known protein that can sense redox and light signals and integrate both. We also identified for the first time a biological function for a bacterial cryptochrome. It regulates photosynthesis genes and is also involved in stress responses. A third photoreceptor consists of a

short LOV (light oxygen voltage) domain. In addition, photosynthetic electron transport has a regulatory function in expression of photosynthesis genes. We aim to understand how a light dependent signal is initiated and transmitted within the cell and finally leads to altered gene expression. We are also interested to unravel the structures of the unusual cryptochrome and LOV protein of *R. sphaeroides*.

Mechanisms of RNA processing in prokaryotes

The processing and turn-over of RNA is an essential process in all living organisms. It is required for the maturation of RNAs and also contributes to regulation of gene expression. We have investigated the underlying mechanisms in different model systems for many years. Presently we focus on the biological functions of the RNA-processing exosome of *Sulfolobus solfataricus* and the biochemical processes involved in catalyzes. We aim to unravel the function of the individual components of the exosome. We would especially like to know how RNA-protein interaction is stabilized at



high temperature and low pH. In addition, we also investigate mechanisms of RNA processing in bacteria, especially in regard to processing and turn-over of small regulatory RNAs. Several regulatory RNAs affect gene expression by pairing to a target mRNA, which then leads to recognition by a double-strand specific RNase and degradation of both RNAs. We identified one regulatory RNA in *R. sphaeroides*, which is specifically processed in the presence of singlet oxygen. Thus, RNA processing may also have a sensing function in bacteria. We are currently identifying the RNases involved in singlet-oxygen specific processing

and analyzing by which mechanisms singlet oxygen can promote RNA cleavage.

Gabriele Klug

phone ++49-641-99-35542

mail Gabriele.Klug@mikro.bio.uni-giessen.de

www.uni-giessen.de/cms/fbz/fb08/biologie/mbio/Forschung/Klug





Experimental Plant Ecology

Institute of Plant Ecology
Faculty 08 — Biology and Chemistry

Prof. Christoph Müller, Ph.D.

The impact of global change on biodiversity and ecosystem processes

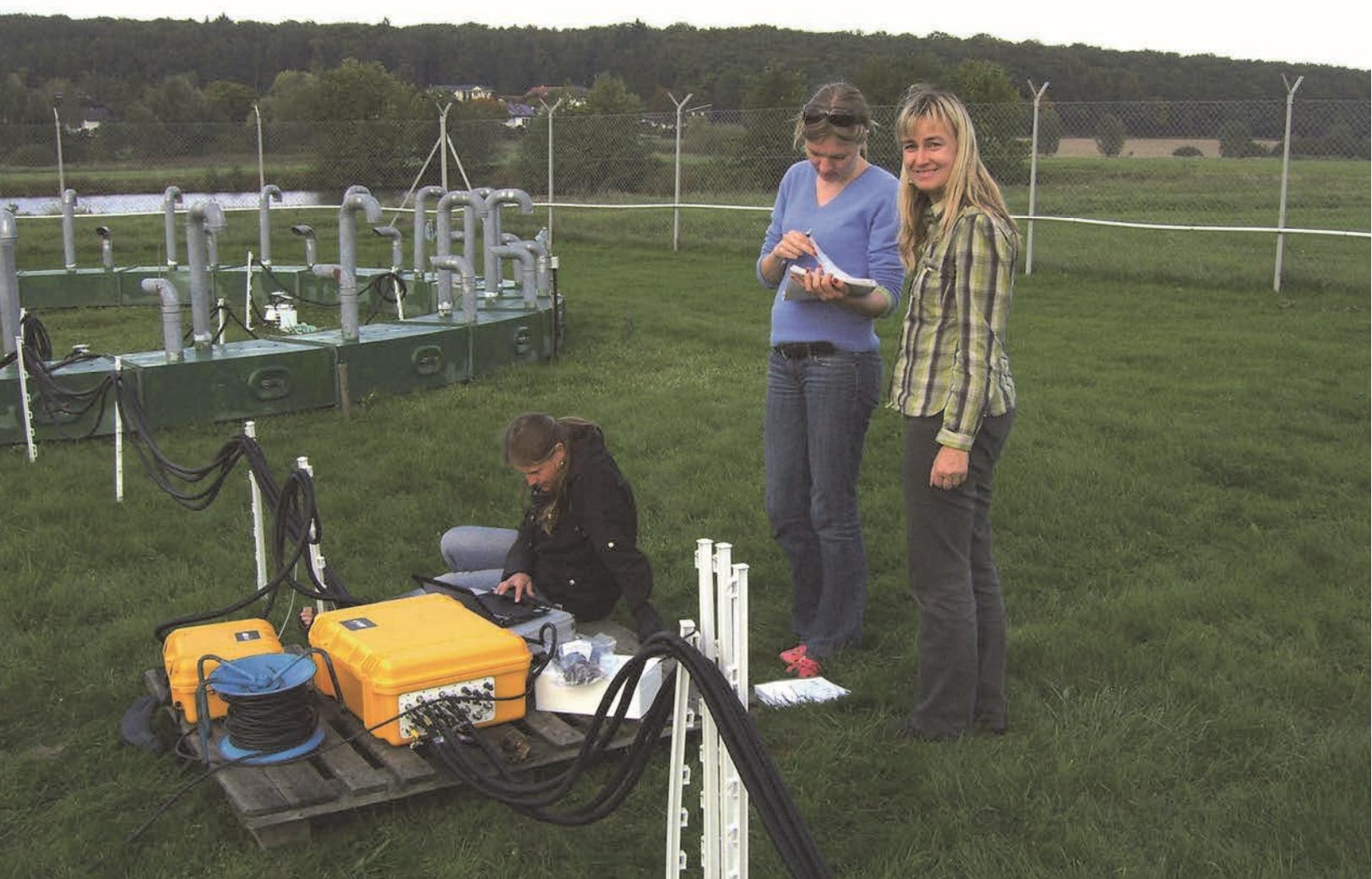
Plant and ecosystem development depends on interactions with the environment. Our research focus is on the evaluation of global change including climate change impacts and land-use changes. Our concept encompasses long-term biomonitoring programs, manipulation experiments to study ecosystem processes under climate change, and evaluation of mitigation options to reduce atmospheric CO₂ concentrations.

Throughout Earth's history, changing environmental conditions were always reflected in the development of specific plant communities. Increase in global temperature, which is linked to the unprecedented increase of greenhouse gases (CO₂, CH₄ and N₂O), and other human-induced changes of our natural environment (e.g. land-use changes) will affect our livelihoods. Ecosystems respond slowly to changing conditions, thus it is pivotal to make observations over long periods of time. In our institute we consider a three-step approach: 1) Study of long-term reactions of plant and ecosystem processes (e.g. plant phenology, micrometeorological studies) via long-term monitoring programs; 2) Investigation of future climatic scenarios (e.g. elevated atmospheric CO₂) on plants and ecosystems via manipulation experiments and 3) Evaluation of mitigation options to counterbalance global climate change. We have two active working groups in Giessen and Dublin (Ireland). The Giessen group has a focus on long-term monitoring programs including one of the longest running FACE facilities on perma-

nent grassland world-wide. The Dublin group has as focus on peatland research to study biodiversity and carbon exchange on drained and restored peatland and also grassland research with the aim to evaluate sustainable options for bioenergy production.

Effect of climate change on plant ecosystem processes

Biomonitoring programs and manipulation experiments to evaluate the effect of climate change on plant growth and ecosystem processes are carried out at the Environmental Monitoring and Climate Impact Research Station Linden. Since 1998 a Free Air Carbon dioxide Enrichment (FACE) study has been in operation, which simulates a 20% higher atmospheric CO₂ concentration which is reached in ca. 2040. Results from this species-rich ecosystem over the past 12 years showed an approximate 10% biomass increase under elevated CO₂ and clear biodiversity shifts towards grass species at the expense of herbs.



One of the world-wide longest continuous trace gas (N_2O , CH_4 , CO_2) emission data sets shows that elevated atmospheric CO_2 stimulates emissions of other climate relevant trace gases. This is most likely related to plant carbon transfer into the soil and a concomitant shift of microbial activities in the ecosystem. Elevated air temperatures have already led to a shift in plant phenology, i.e. timing of recurring life cycle stages such as flowering. Observations are carried out in a phenological garden which is embedded in national and international monitoring programs. Long-term records reveal that the last 20 years have been characterized by reduced dormancy (winter period) and an earlier start of spring. Our results show that long-term observations are pivotal to evaluating the effect of climate change on ecosystem processes.

Mitigation options to reduce climate relevant greenhouse gas emissions

Currently we are evaluating two options to limit the increase and possibly reduce the atmospheric CO_2 concentrations: (1) Long-term sustainability of grass-

land as a source for bioenergy (biogas) production (Dublin group) and (2) Long-term carbon storage in soils in the form of pyrolysed biomass (biochar) (Giessen group). The project in Ireland focuses on the environmental impacts and long-term sustainability of grass biomass for energy production via biogas production in farm-based digesters. Grass has a high energy potential and is suitable for co-digestion in biogas plants. Results show that extensively managed grasslands and fertilizer management utilizing digestate provide the most sustainable option for bioenergy production from grass. Furthermore, biomass yield is also positively affected by biochar application as shown from research on man-made Terra preta soils. Terra Preta research showed that addition of charred organic matter to soil generally leads to an increase of biomass yield and improves soil fertility as a function of mineral and organic soil components. However, biochar research in temperate agricultural soils is still in its infancy. Recently, we developed biotoxicity tests to identify possible ecotoxicological effects of biochar applied to soils. Field studies on permanent grassland have been initiated to identify the effects of biochar on



soil fertility, biomass production and biodiversity as well as greenhouse gas emissions. Preliminary results indicate that biochar may reduce N₂O emissions from soils.

Effect of peatland management on plant biodiversity and C dynamics

Peatlands are Ireland's last great areas of wilderness, providing important retreats for unique and specialist flora and fauna. Actively growing raised bogs, blanket bogs and fens act as long-term carbon stores actively removing carbon from the atmosphere. This trend is reversed if peatlands are damaged. Degraded peatlands result in large net C emissions. Restoration offers the potential to reduce CO₂ emissions and re-establish the C sink function characteristics. Results from a restored peatland on the west coast of Ireland provided convincing evidence that degraded peatlands can be restored within a few years to regain

their function as a C sink. The actively growing peatland community sequestered annually approximately 2.7 t C ha⁻¹ whereas bare peat and open water areas were net CO₂ sources. The research provided clear evidence that re-establishment of the peatlands C-sink functions via rewetting can be successful highlighting the potential of industrial cut-away peatlands to be utilized as C offset projects. This research will be expanded and complemented via studies that are aimed to evaluate the greenhouse gas emissions of organic soils in Ireland, which may be a major source of climate relevant trace gas emissions and play an important role for national inventories.

Christoph Müller

phone ++49-641-99-35300

mail Christoph.Mueller@bot2.bio.uni-giessen.de

www.uni-giessen.de/cms/fbz/fb08/biologie/pflanzenoek



Plant Ecology with Focus on Geocology and Modeling

Institute of Plant Ecology
Faculty 08 — Biology and Chemistry

Successful candidates will be highly qualified to conduct scientific work in the fields of plant ecology, geocology and ecological modeling and possess teaching skills. They should also have an understanding of the future development of ecosystems under climate change and should be willing to closely liaise within the IFZ in the pursuit of its research objectives.



Biometry and Population Genetics

Institutes of Agronomy and Plant Breeding
Faculty 09 — Agricultural Sciences, Nutritional Sciences
and Environmental Management

Prof. Dr. Matthias Frisch

Biometric modeling and computer simulation of population genetic systems

The working group Biometry and Population Genetics in the Institute of Agronomy and Plant Breeding II conducts research on the modeling of complex population genetic systems with biometric models and computer simulations. Our goal is to develop the mathematical foundations that serve as the theoretical basis of crossing and selecting in plant breeding.

In 1908 the Stuttgart based physician W. Weinberg published a biometrical model that was able to explain the inheritance of eye colors in human populations. The British mathematician G. H. Hardy independently found the same result, and the so called Hardy-Weinberg law is regarded as the foundation of population genetics. This discovery initiated research on the factors that influence the characteristics of populations with respect to traits interesting human geneticists as well as plant and animal breeders. While it was known since the beginning of agriculture that planting seeds from the best plants of a crop field results in a steady increase in yield, only with the development of population genetical models, could these changes be theoretically explained. And more importantly, population genetic models can quantify the changes in a population and can suggest methods to determine the parents of crosses and methods to select between their progenies. To suggest crossing schemes and selection strategies for the development of new and better crop cultivars is the goal of population genetics in the

context of agronomy. In our working group, we focus on the population genetic theory of applying state-of-the-art molecular techniques for the development of new crop cultivars with increased yield, better quality, and higher resistance to biotic and abiotic stresses while at the same time maintaining and improving the genetic diversity in the breeding populations.

Increasing the genetic diversity in elite maize with introgression populations

The gene pool of maize is tremendously diverse. Despite this abundance of genetic diversity, the currently grown cultivars relate back to a relatively small set of progenitors and, therefore, their genetic base is narrow. In the tropics, maize has been adapted to very contrasting climates. Under humid conditions in the lowlands, maize is cultivated under a high insect and fungal disease pressure, in other regions maize faces severe droughts and high temperatures. In Andean regions, maize is grown at elevations up to 4000m and



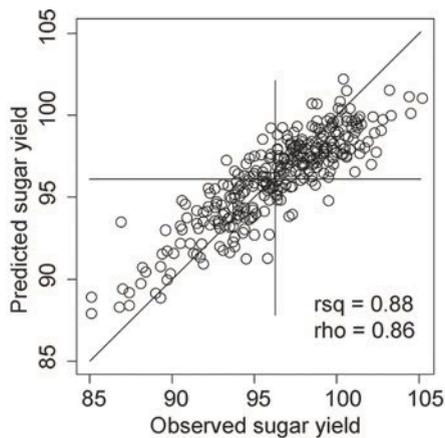
has to cope with very low temperatures throughout its growing season. Tropical maize should therefore present a host of opportunities for the improvement of yield and its stability in temperate germplasm. This high genetic diversity for abiotic and biotic stress tolerances has not been exploited yet systematically. A major bottleneck for the utilization of tropical germplasm is its poor adaptation to our temperate target environments. Photoperiod sensitivity, late maturity, and susceptibility to lodging make it impossible to directly cross tropical with temperate maize and to grow the progenies under temperate conditions.

We investigate the development of novel strategies for the systematic use of tropical germplasm in the improvement of temperate maize. We aim to identify novel genetic variation for biotic and abiotic stress tolerances focusing on three important traits: nitrogen use efficiency, cold tolerance, and resistance to northern corn leaf blight. Our method of choice is introgression populations. These consist of a set of elite maize lines carrying small chromosome segments originating from tropical maize in the genetic background of temperate elite breeding material. We aim to design an

optimal strategy for the construction of genome-covering introgression populations. This includes a cost-effective and time-saving development of introgression populations using novel molecular techniques and optimized crossing schemes. In addition, novel biometric designs and methods will be developed for efficient detection of the genes underlying the favourable properties in introgression populations. Knowledge gained from computer simulations will be directly used for the development of introgression populations by our project partners.

DNA-based identification of superior genotypes in sugar beet populations

Identifying the best individuals in a population of candidate genotypes of a crop is done in classical breeding by testing the candidate genotypes in field trials over several years at multiple locations. These trials are a main reason for the long time span required for the development of a new cultivar and are causing a major part of its costs. New developments in molecular biology delivered high-throughput DNA sequencing



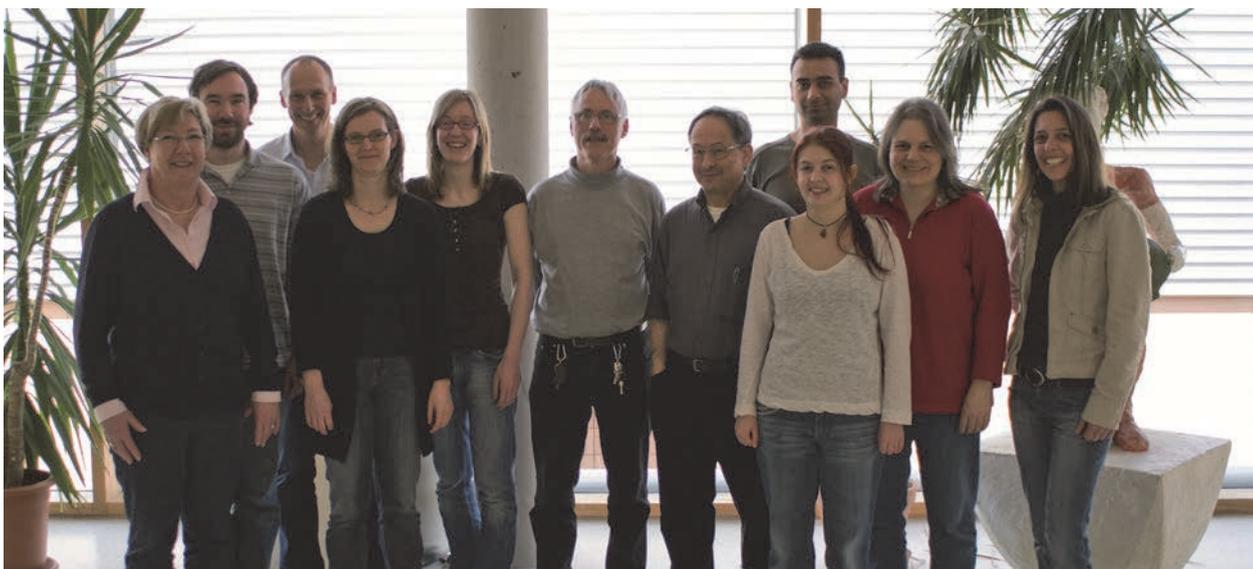
technologies, that enable the genetic fingerprinting of candidate genotypes quickly with relatively low costs. Using such DNA information for drawing conclusions on the field performance of breeding material has the potential to entirely change the way new cultivars are developed and to greatly enhance the efficiency of developing new cultivars with improved yield, quality, and resistance characteristics.

We are developing new biometrical models for predicting sugar yield related traits of the genotypes in breeding populations of sugar beet lines on the basis of information from their DNA sequence. The characteristic properties of the DNA sequences of sugar beet lines are assessed with single-nucleotide-polymorphism markers. At the same time, the performance of the lines is assessed in field trials. Then models are established that relate the DNA information to the field data. These models are used to estimate the effects of DNA sequences on sugar yield related traits.

The concept of DNA based "genomic selection" uses these estimated effects together with DNA analyses of newly bred sugar beet lines to predict the performance of the new lines with respect to sugar yield. This enables the breeder to have a first information on the performance of a new line before it has been grown in the field, based solely on its DNA sequence. Our theoretical and simulation studies are accompanied by the application of our models in practical sugar beet breeding programs by a project partner. This ensures an instant transfer of newly developed population genetic theory into practical cultivar development.

Matthias Frisch

phone ++49-641-99-37540
 mail Matthias.Frisch@agr.uni-giessen.de
www.uni-giessen.de/biometrie





Genomics-based breeding for quality, resistance and yield

The Department of Plant Breeding has diverse research activities in the fields of genetic analysis and breeding for resistance to biotic and abiotic stress, seed quality, vigour and yield in major European crops. A major focus is the development and application of genomics methods for elucidation and selection of important traits.

Crop plants are the fundamental basis of human nutrition and an increasingly important source of renewable energy. As the world population expands there is a demand to continually increase production of high-quality crop products, but with lower agronomical inputs. Increasing yields of major crops in the face of abiotic and biotic stress factors, and improving quality for nutrition and energy use, are therefore ongoing challenges for plant breeders. In the Department of Plant Breeding we work closely with the breeding industry on research solutions for improvements in seed and biomass yield, biotic and abiotic stress resistance, seed quality, developmental and physiological traits. The main crops of interest are oilseed rape, the most important oilseed crop in Europe, the two major cereal crops wheat and barley, along with the emerging energy crop sorghum. A major focus of our research is the use of genomics-based technologies for more efficient use of genetic diversity in breeding programs. Identification and utilization of novel diversity for complex traits is an extremely difficult challenge for breeders,

and by implementing the latest technologies for high-throughput DNA sequencing and marker-based selection we help to accelerate this process. Some examples include the identification and introgression of new resistances against the emerging fungal disease *Verticillium longisporum* into oilseed rape, the improvement of rapeseed meal quality for livestock feeds by locating and using genes for reduced seed fibre, and the use of DNA marker technologies for marker-assisted combination of desired resistance genes in cereals.

Fusarium resistance in wheat

Fusarium head blight (FHB), caused by the fungi *Fusarium graminearum* and *F. culmorum*, is one of the most destructive diseases of wheat and barley worldwide. The mechanisms of pathogenesis and host plant resistance are still poorly understood, and breeding for FHB resistance is extremely challenging since available resistances are complex and pose difficult problems for selection. In this study we performed gene expression profiling of resistant and susceptible wheat

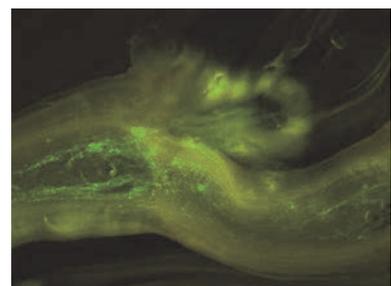
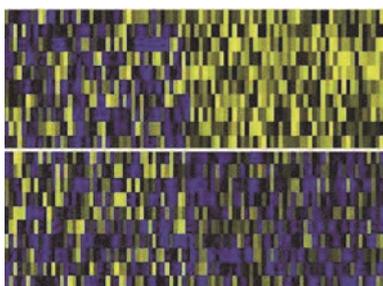


cultivars, using the Affymetrix wheat GeneChip®, in order to gain insight into the molecular pathogenesis of FHB infection. Identification of key steps in disease course, and their relationships to known biological processes, is a first step towards development of new prevention strategies against FHB epidemics. The study revealed different mechanisms that appear to contribute to the defense response in the resistant cultivar “Dream”. The major factor was a jasmonic acid mediated expression of anti-microbial peptides, accompanied by ethylene-regulated elicitors of induced systemic resistance and inhibitors of necrotrophic fungal pathogens, respectively. A second contributing

factor was expression of cell wall defense genes involved in fungal inhibition and degradation. We are now working to further confirm the observed defense mechanisms and analyse specific signalling factors that might have potential to improve resistance against this important pathogen.

Improvement of abiotic stress tolerance in energy sorghum

In recent years interest has grown in the potential use of sorghum as an alternative to maize for biomass production. In comparison to maize, sorghum has a



considerably higher tolerance against water stress, a factor of growing importance in the face of climate change and expanding maize production for biogas and ethanol production. As a tropical plant, however, sorghum is particularly sensitive to low temperatures during early plant development. Thus, tolerance to early-stage chilling needs to be improved to establish sorghum production in temperate regions like Germany. The genus *Sorghum* contains numerous inter-crossable subspecies with considerable biodiversity for biomass yield and stress tolerance. In this research we are investigating chilling tolerance and other abiotic stress factors in genetically diverse sorghum populations and using genomics-based techniques to try to identify the responsible genes and mechanisms. Extensive phenotype data for biomass, developmental, physiological and metabolic traits are collected from field evaluations, greenhouse trials and growth chamber experiments under optimal and stress conditions. By correlating phenotypes with genomic data describing the genetic variation present in the populations we hope to identify chromosome segments, and ultimately genes, associated with the traits of interest.

Associative expression and systems analysis of complex traits in rape

The tri-national ERANET Plant Genomics Consortium ASSYST, coordinated by Rod Snowdon from the De-

partment of Plant Breeding, aims at identifying regulatory genes involved in expression of complex traits in oilseed rape. In cooperation with colleagues in Germany, Canada and the UK, quantitative gene expression data from oilseed rape populations are being integrated with global gene expression data, quantitative metabolite profiles and phenotype data from greenhouse and field trials using a systems genetics approach that combines an analysis of gene co-expression networks with expression mapping approaches. The consortium has developed a new single-nucleotide polymorphism (SNP) array that will be used to find chromosome regions associated with important traits in a set of over 500 genetically diverse *Brassica napus* inbred lines. The project incorporates the most recent technological developments in the field of next-generation sequencing for ultra-deep gene expression profiling and SNP discovery. Gene co-expression network analysis, classical quantitative trait mapping, genetical genomics and association genetics concepts are being integrated in a manner that until now has not been used for functional genomics of complex traits in crop plants.

Wolfgang Friedt

phone ++49-641-99-37420

mail Wolfgang.Friedt@agrar.uni-giessen.de

www.plantbreeding-giessen.de/





Animal Nutrition

Institute of Animal Nutrition
Faculty 09 — Agricultural Sciences, Nutritional Sciences
and Environmental Management

Prof. Dr. Klaus Eder

Molecular animal nutrition

Nutrients are able to activate or inhibit transcription factors which are regulators of gene expression in animal cells. The group of Klaus Eder investigates the interaction between nutrients and transcription factors in farm animals in order to find possibilities to modify the metabolism in a beneficial manner to improve animal performance, health and the quality of animal products.

Nutrition has a variety of important functions in animal production. An adequate supply with energy and nutrients is not only required for the achievement of maximum animal performance (e.g. growth, milk yield) but also for keeping farm animals in a good health condition. Moreover, nutrition influences the quality of animal products. Finally, feeding has an impact on the release of environmentally relevant compounds such as phosphorus, nitrogen, trace elements or greenhouse gases. In farm animals, energy and nutrients are required for anabolic processes, i.e. protein and fat synthesis. However, several nutrients are also able to influence the metabolism by acting as activators or inhibitors of transcription factors. Transcription factors are proteins which are able to activate or inhibit the transcription of numerous genes and thus to modulate the metabolism in a complex manner. Among many transcription factors existing, the peroxisome proliferating-activated receptors (PPARs), the sterol regulatory-element binding proteins (SREBPs) and nuclear factor kappa B (NF-kB) are particularly interesting

from a nutritional view as they are activated or inhibited by several nutrients. PPARs play an important role in energy homeostasis and fatty acid and glucose metabolism. SREBPs play a key role in the regulation of lipogenesis and the synthesis and uptake of cholesterol in mammalian cells. NF-kB is the key regulator of the inflammatory process. While the role of these transcription factors has been well investigated in humans and rodents, less is known about their function in farm animals. The group of Klaus Eder aims to detect links between nutrients and transcription factors in farm animals in order to find possibilities to modify the metabolism in a beneficial manner.

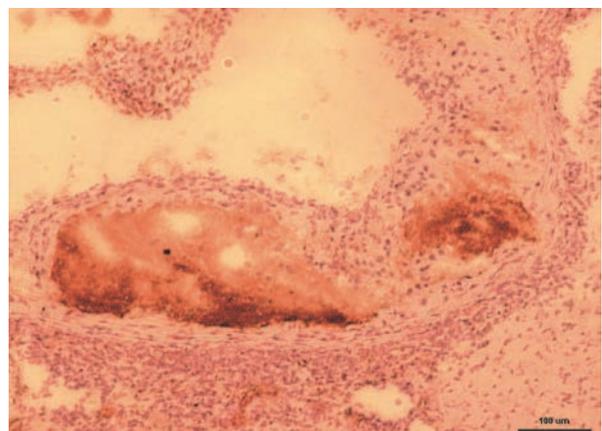
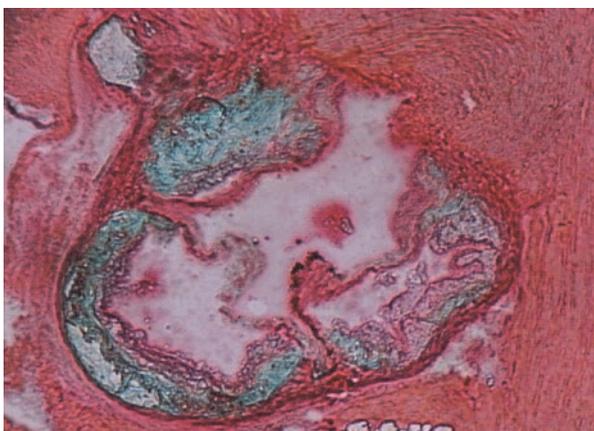
Activation of PPAR α stimulates carnitine synthesis and uptake into cells

Carnitine plays a key role in the β -oxidation of fatty acids. It is derived from the diet but is also synthesized in liver and kidneys. Carnitine from the diet or endogenously synthesized is taken up into body cells by novel



organic cation transporter (OCTN)-2. Until recently, little was known about the regulation of carnitine homeostasis. We investigated the hypothesis that carnitine synthesis and uptake into cells is stimulated by PPAR α . Therefore, we used PPAR α knockout mice and their wildtype littermates to study the metabolism of carnitine. In wildtype mice, treatment with a synthetic PPAR α agonist increased the expression of enzymes involved in carnitine synthesis and OCTN2 and increased concentrations of carnitine in various tis-

sues. In contrast, these effects did not occur in PPAR α knockout mice. In analogy with these findings, we observed that fasting (which leads to activation of PPAR α by release of fatty acids from adipose tissue) and feeding of thermoxidized fats (which contain oxidized fatty acids as nutritive PPAR α agonists) cause also an up-regulation of genes involved in carnitine synthesis and uptake and increased carnitine concentrations in tissues of rats and pigs. Recently, we were able to detect functional PPAR α response elements in



the key enzyme of carnitine synthesis and OCTN2 which is a further proof that carnitine is directly regulated by PPAR α . Altogether, these findings show that PPAR α regulates carnitine homeostasis in rodents and farm animals.

Sterol regulatory element-binding proteins influence genes involved in the synthesis of thyroid hormones

We have recently observed that treatment of thyroid cells with cholesterol down-regulates the expression of genes involved in thyroid hormone synthesis such as sodium iodine symporter (NIS) or thyroid peroxidase (TPO). As cholesterol treatment lowers the expression and activation of SREBPs, we hypothesised that the effect observed was mediated by a reduced activity of SREBPs. In order to investigate this hypothesis we performed experiments in which SREBPs were inactivated by treatment with 25-hydroxy-cholesterol. In these experiments, promoter activity of NIS was strongly reduced. We moreover found that treatment of thyroid cells with thyroid stimulating hormone (TSH) stimulates the activation of SREBPs. These findings strongly indicate that SREBPs play a key role in the synthesis of thyroid hormones. As expression and activation of SREBPs are influenced by nutrition, i.e. dietary cholesterol intake, a novel link between nutrition and thyroid hormone synthesis could be detected.

Activation of PPAR α activates the ubiquitin proteasome pathway

In the animal organisms, proteins are underlying a permanent turnover. The ubiquitin-proteasom system (UPS) is the most important system involved in the degradation of proteins. An up-regulation of this system stimulates protein breakdown in tissues while a down-regulation of this system suppresses proteolysis. The role of the UPS has been most intensively studied in the skeletal muscle where a stimulation of this system causes atrophy. We investigated the hypothesis that this system is activated by PPAR α . We found indeed that activation of PPAR α by a synthetic agonist causes an up-regulation of several components of the UPS in skeletal muscle of wildtype mice but not in PPAR α knockout mice. In more recent experiments, we found that treatment with synthetic PPAR α agonists or oxidized fats cause an up-regulation of this system in rats, pigs and laying hens. The up-regulation of this system led to increased proteolysis in muscle and reduced muscle mass. Altogether, our studies show that an up-regulation of UPS, induced by activation of PPAR α , stimulates proteolysis in muscle and thus enhances "muscle wasting". Dietary strategies to inhibit activation of PPAR α might lower degradation of muscle.

Klaus Eder

phone ++49-641-99-39230

mail Klaus.Eder@ernaehrung.uni-giessen.de

www.uni-giessen.de/cms/fbz/fb09/institute/tierernaehrung



Plant foods are the principal sources of energy and nutrient supply of farm animals. The Feed Sciences group aims to investigate the effect of particular plant ingredients such as secondary plant metabolites on metabolism and health aspects of farm animals.



General and Soil Microbiology

Institute of Applied Microbiology
Faculty 09 — Agricultural Sciences, Nutritional Sciences
and Environmental Management

Prof. Dr. Sylvia Schnell

Understanding the functional role of microorganisms and their interactions in environmental habitats

Ecosystem functions of anaerobic complex microbial communities are studied to understand the interactions of microorganisms with abiotic and biotic environmental factors. Community structure changes upon time, space or altering environmental factors are analyzed using cultivation, molecular, and analytical techniques in habitats such as biogas plants, human intestine, and rice paddies. Relevant microorganisms are identified for further studies concerning their ecological function and interactions with other organisms.

Microorganisms are the most successful organisms on our planet, as they outnumber every other group of organisms. Environments of all climatic regions are inhabited by prokaryotes, as these organisms have adapted to different concentrations of nutrients, a wide range of substrates, and temperatures. Microorganisms have also adapted to extreme conditions including high salinity and can use different organic and inorganic compounds as electron donors and acceptors. Knowledge on diversity and ecological function of microorganisms is still limited, which is in contrast to their important functions in global biogeochemical cycles and the crucial functions in interactions with higher organisms. Many of the important microorganisms are not yet identified, mainly due to the fact that cultivation methods have been shown to be very limited for determination of environmentally abundant microorganisms. Therefore, molecular methods are in use for approaching the microbial diversity and structural community changes upon environmental changes.

Identification of the abundant microorganisms by culture-dependent and molecular culture-independent methods will help to understand the factors controlling interactions of these organisms with the environment and will allow to manipulate them. Our studies may lead to favorable outcomes such as higher salt stress resistance of plants, less greenhouse gas emissions from agricultural soils, and higher biogas production in biogas plants.

Microbial community analysis in biogas reactors

Production of biogas from organic matter involves a community of diverse microorganisms. However, little is known about the key organisms for degradation of certain substrates in biogas plants. This knowledge could help to improve fermentation processes and may enhance biogas formation by optimizing the respective growth conditions for these key organisms.



Therefore, we study microbial communities in lab-scale biogas reactors which were filled with manure. The manure was fermented and diminished in organic carbon before different model substrates were added such as casein, starch, cellulose, and plant oil to follow the corresponding changes in the community structure. Key organisms for the degradation of the added substrates were identified which comprised bacteria of the phyla *Firmicutes* and *Bacteroidetes*. The organisms also represent the most abundant bacteria in the reactors as shown by the high copy numbers of the 16S-rRNA gene fragments detected by real-time PCR. Within the *Firmicutes*, the family *Lactobacillaceae* and *Clostridia* Cluster XIVa turned out to be of highest abundance, both consisting of fermenting bacteria. As detected by molecular fingerprinting methods, organisms of the genera *Cytophaga* und *Alkaliflexus* (both phylum *Bacteroidetes*) have been shown to be most dominant. Community changes according to different substrates have been identified by altered banding patterns. Methanogenic *Archaea* were quantitatively monitored based on detection of the *mcrA* gene encoding the methyl-CoM reductase

involved in the last step of methanogenesis. As determined by quantitative real-time PCR, the copy number of this gene was about 10^8 per g dw. *Methanospirillum* and *Methanobrevibacter* have been identified which were known to utilize hydrogen and methanol. Interestingly, no acetate-degrading methanogens have been detected, which are hypothesized to play an important role in biogas reactors. Further studies will focus on processes induced by more complex substrates and will use rRNA-based techniques.

Does the body weight of persons relate to the composition of their intestinal microflora?

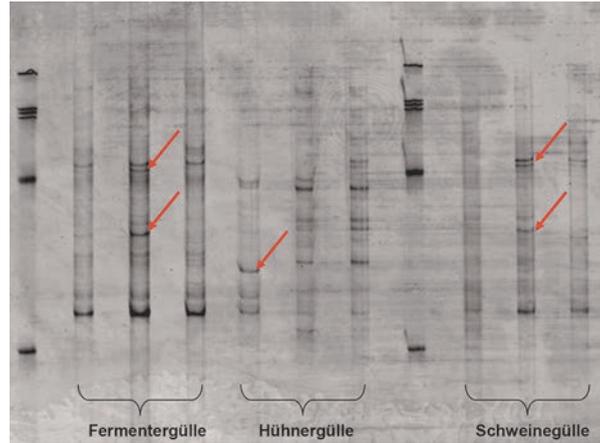
Obesity epidemic is a global phenomenon, both affecting people in developed and developing countries. Formation and manifestation of obesity is due to many factors such as sparse exercise, excessive nutrition, genetic factors or illness. Recent work has shown that the intestinal microflora may also be influenced by interactions with the host system affecting the host energy balance. For understanding of these observati-



ons in more detail, stool samples were collected from healthy persons, either with normal weight or with obesity. All persons represented a homogeneous group regarding age and gender. After extraction of DNA from the stool samples, real-time PCR and molecular fingerprinting were performed. For the analyses, different primers sets were applied which detect the major groups of intestinal flora microorganisms. First results showed significantly higher *Firmicutes* 16S rRNA gene target numbers in the obese group compared to the normal weight control group whereas no differences were found for *Bacteroidetes* and total bacteria numbers. As shown by cloning of the 16S rRNA gene, abundant families within the *Firmicutes* were the *Lactobacillaceae*, *Clostridiaceae*, and *Veillonellaceae*. Banding patterns of 16S rRNA gene fragments acquired by PCR-SCCP (single strand confirmation polymorphism) with *Firmicutes*-specific primers showed prominent bands in samples from the obesity group which are currently sequenced.

Plant growth-promoting bacteria diminishing salt stress of plants

Plant rhizosphere is highly colonized by bacteria which interact with the plants in a mutualistic or pathogenic way. The so-called plant growth-promoting bacteria support plant growth by (i) supplying nutrients as a source of nitrogen or phosphorous, (ii) diminishing stress situations by changing endogenic levels of plant growth regulating substances, or (iii) by replacing location sites of pathogens. Salinity is a major environmental threat for crop production in arid regions of the world. In this project, 119 strains with different plant promoting abilities were isolated and identified from



the rhizosphere of the wild barley *Hordeum secalinum* and of *Plantago winteri* from a natural salty meadow in Münzenberg, Germany. At the beginning of the study, we focused on rhizobacteria containing activity of ACC (1-aminocyclopropane-1-carboxylate) deaminase which is able to reduce the endogenous ethylene level. Several bacterial strains with ACC deaminase activity were isolated and strains were further selected based on their properties to produce indole-3-acetic acid (IAA) and to solubilize phosphorous. Three strains were evaluated for growth-promoting efficacy on crop barley and for effects on root colonization by conducting a pot experiment under axenic conditions at salinity levels of 0, 0.7, 5 and 10 dS m⁻¹. The results indicated that all three strains were able to promote root and shoot growth of barley under salinity stress. Further studies will focus on ACC gene expression under environmental stress conditions and on characterization of further isolates.

Sylvia Schnell

phone ++49-641-99-37350

mail Sylvia.Schnell@umwelt.uni-giessen.de

www.uni-giessen.de/fbr09/mikrobiologie/schnell.html





Recycling Microbiology

Institute of Applied Microbiology
Faculty 09 — Agricultural Sciences, Nutritional Sciences
and Environmental Management

Prof. Dr. Dr. Peter Kämpfer

Diversity analyses of microbial communities from different environments

In different projects the research group is studying the microbial diversity of bacterial communities with both cultivation-dependent and cultivation independent (molecular) methods. The aims of the projects are to gain a better understanding of the composition of the microbial communities and their different roles in complex and often rapidly changing environments.

Microbial diversity on the skin of the medicinal leech *Hirudo verbana*

Medicinal leeches are used today mainly post-operatively in the fields of plastic and reconstructive surgery. Like all living organisms, leeches harbour communities of microorganisms and their application can lead to a bacterial infection. In this project, the bacterial diversity on the skin of the medicinal leech *Hirudo verbana* as well as methods to reduce this diversity before contact with patients are studied. 16S rRNA gene analysis revealed that a high bacterial diversity can be found on the skin of leeches. Isolated strains had high sequence similarities with potentially pathogenic species. To reduce the number of microorganisms on leeches, they were treated with potassium permanganate, antiseptic agents and washed with tap water. Although the numbers of bacteria on the leeches were reduced in most of the experiments, the results were not always consistent. Ciprofloxacin, an antibiotic that was tested, had a negative effect on the

viability of the leeches. On the other hand, washing leeches with water directly before treatment showed the best results. This procedure seems to be an easy to follow and low priced method to lower the number of microorganisms on the leech.

Diversity analysis of indoor *Actinobacteria* from water-damaged building materials

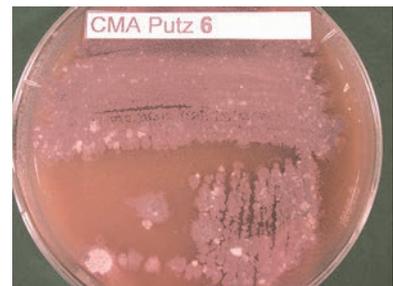
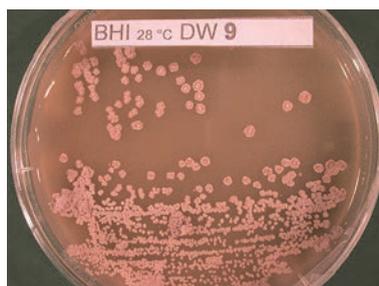
Different building materials damaged by water were investigated by cultivation-based and molecular approaches to compare the communities of *Actinobacteria*. For the identification of the isolates at the genus level, the 16S rRNA gene sequencing approach and chemotaxonomic methods were applied. In addition, genomic DNA extracted directly from building material was used as template for the generation of clone libraries of the 16S rRNA genes. With both methods, 63 different genera of the class *Actinobacteria* were detected. A total of 256 isolates from the 16 materials



were assigned to 34 different genera of the class *Actinobacteria*. By cloning analyses, 16S rRNA gene inserts of 689 out of 1600 clones (45%) from 16 materials were assigned to 53 different genera. Representatives of *Streptomyces*, *Amycolatopsis*, *Nocardiopsis*, *Saccharopolyspora*, *Promicromonospora*, and *Pseudonocardia* were found most frequently. Several novel species belonging to the genera *Promicromonospora*, *Brevibacterium*, *Citricoccus*, *Microbacterium*, *Nocardia*, *Nocardiopsis*, and *Prauserella* could be detected. The results derived from both methods indicate a high abundance and diversity of *Actinobacteria* in water damaged buildings. To obtain a detailed overview of the diversity of *Actinobacteria*, both methods have to be used.

Biogeography and genetic diversity of phyllosphere pink-pigmented facultative methylotrophic bacteria

Phyllosphere methylotrophic bacteria were characterized by their ability to utilize C1-compounds as their sole carbon and energy source. They colonize plant surfaces, mainly leaves, and play an important role in the methanol cycle by utilizing the methanol emitted by plants. In addition, they can produce plant growth promoting substances like auxins. One aim of the current project is to analyse the abundance and genetic diversity of phyllosphere pink-pigmented facultative methylotrophs (PPFM) in dependence on the colonized plant species, the geographic location of the





sampling site and the land-use type. Leaf samples of *Trifolium repens* and *Cerastium holosteoides* were collected from sites with different land-use types from 3 sampling locations in Germany. It was found that the abundance of PPFM was significantly higher on leaves of *Trifolium repens* than on leaves of *Cerastium holosteoides*. Geographic location, land-use type and fertilisation had no significant influence on the abundance of the PPFM on the leaf surfaces. 16 different groups of pink-pigmented isolates were found, which were similar to *Methylobacterium adhaesivum*, *M. me-*

sophilicum, *M. organophilicum* and *M. jeotgali*. The main groups of isolates could be found on leaves of both plant species, in both sampling periods, and at all sampling sites and land-use types.

Peter Kaempfer

phone ++49-641-99-37352

mail Peter.Kaempfer@umwelt.uni-giessen.de

www.uni-giessen.de/cms/fbz/fb09/institute/mikrobiologie/recycling-prozesse





Landscape Ecology and Landscape Planning

Inst. of Landscape Ecology and Resources Management
Faculty 09 — Agricultural Sciences, Nutritional Sciences
and Environmental Management

Prof. Dr. Dr. Annette Otte

Balance between demands of land-use and ecological requirements of biodiversity within the cultural landscape

Our main task is the analysis of patterns and the diversity of interactions of plant populations and plant communities with their environment. We want to understand the relationships of compositional, structural and functional components of biodiversity on different spatial scales. Our research results are aimed to further the balance between the demands of land-use and the requirements of biodiversity within the cultural landscape. Projects within the subject area of Landscape Planning are consequently carried out with the aim to establish scientifically sound foundations for nature conservation. Our current research projects consider the local to the regional scale in different parts of the world and are organized as stand-alone or interdisciplinary projects.

amies - Analysing multiple interrelationships between environmental and societal processes in mountainous regions of Georgia - Interdisciplinary research to foster sustainable land use, land development, and quality of life

Since its declaration of independence in 1991, Georgia has undergone dramatic transformation processes, which have caused environmental problems such as land degradation, soil erosion, and decrease in biodiversity, and resulted in societal changes such as pauperisation followed by migration. Climate change has aggravated the environmental problems. Thus, research that aims to foster sustainable land use, land

development, and quality of life in this part of the world is urgently needed.

In this context, our three-year research project aims at developing and applying an interdisciplinary and multi-scale approach, focussing on two study regions in the Greater and Lesser Caucasus Range of Georgia. The methodological concept of the research project, which has been organised in a network of four project units including eight subprojects, involves three major steps, (1) the development of a consistent hierarchical classification of landscape patterns, (2) the analysis of interrelationships between environmental and societal processes under consideration of these patterns, and (3) the formulation of regionally differentiated recommendations for sustainable land use and land development.



KLIWAS-Project 5.06: Climate change and its impact on flood- plain vegetation

Due to hydrological manipulations and intensified agricultural management flood plain ecosystems belong to the most threatened habitats in Germany and Europe. As a consequence of their rapid decline, habitats such as flood meadows, alluvial forests and ephemeral mudflat vegetation, are listed in the Appendixes of FFH directive. The composition and structure of these plant communities highly depend on the prevailing hydrological dynamics. Especially the flooding tolerance of species during different episodes of their life-cycle leads to the typical zonation of plant communities along the prevailing flooding gradients.

It is expected that in flood plain ecosystems climate change will induce changes in the stream flow, temperature, and precipitation. For the long-term conservation and restoration of floodplain plant communities it is crucial to assess the impacts of climatically induced habitat changes. Beyond modeling the expected shift in plant communities it is important to

understand the underlying processes and mechanisms. To this end, we will address topics of seed ecology, seed bank ecology, germination ecology and vegetation ecology in field and lab experiments.

Range expansion of *Ceratocarpus claviculata*

As a consequence of global change, the ranges of species are expected to change dramatically in the future. Therefore, the identification of factors that enable or limit range expansions is essential for the understanding and potential management of range changes. Ongoing range expansions offer unique opportunities to study the relative importance of ecological, genetic, and climatic factors for distribution and abundance of plant species. In one research project, we study these processes in the expanding short-lived plant *Ceratocarpus claviculata*, an atlantic species of the forest understory that has spread east- and northwards during the last decades. The project consists of field studies in the native and the newly invaded range, molecular analyses (AFLP), and controlled



experiments. First results suggest that the species has successfully established new populations despite low genetic diversity across large parts of its range. The colonisation of new sites seems to be facilitated through anthropogenic disturbance of forest stands. In seed sowing experiments, seed germination varied strongly, indicating that without disturbance the species range may be limited through certain types of soil cover, temperature and humidity.

Annette Otte

phone ++49-641-99-37160

mail Annette.Otte@umwelt.uni-giessen.de

www.uni-giessen.de/cms/fbz/fb09/institute/ilr/loek





Resource Management

Inst. of Landscape Ecology and Resources Management
Faculty 09 — Agricultural Sciences, Nutritional Sciences
and Environmental Management

Prof. Dr. Hans-Georg Frede

Land use impact on hydrological and biogeochemical fluxes

Landscapes provide the grounds for agriculture, forestry and energy production. Hans-Georg Frede and his team investigate the associated impacts on environmental conditions with a focus on water resources. Based on improved system knowledge they develop alternative land use concepts for the future.

Since the settlement of mankind, humans have actively shaped the environment for food production, building space for settlements and exploitation of energy resources. These activities resulted in landscapes of which many are seen nowadays as our cultural heritage such as the meadow orchards in Hesse, the Lüneburg heath, the Mediterranean Macchie or the rice terraces of the Philippines. Apart from these appreciated impacts, land use also has a long list of negative ones such as eutrophication, reduced water availability and quality, soil erosion, or desertification. And even today, landscapes evolve that represent the dark side of our activities: lignite mining areas in Germany, rainforest clear cut for palm oil production in Indonesia or cotton monocultures in Uzbekistan to name a few.

Given the scale of land use and the resulting impacts we mainly focus on research at the landscape scale, often delineated by watersheds. Hydrological as well as biogeochemical fluxes and processes are the major topics we investigate. Our objective is to combine experimental as well as modeling approaches to improve our understanding of the systems.

The focus of our research is to investigate the seeming contradiction of land use: production and protection. Based on analyses of multiple ecosystem services we are looking for improved land use options that optimize the different ecosystem services. It allows us to not only develop sustainable concepts of land use with the smallest environmental impact possible, but also to evaluate their economic performances and societal acceptance. This cross-disciplinary approach requires the cooperation with scientists of different disciplines which is reflected in our participation in a variety of coordinated projects.

Project outlines

Field experimental work is a precondition to improve our knowledge about the processes that lead to runoff generation, water losses, and biogeochemical turnover. Work in previously ungauged basins such as the Xilin in Inner Mongolia (China) (*DFG-Forscherguppe 536*) or the Rio San Francisco in the south of Ecuador (*DFG-Forscherguppe 816*) has revealed new insight



on how rain becomes runoff. In both catchments, base flow has been underestimated as a contribution to discharge. We use ^2H and ^{18}O isotopic analyses and large tracer sets of water solutes to derive flow path understanding and water provenance, which helped in understanding the composition of the hydrograph. State of the art analytical instruments such as Inductively Coupled Plasma - Mass Spectrometry (for elemental water solutes) and Cavity Ring Down Spectroscopy (for isotopic analyses of water) are used along with classical field methods such as permanent discharge gauging stations or monitoring of groundwater level. UV hyper spectrometry is another new promising method with high temporal resolution that we currently test to gain insight in carbon and nitrogen export dynamics of streams.

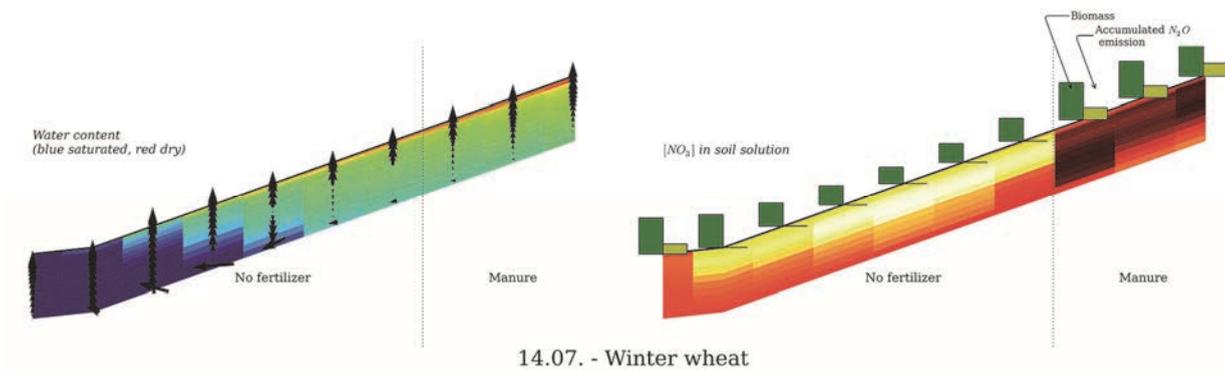
Based on our experimentally derived knowledge of hydrological and biogeochemical turnover processes, we apply, improve and develop modeling concepts that facilitate the simulation of these processes on the landscape scale (*NitroEurope IP*). Besides hypotheses testing based on these models we aim at making projections and predictions into the future: how will water

resources react to altered climatic conditions? What impact will land use and management changes have on stream loads of nitrogen, carbon or other nutrients?

In cooperation with social and economic researchers we even go one step further and investigate a broad set of ecosystem services and ask questions such as to which degree these global changes will have an impact on humans' well-being (*DFG Collaborative Research Centre 299 and the associated Transferproject on Bio-Energy Production*). Together we develop alternatives and adaptation strategies, assuming that there are trade-offs and win-win situations for a variety of land use options.

Recently, we developed the *Catchment Modeling Framework* that overcomes the classical set up of hydro-biogeochemical models. Instead of working with one fixed source code we created a flexible environment with which researchers are able to adjust the model to their needs and the available model input data.

Research at ILR is conducted worldwide on almost all continents. Due to several coordinated projects, Cen-



tral Asia has become a focus of our research. The *Central Asian Water project CAWa* was set up by the German Federal Foreign Office in view of the tremendous water-related challenges in the region, such as water scarcity, degrading water quality and inefficient water use. As these already existing problems are most likely aggravated by climate change, we initiated the DAAD funded *Climate Change Network for Central Asia, CliNCA*. This post-graduate project as well as the *LUCA (Land Use, Ecosystem Services and Human Welfare in Central Asia)* funded by the Volkswagenstiftung) project provide training and research for young scientists from Central Asia. Agriculture is by far the most important consumer of water -

and at the same time the worst contaminator. Improved land use strategies are needed to prevent any further unsustainable utilization of water resources. Together with a large consortium of partners from Germany and Central Asia we develop adapted management strategies of water resources.

Hans-Georg Frede

phone: ++49-641-99-37395

mail hans-georg.frede@umwelt.uni-giessen.de

www.uni-giessen.de/cms/fbz/fb09/institute/ilr/ilr-frede





Waste and Resources Management

Inst. of Landscape Ecology and Resources Management
Faculty 09 — Agricultural Sciences, Nutritional Sciences
and Environmental Management

Prof. Dr. Stefan Gaeth

“Ideas for Waste” – how to minimize pollutant accumulation in matter cycles and risks for the environment

The continuously growing world population and increasing wealth, most notably in Asia, implicate an arising demand for aliment and drinking water on the one side, and on the other side the availability of energy and resources has to be ensured. In this context, the Waste and Resources Management group searches for possibilities and potentials to use waste and waste ingredients for the substitution of natural resources. Another work field is the optimization of the resources efficiency of processes by improving technologies, production steps as well as processes and the implementation of efficient management systems. Thus, waste accruing in private households, trade or industrial plants can be avoided and costs will be reduced. Further projects of the group focus on the production of microalgae as renewable biomass and on the behavior of metals in soils originating from fertilizer application in plant nutrition. The Waste and Resources Management group supports the transfer of technologies by application-oriented projects conducted in cooperation with companies of different sizes. Furthermore, the group is incorporated in a wide network in different fields of technologies and research institutions.

Microalgae: Potential for utilization of heat and CO₂ in waste treatment plants

Heat and CO₂ accrue in nearly all kinds of waste treatment plants. Well thought utilization concepts for both components are extremely rare. Especially in the fields of biological waste treatment and use of landfill gas the potentials remain unused. A sustainable option for utilization of heat and CO₂ is the production of biomass by means of microalgae.

Microalgae are aquatic plants which are able to fix CO₂ in their biomass through photosynthesis. Hence, fertilization with CO₂ leads to an increased growth

rate. Furthermore, microalgae consume heat and nutrients for their growth. The generated biomass constitutes a high value of natural raw material, which can be used in a lot of application areas like energy production, food or feed.

In the project, different microalgae strains were analyzed for biomass production and content of lipids considering varying growth conditions (temperature, pH, nutrients, etc.). Furthermore, a pilot plant was established which aimed at producing microalgae biomass through CO₂ fertilization. It is connected with a biogas plant using the surplus heat and flue gases of the co-generation unit. The generated biomass is redirected



to the fermenter for energy production. This set up allows for a closed system without accumulation of waste and residuals.

Sorption of uranium in soils and consequences for the application of phosphate fertilizers in plant nutrition

The contents of uranium in natural soil are highly variable depending on geochemical background and soil formation processes. Average values for total uranium contents in soils range between 0.5 and 4.2 mg kg⁻¹. Additionally, the application of phosphate fertilizers may cause considerable uranium inputs into top soils and currently it is not clear whether this uranium can be sorbed on soil matrix and to which extent this happens. The project therefore investigates the fate of uranium in soil and soil solution. First of all, we examine soil characteristics which dominantly influence uranium sorption processes. The sorption experiments are done for nearly 100 soil samples varying in contents of clay, organic matter and carbonates as well as pH values. Based on these experiments, uranium

sorption isotherms will be derived including the relevant soil properties. As a result, pedotransfer function shall be developed which can be integrated in a balancing tool for metals in soils (ATOMIS) to allow the assessment of the behavior of uranium in soils when U-containing phosphate fertilizers are applied. Pot experiments in the greenhouse with different soils and plant species can provide useful data for the model validation.

Resources potential in selected German landfills

The resource potential of landfills is one source in Western Europe to encounter the depletion of raw natural materials. In this regard the project investigates three landfills to assess the feasibility of dismantling a landfill as a raw materials warehouse considering economic and environmental conditions. The main questions the project deals with are: Which resources are in a landfill and where they are? How will the prices for raw materials develop in the future? Which technical requirements are necessary and fit for prac-



tice? Finally, the results of the first three working steps will be used to create a mass flow model. This mathematical model should allow the assessment of the sustainability of resources recovery and therefore may be used as a decision support tool. First results show for investigated landfills that currently landfill mining can not be realized economically, but surely in the future. At present, the costs of dismantling are considerably higher than the benefit. The deficits may be covered in the future by better marketing opportunities

of secondary raw materials. Also greenhouse gas emission certificates could be a source of financing.

Stefan Gaeth

phone ++49-641-99-37383

mail Stefan.A.Gaeth@umwelt.uni-giessen.de

www.uni-giessen.de/cms/fbz/fb09/institute/ilr/abfall-und-ressourcenmanagement





Molecular Nutrition Research

Institute of Nutrition Sciences
Faculty 09 — Agricultural Sciences, Nutritional Sciences
and Environmental Management

Prof. Dr. Uwe Wenzel

Interactions between food ingredients and genes affect stress resistance and ageing

Ageing processes can be influenced in organisms by a number of genes. Uwe Wenzel investigates in the nematode *Caenorhabditis elegans* and in the red flour beetle *Tribolium castaneum* which genes mediate the effects of various physiologically and toxicologically relevant food ingredients on stress resistance and lifespan.

Ageing is a physiological process that is characterized by functional impairments of cellular activities that result, e.g. in diminished stress resistance. A major aim of ageing research is to identify the molecular mechanisms underlying ageing processes and to identify factors that prolongate such processes in order to maintain a good health status. The nematode *Caenorhabditis elegans* and the red flour beetle *Tribolium castaneum* are two model organisms which are used in this context. Both organisms display considerable genetic sequence homologies to the human genome which allow us to draw general conclusions from the reactions of such simple organisms at least when conserved pathways and mechanisms are considered.

The great advantage of *C. elegans* is the convenient adaptation of RNA-interference (RNAi) technology for genome-wide loss-of-function analysis and the availability of numerous mutant strains that help to define the role of distinct genes in physiological and pathophysiological responses. *T. castaneum* provides considerable advantages when whole foods should be tested since the organism can be fed by mixing

freeze-dried foods with their natural food, which is flour. On the other hand, RNAi is more complex in *T. castaneum* because the plasmids coding for double stranded RNA must be constructed first by RT-PCR amplification from total RNA. After both organisms have been fed by compounds or foods to be investigated lifespan is measured under heat stress (37°C for *C. elegans*, 42°C for *T. castaneum*) in order to cause the die-off of the population within 24 h (*C. elegans*) or 1 week (*T. castaneum*).

Polyphenols protect *C. elegans* from glucose-induced damage

In this project it is studied how the feeding of glucose, simulating a high-caloric diet or a diabetic situation according to the efficient absorption, affects lifespan in *C. elegans*. It is found that glucose reduces the lifespan of *C. elegans* drastically which can be completely prevented by 1 µM of polyphenols that occur in red wine or apples, such as resveratrol or quercetin. Such concentrations of polyphenols can be reached in



human plasma by a Mediterranean diet rich in fruits and vegetables. Knock-down of *sir-2.1*, a histone deacetylase which is an important mediator of lifespan extension by caloric restriction, blunts the lifespan rescuing activity of polyphenols, indicating that *sir-2.1* is a key target for the polyphenol action. The gene coding for heat-shock factor-1 (*hsf-1*) is another target unraveled to be essential for the polyphenol's action to prevail, and *hsf-1* has been shown in former studies to be required for enhanced thermotolerance, suppression of proteotoxicity, and lifespan extension by dietary restriction.

Cholesterol supply by vitellogenins affect stress resistance in different ways depending on the stressor

This project deals with the impact of vitellogenins, a class of precursors of the major egg storage protein vitellin, on stress resistance. Vitellogenins are homologous to human Apolipoprotein B100 which is a crucial component of low density lipoprotein particles that feed cells with cholesterol. Moreover, they have an

estrogen-response-element in their promoter sequence making their expression highly sensitive to endogenous and exogenous estrogens. RNAi-experiments revealed that vitellogenins increase the resistance versus *Photorhabdus luminescence*, a bacterium which is pathogenic for *C. elegans*. On the other hand, knock-down of *zmp-2*, a matrix metalloprotease expressed e.g. in neuronal cells, caused lifespan reduction which is dependent on the presence of vitellogenins. These results therefore suggest that interference of vitellogenins with different signaling pathways exist which can provoke lifespan extension or shortage dependent on the stressor. So far, a clear difference between the two responses has been identified in as far as lifespan extension by vitellogenins requires *daf-9*, a cytochrome P450 enzyme which produces a number of steroid hormones involved in stress resistance and ageing, whereas lifespan reduction by the same proteins does not. Currently, it is investigated how cholesterol supply affects those phenomena and moreover what impact phytoestrogens from dietary sources have on stress resistance.



Broccoli extends the lifespan of *T. castaneum*

We applied a number of freeze-dried vegetables to *T. castaneum* and observed that broccoli at a concentration of 1% in the flour extended the lifespan under heat-stress by 40%. The life extension is dependent on the *C. elegans* homologue *skn-1*, coding for a transcription factor that activates detoxification enzymes of phase-II xenobiotic metabolism. The analogies to human physiology are again evident, since cruciferous vegetables, such as broccoli, has been shown to provide cancer protective activities in persons with a distinct polymorphism of a phase-II enzyme, the glutathione-S-transferase. Interestingly, none of the tested food supplements, originating e.g. from broccoli, were able to prolong the lifespan significantly, demonstrating how valuable *T. castaneum* can be with regard to exploring the effects and mechanisms of complex foods. Moreover, *T. castaneum* but also *C. elegans* can be used for studying toxicological phenomena. In this regard, we are currently assessing the lifespan reducing activities of benz(a)pyrene, which plays a prominent role in human toxicology as well, and in how far the activities of phase-I and phase-II enzymes of xenobiotic metabolism influence the response to those polycyclic aromatic hydrocarbons.

Uwe Wenzel

phone ++49-641-99-39220

mail uwe.wenzel@ernaehrung.uni-giessen.de

www.uni-giessen.de/fbr09/mol-nutr-res/





Nutritional Biochemistry

Institute of Nutrition Sciences
Faculty 09 — Agricultural Sciences, Nutritional Sciences
and Environmental Management

Prof. Dr. Katja Becker

Cellular redox and energy metabolism in man and malarial parasites

Redox processes are important to maintain a reducing milieu within living cells. The Becker lab investigates how malaria parasites and other eukaryotic cells deal with toxic reactive oxygen species, how they maintain an adequate redox balance including redox signalling, and how these processes can be employed for therapeutic intervention strategies.

Reactive oxygen and nitrogen species are continuously generated in metabolically active tissues. During infections this production is increased. *Experimentalis naturae*, like human glucose 6-phosphate dehydrogenase deficiency, indicate that limited availability of reducing equivalents in the form of NADPH confers protection from malaria. This underlines the fact that the protozoan parasite *Plasmodium falciparum*, causing tropical malaria, is particularly susceptible to oxidative and nitrosative stress. The multiple biochemical pathways involved in the generation of oxidative stress and in its detoxification represent a range of potential targets for interfering with redox balance.

The enzymes thioredoxin reductase and glutathione reductase as well as their substrates represent cornerstones of the cellular defense against oxidative stress. They are involved in a number of different metabolic pathways including cell proliferation and differentiation as well. Therefore, also other antioxidant enzymes represent promising target molecules for the rational drug design against infectious diseases and cancer.

By studying the redox metabolism of malaria parasitized cells we hope to learn about parasite biology and to contribute to the development of new antimalarial drugs. For this purpose genes coding for redox active proteins from man, *Plasmodium*, and the malaria transmitting mosquito *Anopheles* are cloned and overexpressed. Comparative structural and functional characterization of the proteins and their substrates are performed. Drug screening on malaria parasites and isolated enzymes combined with structural knowledge leads to optimized compounds.

Compartmentation

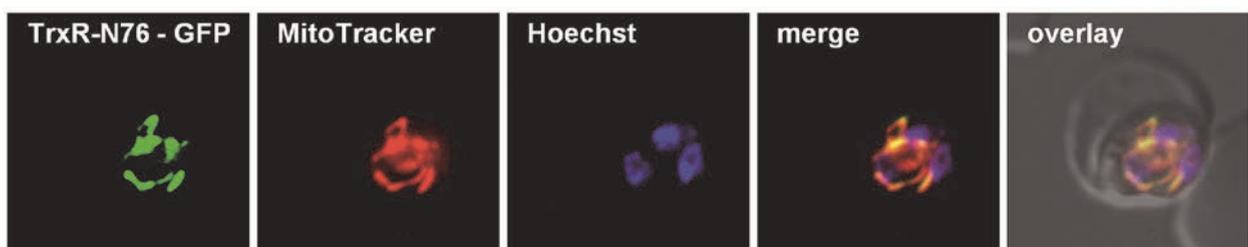
In order to further understand functions and networking of redox-active proteins in malaria parasites, we systematically study the subcellular compartmentation of redox networks. We e.g. recently demonstrated the targeting of two plasmodial peroxiredoxins and a putative glyoxalase system to the apicoplast, a non-photosynthetic plastid. We furthermore obtained a

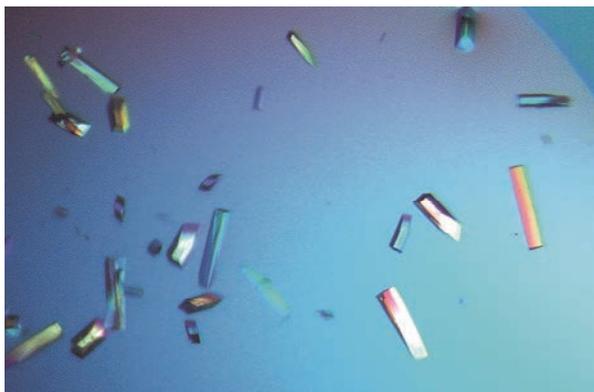


complete picture of the compartmentation of thioredoxin- and glutaredoxin-like proteins. Most interestingly, for the two major antioxidant redox enzymes – glutathione reductase (GR) and thioredoxin reductase (TrxR) – an alternative translation initiation (ATI) was identified producing protein isoforms with different subcellular localisation. The previously unidentified isoform of GR is targeted to the apicoplast, the newly described isoform of TrxR is localised to the mitochondrion. The differentiated control of ATI-sites may furthermore provide a mechanism for the fine tuning of the ratio between the synthesised protein isoforms. Identification of further genes that might have evolved dual targeting capability because of ATI-sites is likely to change our *in silico* view of organelle function.

The interactome of thioredoxin-related proteins in *P. falciparum*

Plasmodium falciparum possesses a functional thioredoxin and a glutathione system. Thioredoxin (Trx), glutaredoxin (Grx), and plasmoredoxin (Plrx) are redox-active proteins involved in antioxidant defense and cellular redox regulatory processes. Since only few of their target proteins are known in *Plasmodium*, we studied the inter-actome of the redoxins by performing pull-down assays. We could identify around 30 potential interaction partners of Trx, Grx, and Plrx. Among the captured proteins we identified known interaction partners as well as newly discovered target proteins involved in energy metabolism, protein biosynthesis and signal transduction. The results were





verified and studied in detail by examining the binding properties of selected enzymes using BIAcore surface plasmon resonance analysis and enzymatic assays. We could show that the redoxins interact with ornithine δ -aminotransferase (OAT). PfOAT is involved in ornithine homeostasis and proline biosynthesis, and is – in contrast to its human counterpart – activated by thioredoxin by a factor of 10. We solved the three-dimensional crystal structure of PfOAT at 2.3 Å resolution. The overall structure is very similar to human OAT. However, in plasmodial OAT, a loop involved in substrate binding contains two cysteine residues, which are lacking in human OAT. Site-directed mutagenesis of these cysteines and functional analysis demonstrated that they mediate the interaction with Trx. These two cyteins are highly conserved in *Plasmodium*, but do not exist in other organisms, suggesting that redox-regulation of OAT by Trx is specific for malaria parasites.

thereby allowing the visualization and improvement of protein-inhibitor contacts. During the last years our group solved the structures of several malarial enzymes like GR, GST, AOP, and OAT. Interesting results are e.g.: the sole malarial GST is unique since it possesses a wide open binding site for the second substrate, it represents the member of a new GST family. The PfOAT was shown to be activated 10x with PfTrx, a phenomenon not known for this class of enzymes before. Since autumn 2010, the group is supported with an automated pipetting system to increase the attempts to crystallize more interesting targets and also other proteins.

Katja Becker

phone ++49-641-99-39120

mail katja.becker@ernaehrung.uni-giessen.de

www www.uni-giessen.de/cms/fbz/fb09/institute/ernaehrungswissenschaft/ag/becker

Functional and structural characterization of drug targets

The discovery of new drug targets and the development of new drugs is one of the most important gateways to combat malaria. Structural and functional differences in redox active proteins of parasite and host can be exploited to develop novel antimalarial strategies and compounds. Coupling the *Plasmodium* sequence data with bioinformatics, proteomics, and RNA transcript expression profiles opens unprecedented opportunities for exploring new malaria control strategies. Ideally, proteomic and genomic approaches are complemented by crystallographic studies characterizing target proteins and protein-inhibitor complexes



Food Sciences

Institute of Nutrition Sciences
Faculty 09 — Agricultural Sciences, Nutritional Sciences
and Environmental Management

Successful candidates will be highly qualified to conduct scientific work in the field of food sciences and possess excellent teaching skills. Research should focus on food analysis, the effects of technology and environment on food quality, also considering physiological, metabolic and toxicological aspects.



Applied Entomology

Institute of Phytopathology and Applied Zoology
Faculty 09 — Agricultural Sciences, Nutritional Sciences
and Environmental Management

Prof. Dr. Andreas Vilcinskis

Pioneers in insect biotechnology

Insects are the most successful group of organisms regarding biodiversity which can be expanded beyond the species level to include their tremendous arsenal of bioactive molecules used, for example, in defense against pathogens, parasites, predators and competitors. The Vilcinskis lab is pioneering insect biotechnology in Germany in a joint venture between Fraunhofer and the JLU. This innovative cutting-edge discipline (called yellow biotechnology) explores the use of insects and insect-derived cells or molecules in medical (red biotechnology), agricultural (green biotechnology) or industrial (white) biotechnology as well as in bionics aiming at the systematic transfer of solutions from nature to the technical world.

Insects inspire negative reactions in many people. They are our main competitors for food, destroying crops over vast areas and consuming or spoiling stored products. They are also vectors for important diseases, e.g. mosquitoes transmitting malaria and fleas spreading plague. However, insects are also highly beneficial to humans. More insect species feed on other insects than on plants, so these beneficial insects are the primary eliminators of pests and disease vectors. Insects are also pollinators, and without them our ability to cultivate fruit and vegetable crops would be restricted, and the diversity of our food would be limited. In this context, the honeybee is the third most economically valuable species to humans, after cattle and pigs. The rapid evolution of molecular biology and biotechnology has opened up new opportunities for the exploitation of beneficial insects.

LOEWE focus group “Insect Biotechnology“

Insect biotechnology can be defined as any technological application using insects or insect-derived cells and molecules to make or modify products or processes for specific use in medicine, agriculture or industry. This cutting-edge technology shall be developed in cooperation with Fraunhofer for the first time in Germany and integrated in the Justus Liebig University life sciences concept. Thinking of the enormous potential of the new research area, the state of Hessen has awarded both 4 Mio. Euro in initial funding allowing the Fraunhofer Institute of Molecular Biology and Applied Ecology (IME) to establish and develop the Fraunhofer Bioresources group, which is currently located in the Technology and Innovation Centre Giessen (TIG), and



4.5 Mio. Euro for the LOEWE focus group “Insect Biotechnology”. Prof. Vilcinskis, spokesman of the LOEWE focus group “Insect Biotechnology” and head of the Fraunhofer Bioresources group, has edited the first book about “Insect Biotechnology” which has been published in 2010 by Springer. At present, insect biotechnology is the largest interdisciplinary IFZ project and encompasses the labs of Prof. Dr. Katja Becker, Prof. Dr. Friedt and Prof. Dr. Kogel.

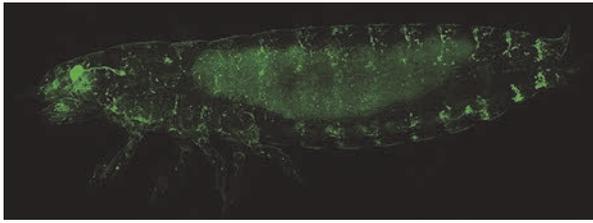
Genome biology and RNA interference

Since it has been recognized that insectivore insects or parasitoids are important allies in fighting against pest or vector insects, and that other beneficial insects such as bees play an economically important role as pollinators, it turned out that sustainable and environment friendly approaches require the availability of selective insect control measures. Targeted fighting against pests or vectors insects has become imaginable since scientific breakthroughs in molecular biology such as the RNA interference technology can be combined with the expanding knowledge about insect genomes. Prof. Vilcinskis is a member of several inter-

national consortia which have sequenced or sequence the genomes of model insects such as the red flour beetle *Tribolium castaneum* or the pea aphid *Acyrtosiphon pisum*. The outcome of collaborative projects between him and the groups of Prof. Friedt, Dr. Freitak and Prof. Kogel in the future may be crops expressing double-stranded RNA mediating silencing expression of essential genes in pest insects without impeding non-target organisms.

LOEWE focus group AmbiProbe

Prof. Vilcinskis is among the project leaders of the LOEWE focus group AmbiProbe, a high-tech focus on developing chemical detection methods and devices for the fields of health, environment, climate, and security. These devices and methods will be miniaturized, mobile, and deployable directly on site. Such so-called in situ techniques should be developed for various areas of application such as the identification of toxins, drugs and explosives at airports. Since insects have acquired the most effective chemical sensors during evolution, the Vilcinskis lab aims to use their antennae as components or templates in developing



new biosensors for in situ-analysis. This bionic approach combines newly developed mass spectrometers with the so-called electroantennography. The latter is a method for amplification and recording of electrical potentials from insect antennae which are produced upon binding of particular volatiles to corresponding receptors. This key event in olfactory perception of insects can be exploited for the development of signal transducers in transportable biosensors. Such a transfer of solutions from nature to the technical world enables the detection of particular, for example, insect pheromones, which are applied in modern plant protection measures.

Insect as models in host-parasite-coevolution

Some insects such as the larvae of the greater wax moth *Galleria mellonella* prosper worldwide in use as surrogate model hosts for human pathogens which are ethically more acceptable than mammalian hosts. In addition to the growing importance of *Galleria mellonella* in medical research this lepidopteran has also emerged as a powerful model host in evolutionary biology. The unifying goal of the DFG Priority program

1399 “Host-parasite coevolution – rapid reciprocal adaptation and its genetic basis” is to establish host-parasite coevolution as a powerful and versatile model for analyzing the causes and processes of evolutionary adaptation, including direct observation of evolution in action. The major objectives are (1) to study adaptation and counter-adaptation of hosts and parasites under different coevolutionary conditions in field and experimental laboratory settings, (2) to identify important ecological and life-history constraints on host and parasite evolution, (3) to determine the molecular genetic basis of evolving immunity and virulence, (4) to identify how genetic variability within host and parasite populations is generated and maintained. The Vilcinskis lab contributes to the DFG priority program with a project entitled “Reciprocal genetic diversification and adaptation of host proteinase inhibitors and parasite-associated proteinases during coevolution of insects and entomopathogenic fungi”.

Andreas Vilcinskis

phone ++49-641-99-37600

mail Andreas.Vilcinskis@agrar.uni-giessen.de

www.uni-giessen.de/cms/fbz/fb09/institute/ipaz/abt/phyto





Phytopathology

Institute of Phytopathology and Applied Zoology
Faculty 09 — Agricultural Sciences, Nutritional Sciences
and Environmental Management

Prof. Dr. Karl-Heinz Kogel

Committed to improvement for better crop plants

The Kogel lab mission is to advance and communicate scientific knowledge in plant biology to improve agriculture, protect the environment, and enhance human health. To accomplish this, IPAZ conducts research on different levels of the food chain. We seek, for instance, to understand the basis of sustainable plant production by fortification of plant health by beneficial root microorganisms. In other projects we seek, for instance, to improve cereal plants to meet the requirements of celiac patients. In a third project, we investigate the communication of microorganisms with their host in the plant rhizosphere.

Mechanisms of compatibility – why can microbes colonize their host?

The FOR 666 consortium (*DFG Forschergruppe 666*) aims at a concerted in depth comparative analysis of “compatibility mechanisms” in plant-microbe interactions by comparing parasitic and mutualistic lifestyles of fungal model microbes. A central strategy of the consortium is defining complementary projects that collaboratively investigate both, the plant and the microbe side of an interaction, with a strong focus on the central experiment (CET) guided and supervised by a bioinformatics platform that computes all the transcriptome and metabolome data from the different systems. It is the principal goal of the consortium to seek for sustainable solutions in plant production. The future program of FOR 666 is based on the data obtained in the first funding period and is in line with the initial work schedule: to identify compatibility-related fungal

and plant genes and to carry out a detailed analysis of such genes in the present funding period.

Agronomic background of the science-based approaches of FOR 666

Disadvantageous side effects of intensive agricultural cropping systems are evident by irreversible damage of arable land, reduced biodiversity, and eutrophication of fresh water resources. Despite the intensified measures taken to protect crops from diseases and pests, recent evaluations have shown that continuously rising total crop production is accompanied by increasing yield loss rates. One solution for the problem is to improve crop production strategies, to make them more reliable for the producer and safer for consumers and the environment. A key towards this aim is increasing the knowledge of the intricate and dynamic communications between crop plants and their inter-

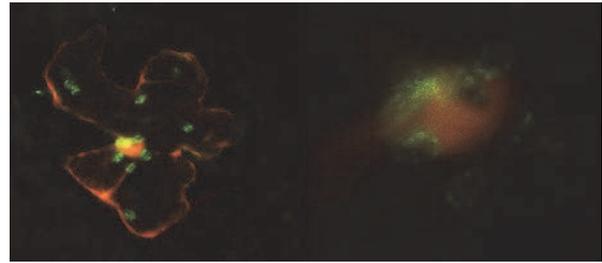
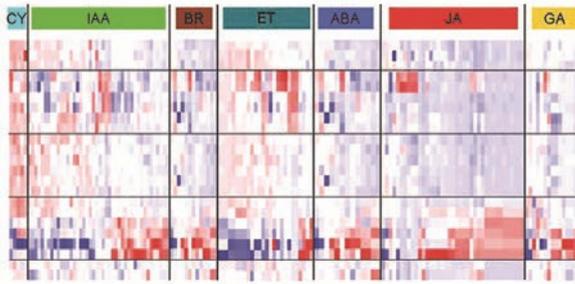


acting parasitic or beneficial microbial partners. By elucidating “compatibility mechanisms”, i.e. mechanisms either of disease or beneficial symbiosis, key processes in crop plants can be identified and exploited for more sustainable measures based on either novel chemicals or genetically improved plants. If compatibility factors like those involved in establishment and maintenance of green islands are associated with primary plant metabolism, they might also be key players for directed carbon flow and could be used for yield improvement.

Wheat for celiac patients and improved disease prevention: future therapeutic options for celiac disease

Wheat and its products are potential elicitors for an autoimmune response (celiac disease) in susceptible patients due to the ingestion of seed storage proteins (gluten) of cereals. Gluten is a mixture of 149 storage proteins. Different celiac patients react with an autoimmune response to different members of these storage proteins. The autoimmune response results in the very

painful destruction of the microvilli of the intestine. The destroyed intestine epithel is unable to absorb nutrients. The autoimmune response results from the resistance to digestion of certain proline/glutamine rich peptides (epitopes) in gluten proteins by our gastric, pancreatic and brushborder membrane proteases. In general, wheat proteins also are poor in nutritional quality because of their imbalanced amino acid composition and deficiency of one of the essential amino acids, lysine. Among the known food allergy cases triggered by wheat and wheat products, most belong to celiac disease. The only effective therapy known to date is strict dietary adherence to a gluten-free diet, which often leads to nutritional deficiencies in celiac patients. In view of the above, we undertake a profound cooperation with Prof. D. von Wettstein of the Washington State University, Pullman (WA), with the ultimate objective of eliminating the prolamins from wheat grains that contain a majority of epitopes causing celiac disease. Eliminating these proteins will also address the issue of imbalance in the amino acid profile of wheat proteins.



Plants hear their pathogens talking

Pathogenic bacteria use a variety of virulence factors for successful infection of their hosts. Those factors are not expressed constitutively but induced during early steps of infection. Their induction requires the presence of a host organism and an adequate density of a bacterial population. In order to sense their population, bacteria use quorum sensing (QS) mechanisms. In human pathogens *Salmonella*, *Yersinia*, and *Pseudomonas* but also in plant colonizing *Rhizobia*, quorum sensing relies on production of bacterial diverse QS molecules that influence gene transcription once detected by a companion.

We and others have recently discovered that hosts for those pathogenic bacteria can perceive and respond to QS molecules. In mice, N-3-oxo-dodecanoyl-L-homoserine lactone (oxo-C12-HSL) leads to increased inflammation via induction of interleukin-1alpha (IL-1alpha) and IL-6. In plants, perception of HSLs induc-

es defense responses and subsequently higher resistance towards diverse pathogens through a yet unknown mechanism. Moreover, a specific class of HSLs, defined by their carbon moieties, does promote plant growth and yield – an even more interesting effect when agronomic questions come into consideration. In the present project – a cooperation among IFZ groups and JLU Chemistry (Prof. Maison) – we want to exploit the newly discovered phenomenon.

Karl-Heinz Kogel

phone ++49-641-99-37490

mail Karl-Heinz.Kogel@agrar.uni-giessen.de

www.uni-giessen.de/cms/fbz/fb09/institute/ipaz/abt/phyto





Salt resistance of maize plants – a contribution to secure global food, feed, and fuel production

Salt resistance of plants is a multi-genic character that is difficult to improve by plant breeding. A new concept, which combines the identification of physiological bottlenecks with conventional breeding methods allowed us to develop new maize genotypes with improved salt resistance.

World-wide billions of hectares of agricultural land are unproductive due to salinization. This is a problem particularly of arid regions and affects many developing countries. The amelioration of salt-affected soils is restricted by limited resources of high-quality water for the leaching of toxic salts. Therefore, it has been suggested long ago to improve the salt resistance of crop plants. However, despite extensive research activities the success is negligible because salt resistance is inherited by many genes that partially show antagonistic behavior. A new approach has recently resulted in the development of salt-resistant maize genotypes. The concept is based on the identification of superior physiological strategies that rely on specific mechanisms. In general, salt stress is differentiated into two phases. In the first phase, osmotic problems prevail and the plants look stunted and show a dark-green color due to a decrease in cell-extension growth. In the second phase ion toxicity develops. For maize, we have shown that sodium accumulation results in necrotic lesions of leaves in this phase. While the problems of ion toxicity in the second phase of salt stress

have been solved with the development of our new maize hybrids, salt resistance in the first phase of salt stress still has to be improved. Presently, the following projects are in progress to further improve the maize hybrids:

- ⊗ Identification of mechanisms that contribute to growth reduction of maize shoots
- ⊗ Characterization of root signals that trigger growth reduction of maize shoots
- ⊗ Investigation of reasons for poor kernel set during flowering

Growth reduction in the first phase of salt stress

As described by the acid-growth theory, cell-extension growth depends on the acidification of cell walls. Protons released by ATPase activity exchange calcium ions from pectinates and thus increase the cell-wall extensibility. In addition, pH-sensitive proteins such as expansins help to reduce the rigidity of cell walls.

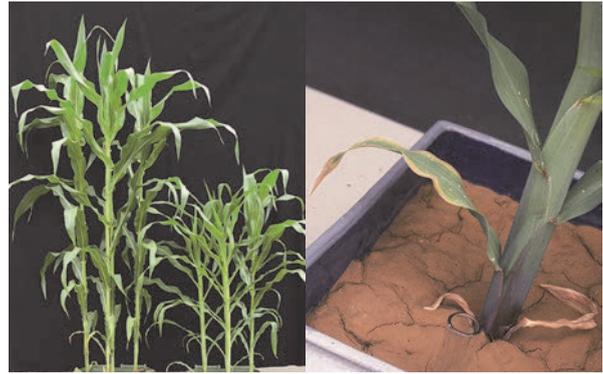


Using *in vitro* methods and *in vivo* ratio-imaging techniques we have shown that the resistant hybrid SR 03 is able to maintain proton pumping and cell-wall acidification under salt stress whereas the sensitive genotype Pioneer 3906 showed reduced proton pumping and an alkalization of cell walls in young leaves relative to control plants. As a probable reason we identified the expression of inefficient ATPase isoforms in Pioneer 3906 in salt-treated plants. However, additional mechanisms are responsible for differences in resistance during the first phase of salt stress. Thus, hybrid SR 12 that shows similar resistance as SR 03 was unable to maintain proton pumping and cell-wall acidification under salt stress. It is possible that earlier and/or more pronounced lignification contributes to the stiffening of cell walls in maize leaves under salt stress.

Root signals trigger shoot growth reduction in the first phase of salt stress

It has been shown earlier that salt stress in the first phase may inhibit shoot growth without reducing cell

turgor. We have recently demonstrated that transpiration rates of plants under salt stress may be not reduced but rather increased. This indicates that shoot growth reduction as a stress avoidance strategy helps to adjust plant growth to the limited water availability. According to this theory, plant roots perceive limited water availability in the rhizosphere and release integrating signals that help to co-ordinate shoot growth. Various root-derived signals are presently discussed. Among them are peptides, hydraulic and pH signals and the plant hormone abscisic acid (ABA). The latter is accumulated in shoots under salt stress but various maize genotypes show different ABA concentrations when exposed to salt stress in the first phase. In addition, leaves of different maize genotypes differ in ABA sensitivity. Whereas exogenously applied ABA reduced proton pumping and cell-wall acidification in the sensitive genotype Pioneer 3906, it increased proton pumping and cell-wall acidification in the resistant genotype SR 03.



Reduced kernel set during the first phase of salt stress

Relative to the sensitive maize genotype Pioneer 3906 which showed a decrease in grain yield to 60% under a salinity stress relative to control conditions, our new salt-resistant hybrids maintained grain yield at 79 - 91%. The limiting process under salt stress was not grain filling but kernel set. Unchanged or increased transpiration rates in the first phase of salt stress indicate that photosynthesis may not be limiting assimilate supply for flowering or kernel development. This is also supported by the observation that sugars accumulate in plants in the first phase of salt stress. In contrast, ABA accumulation may trigger kernel abortion. The root-derived signal may also be responsible for a decrease in invertase activity that plays a central role

in phloem unloading and sink activity. Low invertase activity prevents the hydrolytic cleavage of sucrose into the hexoses glucose and fructose that are selectively taken up by the sink cells. Particularly during the initial phase after fertilization the support of ovaria with hexoses may determine whether or not the zygotes can develop to kernels. A comparison of genotypes that differ in kernel set may help to identify the limiting steps in grain yield formation in the first phase of salt stress.

Sven Schubert

phone ++49-641-99-39160

mail sven.schubert@ernaehrung.uni-giessen.de

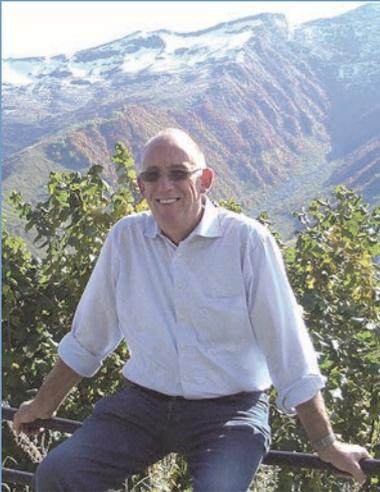
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Biochemistry of Plant Nutrition

Institute of Plant Nutrition
Faculty 09 — Agricultural Sciences, Nutritional Sciences
and Environmental Management

Successful candidates will be highly qualified to conduct scientific work in the fields of biochemistry of plant nutrition / plant metabolites and possess teaching skills. Research should focus on the development and functioning of root systems, in particular on aspects of nutrient efficiency and stress resistance.



Did you know that it takes several hundred years to produce one centimeter of soil?

Soil, the fragile skin of the earth, is being studied in terms of sustaining its numerous important functions for ecosystems and human well-being. Investigating fundamental soil properties is essential for understanding and protecting soil functionality. Adverse impacts of both inorganic and organic contaminants in soils are being assessed using advanced analytical methods.

Soils fulfill important social and ecological functions and services. They provide sustenance to people, animals, plants and microorganisms. More than 90% of all food is produced on soils. Man also needs soil for building construction and raw materials such as sand, gravel, and clay. Healthy soils have natural cleaning capabilities and buffering systems for contaminants, thus protecting groundwater resources. In densely populated countries, damage to soils (sealing, contaminant input, erosion, soil compaction and acidification) can jeopardize its multifunctionality and affect soil sustainability. The responsible use of soil is only possible if we can appreciate and recognize its key role in the natural ecosystem and its vulnerability. Accordingly, we must acquire extensive knowledge about soil formation and distribution as well as soil properties and functions. The Institute of Soil Science and Soil Conservation, directed by Prof. Dr. Peter Felix-Henningsen and PD Dr. Rolf-Alexander Duering, is at the cutting edge of generating such knowledge.

Below we provide a selection of our current research activities in the institute.

Metals in soils and in the food chain

Within an interdisciplinary research project funded by the “Volkswagenstiftung”, the Institutes of Soil Science, Applied Microbiology and Plant Nutrition are cooperating in research on soil processes, functions and remediation of **soils contaminated with heavy metals**. The fertile agricultural soils of the Mashavera valley (SE Georgia) are contaminated with heavy metals resulting from irrigation with contaminated water of the Mashavera River. Primarily copper, zinc and cadmium exceed German and international threshold values for soils. To avoid impacts on human health through transfer of heavy metals into the food chain, the project focuses on four scientific approaches including the spatial monitoring of heavy metal transfer into food crops, identification of heavy metal mobility in alkaline soils, development of an in-situ remediation



strategy and determination of changes in soil microbial activity. Furthermore, at different field sites in Hesse, Germany, **transfer of heavy metals into plants** is being systematically investigated with special attention to fertilization and site characteristics. **Rare earth elements (REE)** are released to the environment because of their increasing use in industry and agriculture, and soils are the natural sink. Occurrence and bioavailability of REE are being investigated comprehensively using representative soil samples from different landscapes in Hesse, Germany.

Soil properties

Sandy soils of the arid/semiarid dune fields of the Palestinian Gaza Strip and the Israeli NW Negev are extensively covered by **biological soil crusts (BSC)**, which stabilize the surface and inhibit desertification processes. Inappropriate land use and grazing can lead to destruction of the BSC and initiate sand mobility. In an interdisciplinary project, funded by the “DFG”, the influence of environmental factors on the vitality, stability and the recovery potential of the BSC are

being investigated in order to evaluate the stability of these fragile surfaces. This is being achieved by incorporating molecular biology and physiology, in combination with physical and soil chemical processes, ranging from the molecular to the landscape scale. **Ground penetrating radar (GPR)** has gained popularity in soil science owing to its non-invasive nature and speed; it uses electromagnetic waves to image the shallow subsurface. The most important parameter affecting the behaviour of the emitted waves (propagation velocity, strength of reflections at layer boundaries) is the complex effective relative permittivity $\epsilon_{r,eff}^*$. Thus, knowledge of soil permittivity is important to interpret radar images. A new measurement technique has been developed to determine $\epsilon_{r,eff}^*$ of soils at their natural *in situ* structure. The suitability of the measurement method has already been demonstrated by measuring standard materials.

Organic pollutants

Soils and water bodies suffer from the impacts of organic contaminants. Chemicals such as the well-



known PCBs and Dioxins can be dispersed into the environment and end up in soils. Other, so-called “emerging contaminants”, are increasingly of public concern. Most of them have been used and released into the environment for decades. However, they are only now becoming detectable due to recent improvements in analytical chemistry. For different projects, the environmental behaviour of organic pollutants and their analysis are being investigated and optimized. The research includes developing and applying new miniaturized methods, **sorption and desorption** behaviour of hexachlorobenzene from sediments of the river Rhine, accumulation of flame retardants in high alpine glaciers, and **transfer of dioxin-like PCBs from soil to plant**. The suitability of micro methods for fish bioconcentration studies is examined in coopera-

tion with Fraunhofer Institute for Molecular Biology and Applied Entomology (IME). To assess biological effects of these pollutants, close cooperation is being carried out with ecotoxicology institutes. A method to use insect antenna as highly **sensitive biosensors** for the detection of volatile organic pollutants is under way within the interdisciplinary research project “AmbiProbe” - mass spectrometric *in situ* analysis for health, environment, climate, and safety (LOEWE focus group).

Peter Felix-Henningsen

phone ++49-641-99-37100

mail Peter.Felix-H@umwelt.uni-giessen.de

www.uni-giessen.de/cms/fbz/fb09/institute/bkbe





Integrative Sensory Physiology

Institute of Animal Physiology
Faculty 08 — Biology and Chemistry

Prof. Dr. Reinhard Lakes-Harlan

Integrative sensory physiology

Mechanosensory systems of insects are in the focus of the group of Integrative Sensory Physiology. The evolutionary transition from vibration receptors to hearing organs and the biodiversity of auditory systems are used for research on sensory ecology and evolution. The different systems also provide a basis for projects dealing with neuroregeneration and bionics.

Mechanosensory systems are evolutionary old systems. Within the insects some of these systems have been transformed during evolution into hearing systems. These processes result in a variety of systems with different specialized characteristics. Therefore auditory systems provide a good opportunity for studying evolution as well as ecophysiological adaptations. The perception of substrate vibrations or air borne sounds is based on internal sensory receptors of the same type. These receptors can be compared to some human mechanoreceptors and the basic sensory mechanisms are of widespread interest. In this respect the function of cell surface molecules are in our focus. The variety of sense organs based on one receptor type also allow other comparative neurobiological projects, like experiments dealing with the wiring of neuronal networks during development or during regeneration.

These receptor organs are widely distributed within the body of insects. Vibration receptor organs are mainly found in the legs, with a very sensitive sense

organ inside the tibia. Auditory organs can be found on the different body parts in different insect groups. Examples for the locations of hearing organs are: the foreleg tibia of Ensifera, the first abdominal segment of Caelifera, the second abdominal segment of cicadas and the prothorax of Diptera. All ears have a homolog organ in non-hearing species and the hearing function is mainly based on transformation of external structures, like a tympanal membrane and tracheal specializations. The evolutionary transition from vibration receptor to hearing organ and the biodiversity of auditory systems are used for projects on sensory ecology and evolution.

Sensory ecology and bionics

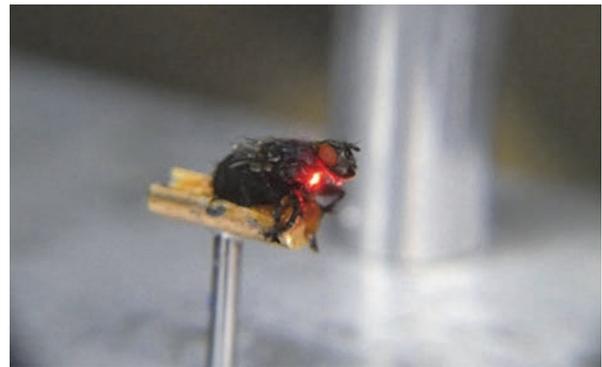
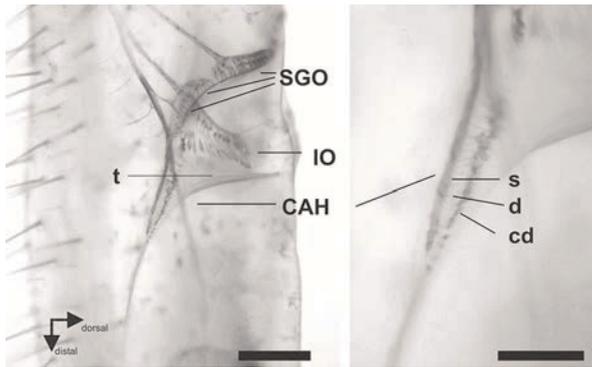
In this project we investigate the adaptation of sensory organs (and the animals) to signals in the environment. A model system is a parasitoid-host system in which a parasitoid fly acoustically locates a host cicada. The calling song of the cicada is exploited by



the fly and therefore sexual selection as well as natural selection acts on the acoustic signal. The adaptations of both species in life history and sensory ecology are investigated. The auditory sense of the fly seems to be perfectly adapted to the host's biology, for example, the acoustic behaviours of both species depend on the same abiotic factors. The search strategy of the fly using the acoustic signals is investigated and modelled. During search they often use landmarks for orientation. From these orientation points the signal direction is determined in all three dimensions. However, only little is known about the underlying mechanisms for locating elevated sound sources. The minute ear of parasitoid fly represents a good model system for these questions. Biophysical investigations of this ear show that probably frequency-specific attenuation processes are important for three-dimensional orientation. These results are now transferred to bionics with the construction of a small microphone with similar properties.

Auditory systems: evolution and biodiversity

By contrast to vertebrates, insects have evolved auditory sense organs multiple times. This richness of different sense organs allows comparative investigations of constraints and prerequisites for evolution and function. Currently, the ear and predecessor organs in Ensifera are in the focus of research with comparative investigations of ensiferan groups like the Stenopelmaticidae, Schizodactylidae and Gryllacrididae. It was shown that these groups have sense organs in their legs from which the ear of the Tettigoniidae could have evolved. The results are now part of a data matrix for the ensiferan phylogeny. Currently the unknown function of these sense organs is under investigation. Biophysical measurements with Doppler-laservibrometry and neurophysiological recordings will unravel the functional properties of the sensory organs. The arrangement of sensory cells inside the organ is different from other sense organs and therefore they probably react to specific parameters of vibratory signals. For the experiments, a unique stimula-



tion setup with complex vibratory signals that can be delivered from different spatial orientations is designed. The analysis is extended to evolutionary reduction of sense organs. This process is often underestimated in its importance for properties of sensory perception in recent insects. The Lepidoptera provide an excellent research basis for solving these questions.

Acoustic communication: biodiversity and ecology

Many insects have intra- and interspecific acoustic communication signals. The intraspecific communication signals can be used to evaluate biodiversity and to identify species. In the mainly African group of Heterodinae (Tettigoniidae), we investigate these signals (and the neuroanatomy and – physiology) to characterise the different species. The taxon is relatively rarely studied, despite that some species can have pest status in agriculture. Morphological species identification is difficult, because the species are rather similar and the morphology within a species is very

variable. Acoustic signals which function as a pre-mating isolation barrier should be more specific. The acoustic signals of different species are recorded during field excursions in Namibia and in the laboratory. Analysis with modern software tools shows that the acoustic signals are indeed species specific, although in some cases with only small differences. The main differences are not within the frequency spectra of the signals, but within the temporal structures. Interestingly, behavioural analyses indicate that at least one species is rather inselective and that a pre-mating isolation barrier of acoustic signals is not ubiquitous. Further investigations are required whether this represents a recent species separation or whether in sympatric areas a separating character displacement occurs.

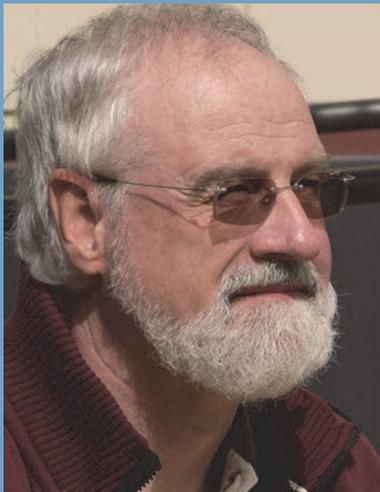
Reinhard Lakes-Harlan

phone ++49-641-99-35270

mail Reinhard.Lakes-Harlan @ uni-giessen.de

<http://www.uni-giessen.de/cms/fbz/fb08/biologie/tphys/sin>





Molecular Cell Physiology

Institute of Animal Physiology
Faculty 08 — Biology and Chemistry

Prof. Dr. Wolfgang Clauss

Molecular physiology of ion channels

The physiology of ion channels and ion transporting molecules are the focus of the group of Molecular Cell Physiology. The identification as well as the regulation of ion channels and transporters delivers the basis for the understanding of the physiology as well as pathophysiology of different organs, like the kidneys or the lung.

The transport of ions via ion channels or ion transporters is a biologically fundamental mechanism establishing homeostasis or cell communication in all organisms. For example, those molecules are responsible for the uptake of electrolytes from the outer milieu, for the maintenance of ion homeostasis in- and outside of cells or the conversion of inputs from sensory structures to electrical signals. Thus ion channel/transporter research is an important field for the understanding of general physiology.

Our group is mainly interested in ion channels and ion transporting molecules of epithelial tissues. Epithelia in organisms have two main functions: they serve as barriers and separate compartments, and they guarantee a regulated vectorial exchange of substances (absorption and secretion) between such compartments. Both functions, barrier and exchange, are tightly associated with ion channels and ion transporters in epithelial cells.

Physiological importance of ion channels and transporters in the lung

Ion channels and transporters in the pulmonary epithelium are important regulators of lung function in health and disease. Our group strongly focuses on the physiological importance of those molecules in lung cells. For example, we are interested in the function of different ion channels (Na^+ channels, K^+ channels, Cl^- channels) and transporters ($\text{Na}^+/\text{K}^+/\text{Cl}^-$ cotransporters etc.) in the pulmonary epithelium. Here, the concerted action of those ion transporting molecules is responsible for transepithelial ion transport. As this ion transport is tightly connected to fluid movements across epithelia, ion transport is the major regulator of pulmonary fluid dynamics. For example, disturbed ion transport in the alveolar epithelium leads eventually to an accumulation of fluid in the alveoli – a situation which is referred to as pulmonary edema. On the other hand, epithelial ion transport also regulates the volume of a thin liquid layer that lines the airway epithelia

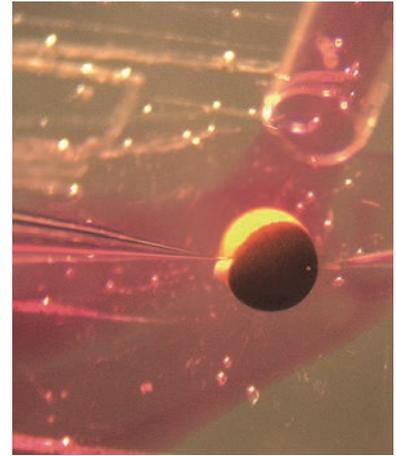
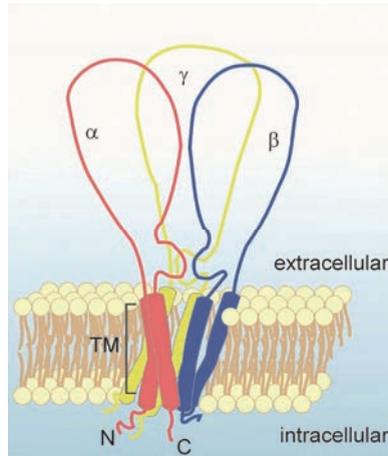
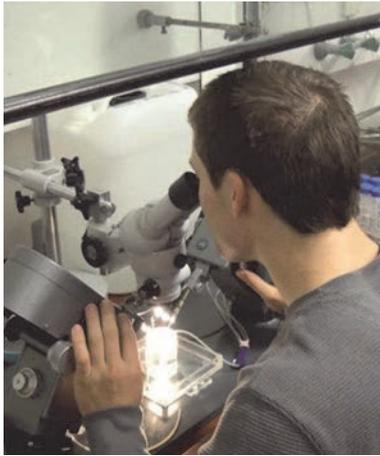


of the trachea or bronchi. Those epithelia contain cilia, which are covered with a mucus layer. Since the lung is the organ in the human body which is highly exposed to the environment, this mucus layer is of particular importance: inhaled particles and pathogens are trapped in this mucus and – due to ciliary beating – transported out of the lung. The mentioned fluid layer, which lines the epithelia, enables optimal beating of the cilia. Therefore, disturbed fluid contents – as a result of impaired ion transport – can directly affect the so-called mucociliary clearance and result in lung diseases associated with infections (e.g. cystic fibrosis).

Therefore, we characterise the ion channels and transporters in pulmonary epithelia of different models, including amphibia, mice and humans. With the identification of those ion transporting systems and their regulation, we hope to better understand the physiology of lung epithelia and the pathogenesis of lung diseases with malfunctioning ion transport.

Molecular physiology of epithelial sodium channels

Epithelial sodium channels (ENaCs) are sodium selective ion channels which are expressed in epithelial tissues including those of the lung or kidneys. Since ENaCs represent the rate-limiting step for sodium and consequently water reabsorption across epithelia, these ion channels are crucial for the maintenance of sodium and water balance in the human body. Accordingly, deregulated activity of ENaCs contributes to the pathogenesis of human diseases, which are associated with a disturbed sodium and/or water homeostasis. In the lungs, hyperactivity of ENaC can lead to depletion of the fluid layer covering the airway epithelium leading to cystic fibrosis like lung disease. By contrast, hypoactivity of ENaCs contributes to the development of pulmonary edema due to impaired alveolar fluid clearance. In the kidneys, hyperactive ENaCs are the reason for a hereditary form of hypertension, which is referred to as Liddle syndrome. Hypoactivity of ENaCs on the other hand contributes to the renal salt-wasting syndrome pseudohypoaldosteronism type 1.



Beside their importance for epithelial physiology, recent findings confirm the expression of ENaCs in non-epithelial tissues like the endothelium, skin, taste buds or the brain. However, their function in these tissues remains to be clarified.

Due to the physiological as well as pathophysiological importance of ENaCs, our group focuses on the molecular regulation of these ion channels in various cells and tissues. Using heterologous expression systems (*Xenopus* oocytes) as well as the Patch-Clamp technique, we are monitoring the behaviour of single ion channels, thus single proteins, *live* in response to various stimuli. We believe that elucidating the physiological regulation of ENaCs and their deregulation under certain pathological conditions will contribute to a better understanding of the pathogenesis of various human diseases and the development of novel therapeutic strategies.

Comparative physiology of pulmonary ion transport

Beside the molecular medicine-related interest in the physiology and pathophysiology of pulmonary ion transport, our interest as biologists is also in the comparative physiology of ion transport in the lung. We have established an amphibian model of pulmonary ion transport: the lungs of the South-African clawed frog, *Xenopus laevis*. Amphibia are interesting models in terms of lung function, for two reasons: (1) they are of evolutionary interest related to “water-land transition” since they are the first vertebrate class in which

air breathing has been established and where pulmonary ion transport mechanisms have been developed (2) the lungs of amphibians have a relatively simple macroscopic anatomy that allows their preparation for pulmonary ion transport studies, although the morphology is similar to that of other vertebrate lungs. We identified the major components of the ion transporting machinery that also exists in mammalian lungs in that model. Therefore the *Xenopus* lung represents an interesting tool to study ion transport in an evolutionary as well as comparative physiological context.

Wolfgang Clauss

phone ++49-641-99-35051

mail Clauss@bio.uni-giessen.de

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