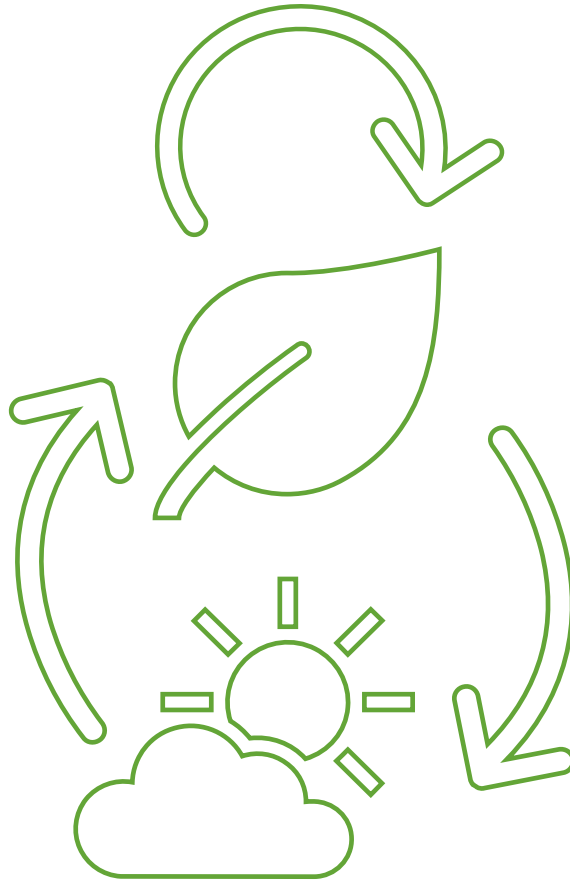


Plant Health and Environment Interactions



Kiel Plant Center – Summer Symposium 2019

22nd – 23rd of July 2019
Zoological Museum and
Botanical Garden Kiel



Contact and Organization:

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KPC steering committee and organization:

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Christian Zidorn

Sponsors:



Max-Planck Institut für
Evolutionärsbiologie, Plön



Christian-Albrechts-Universität zu Kiel



Meeting venue:

Zoological Museum Kiel
Hegewischstr. 2
24105 Kiel



How to get there:

1. Bus lines to *Kunsthalle*
2. Bus lines to *Schlossgarten*
3. Bus lines to *Hospitalstrasse*

41 42 43

32 42 61 62

32 42 61 62

Additional information can be found on the online bus schedule:

<https://netzplan-kiel.de/index.php/de/netzplan>

Evening program:

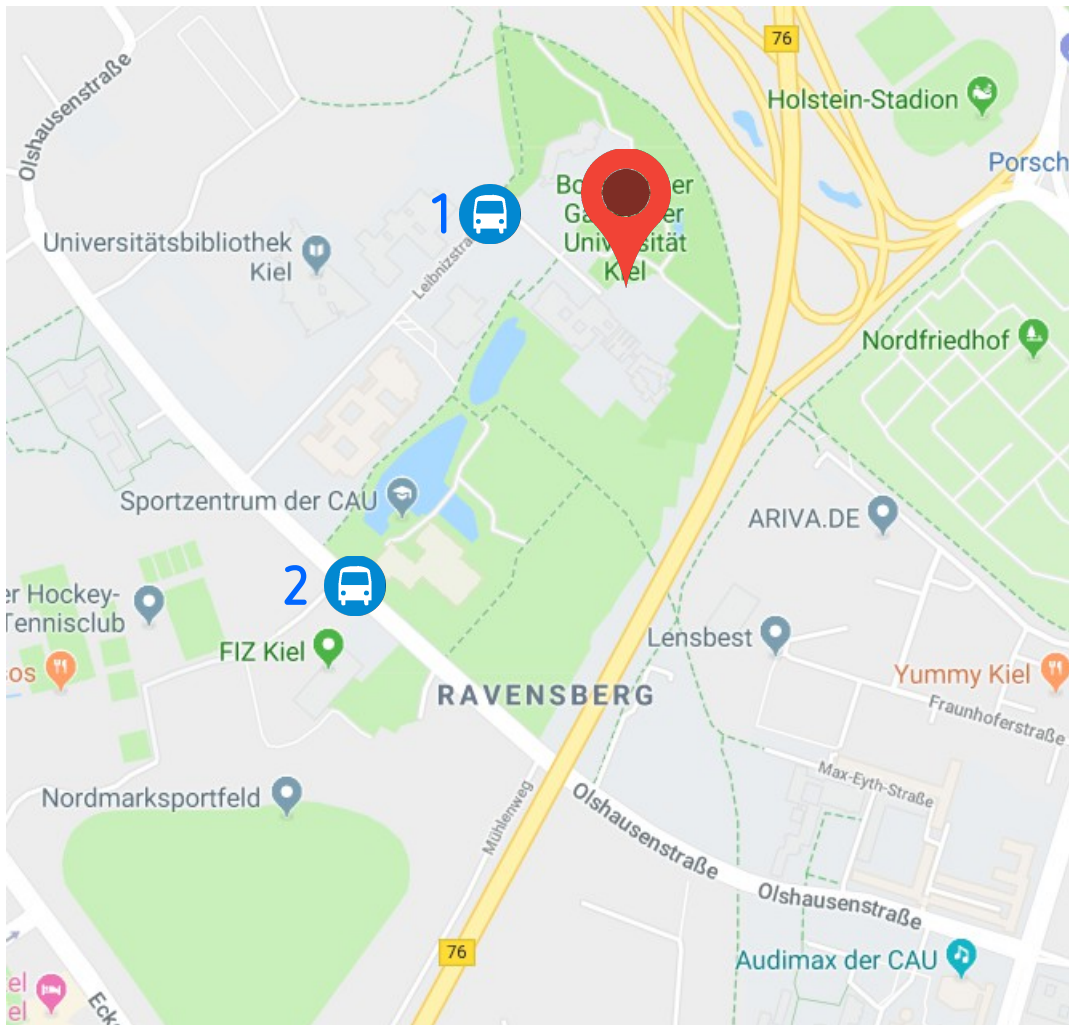
Monday 22nd of July at 6:30 pm

Zentrum für Molekulare Biowissenschaften (ZMB)

Am Botanischen Garten 11

24118 Kiel

(Seminar Room 4th floor)



How to get there:

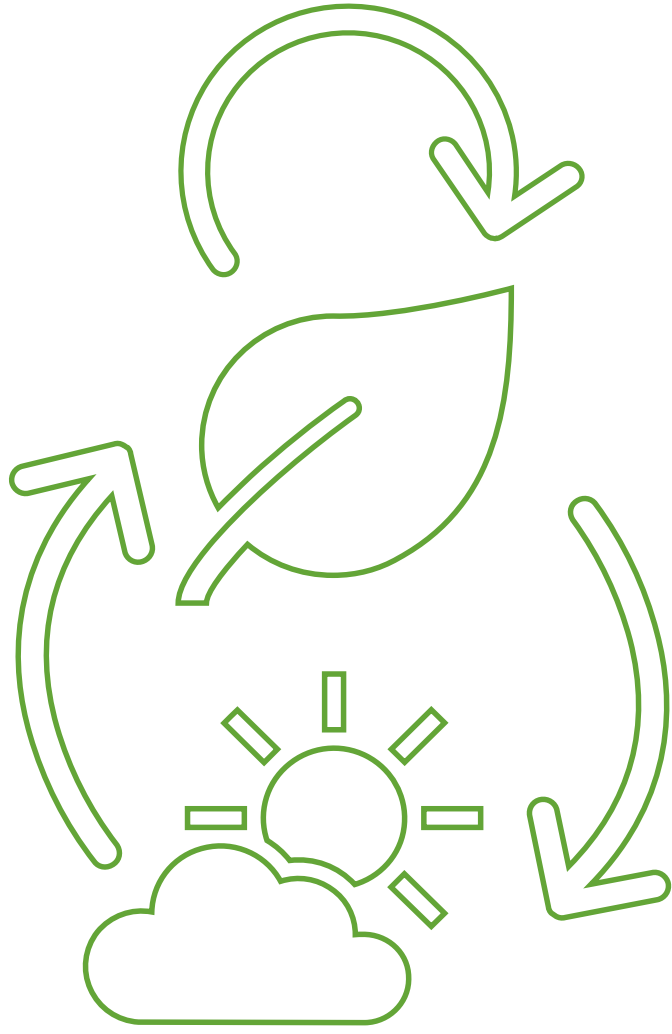
1. Bus lines to *Botanischer Garten*

60S 50 81

2. Bus lines to *Uni-Sportstätten*

60S 50 81 61 62 6

Please note: The last bus departing from *Botanischer Garten* leaves at 22:09 pm. After that time only busses departing from *Uni Sportstätten* can be taken



Scientific Program

Monday July 22nd

Zoological Museum Kiel

From 12:00 *Lunch and registration*

13:00 Welcome by Eva Stukenbrock (Botanical Institute, CAU, Kiel and MPI, Plön)

13:10 - 16:40 **Session I**

Chair: Janine Hauelsen (Botanical Institute, CAU, Kiel and MPI, Plön)

13:10 *Invited Speaker:* Rüdiger Hell (Dept. Molecular Biology of Plants, Heidelberg University)

How plants grow – the integration of metabolism

14:00 Christian Jung (Plant Breeding Institute, CAU, Kiel)

Breeding for resistance to plant parasitic nematodes

14:20 Daguang Cai (Institute for Phytopathology, CAU, Kiel)

Deciphering the function and regulation of noncoding microRNAs in plant response to a/biotic stresses and its potential for improving plant resistance

14:40 Heike Seybold (Botanical Institute, CAU, Kiel and MPI, Plön)

Hemibiotrophic fungal pathogen induces systemic susceptibility and systemic shifts in wheat metabolome and microbiome composition

15:00 *Coffee break*

15:30 *Invited speaker:* Tina Romeis (Dept. Biochemistry of Plant Interactions, IPB Halle)

Regulation and function of Calcium-Dependent Protein Kinases as decoders of calcium changes during stress signalling in plants

16:20 Kirsten Krause (Dept. Arctic and Marine Biology, Tromsø, Norway)

"Hide and seek": Interactions between parasitic Cuscuta and its hosts

16:40 End of symposium at Zoological Museum

18:30 Evening program at the *Botanical Garden, CAU, Kiel*

19:00 *Evening lecture:* Prof. Andreas Graner (Dept. of Genebank, IPK Gatersleben)
Ex situ genebanks: transition from seed repositories to bio-digital resource centres

Poster Session and flying buffet

Tuesday July 23rd

Zoological Museum Kiel

9:00 - 12:30 Session II

Chair: Nazgol Emrani (Plant Breeding Institute, CAU, Kiel)

9:00 *Invited speaker:* Dr. Claire Gachon (Scottish Association of Marine Sciences)

9:50 Margret Sauter (Botanical Institute, CAU, Kiel)
Root system adaptation to flooding

10:10 Wolfgang Bilger (Botanical Institute, CAU, Kiel)
Resistance mechanisms in plants against UV radiation

10:30 Coffee break

11:00 Deniz Tasdemir (Marine Natural Products Chemistry, GEOMAR, Kiel)
Surface-based host-microbe interactions in seaweed and seagrasses: Untargeted and spatial metabolomics coupled with microbiome and bioassay analyses

11:20 Tobias Demetrowitsch (Institute for Human Nutrition and Food Science, CAU, Kiel)
Investigation of the secondary plant substances profile affected by microorganisms in various environments using different analytical approaches

11:40 Birgit Classen (Pharmaceutical Institute, CAU, Kiel)
Arabinogalactan-proteins: Signalling molecules of plant cell wall

12:00 Lunch

13:30 - 15:00 Session III

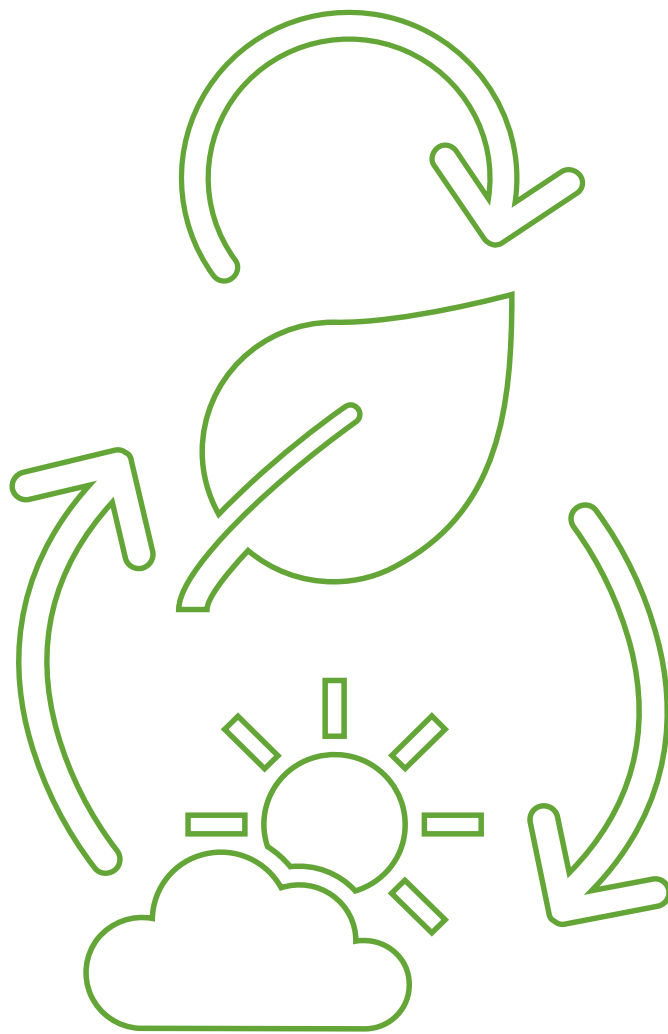
Chair: Opayi Mudimu (Botanical Institute, CAU, Kiel)

13:30 *Invited speaker:* Jürgen Gross (Institute for Plant Protection in Fruit Crops and Viticulture, Julius Kühn Institute, Dossenheim)
Exploring the mechanisms of chemical communication for application in sustainable agriculture

14:20 Ralf-Udo Ehlers (Gesellschaft für Biotechnologie und biologischen Pflanzenschutz, Schwentinental)
Use of microorganisms and nematodes in crop production

14:40 Elisabeth Kaltenecker (Botanical Institute, CAU, Kiel)
Defence de-escalation as answer to adapted herbivores

15:00 Closing



How plants grow – the integration of metabolism, stress and development

Rüdiger Hell

Centre for Organismal Studies, Heidelberg University

Plants can respond to environmental challenges with comprehensive developmental transitions. This developmental plasticity is based on the redirection of metabolic processes to cope with stress factors. Drought and nutrient deficiencies are particular examples for redirection of metabolite fluxes and allocation between shoot and root that leads to massive changes in growth and development of both organs. Using the limitation of the nutrient sulfate as an example it is shown that antagonistic activation of the Target of Rapamycin (TOR) sensor kinase in the root and the shoot is essential for the acclimation of the root-to-shoot ratio. TOR regulates the sulfate limitation-induced activation of autophagy and growth arrest in leaves resulting in carbon allocation to the root. This process is facilitated by specific upregulation of the sucrose-transporters and provides a signal for tuning root apical meristem activity. This sequence of events supports root growth for mining new sulfate resources in the soil. These findings help to explain environment triggered organismal plasticity in plants in general, but also enable new modification strategies towards crop plants with enhanced nutrient use efficiency.

Breeding for resistance to plant parasitic nematodes

Christian Jung, Avneesh Kumar, Smit Shah
Plant Breeding, Kiel University

Plant parasitic nematodes are important pests in crop production worldwide. We are working with two different kinds of plant parasitic nematodes. Cyst nematodes invade the root to establish a specific feeding cell called syncytium. The females stay within the root for the rest of their life. Root lesion nematodes move to the cortex destroying all cells they are feeding from. They can lay eggs within or outside the root and they can also leave the root. The beet cyst nematode *Heterodera schachtii* is the most important pest in sugar beet (*Beta vulgaris*) production. We have mapped a major resistance gene *Hs2* to a translocation from a wild species at the end of chromosome 9. We have sequenced the translocation and we have delimited a region of ca. 200 kb where the gene is located at. Presently we are characterizing candidate genes from this region by CRISPR-Cas knockout and overexpression analysis in hairy roots. Root lesion nematodes of the genus *Pratylenchus* are gaining importance in Europe due to narrow crop rotations. We have mapped QTL for reduced infection rates in barley and wheat. Presently, we perform fine mapping by a GWAS using NGS data from hundreds of barley and wheat accessions. A major QTL in barley is fine mapped by a mapping by sequencing approach to clone candidate genes from this genome region.

Deciphering the function of noncoding microRNAs in plant response to a/biotic stresses and its potential for improving plant resistance

Daguang Cai

Molecular Phytopathology, Kiel University

Increasing data evidence that noncoding microRNAs (miRNAs) play an important role in regulating plant responses to various stress factors. Deciphering the function and regulation of noncoding microRNAs in plant responses is one of currently the most interesting cutting-edge research topics in the life science, worldwide. In recent years, identification and understanding of the role of miRNAs in regulating plant-pathogen interactions is one of major research activities in our lab. (D. Shen et al. 2014, E. Shen et al. 2015, Y. Shen et al. 2017, F. Behrens et al. 2018, Z. Zhou et al. 2019). We demonstrated e.g. that the pathogenic fungus *Verticillium longisporum* is able to suppress plant immunity by interference with plant miRNAs and reprogram plant gene expression to achieve its infection in its hosts. Thus, the interference with miRNA-target interactions provides a promising alternative to reduce host susceptibility to the pathogen infection and a novel approach for improving plant disease resistance. Molecular Phytopathology CAU Kiel is one of the leading groups in the field of miRNA researches in rapeseed and has archived necessary tools, technologies and knowledge and experience for a deeply deciphering the role and regulation of noncoding miRNAs in plant response to a/biotic stresses.

Hemibiotrophic fungal pathogen induces systemic susceptibility and systemic shifts in wheat metabolome and microbiome composition

Heike Seybold, Tobias Demetrowitsch, M. Amine Hassan,

Silke Szymczak, Ekatarina Reim, Janine Haueisen, Sören Franzenburg,

Andre Franke, Karin Schwarz, Eva H. Stukenbrock

Environmental Genomics, Kiel University and MPI Plön

Yield losses caused by fungal pathogens represent a major threat to global food production. One of the most devastating wheat pathogens is the fungus *Zymoseptoria tritici*, which overcomes immune defenses in susceptible wheat cultivars. The underlying mechanisms of plant-pathogen interactions are poorly understood despite the importance of this pathogen. We combined coinfection assays, comparative metabolomics, and microbial profiling to demonstrate that *Z. tritici* actively suppresses the production of immune-related metabolites in a susceptible wheat cultivar. We show that fungus-induced immune suppression spreads in distal leaf tissues and even to other leaves, a phenomenon that we termed “systemic induced susceptibility”. In contrast, *Z. tritici* induces systemic acquired resistance in a resistant cultivar. With a comparative metabolomics approach based on FT-ICR-MS, we identified defense-related biosynthetic pathways that are suppressed and induced in the susceptible and resistant wheat cultivars, respectively. We show that these fungus-induced changes also have dramatic effects on the microbiome of wheat leaves. Our findings emphasize that immune suppression by this hemibiotrophic fungal pathogen affects specialized plant metabolism, indirectly manipulates plant microbial biodiversity, and renders wheat vulnerable to subsequent pathogen infections.

Regulation and function of Calcium-Dependent Protein Kinases as decoders of calcium changes during stress signalling in plants

Tina Romeis

Leibniz Institute of Plant Biochemistry, Halle (Saale)

Calcium-triggered intracellular signalling is a prerequisite to mount abiotic and biotic stress responses, and evidence for Ca²⁺-dependent regulation of plant growth and development exists. Calcium-dependent protein kinases (CDPKs) combine within a single molecule a calcium-sensing domain which contains in general 4 EF-hand calcium-binding motifs and a protein kinase effector domain. Accordingly, CDPKs function as decoders that sense and translate (induced) cytoplasmic changes in Ca²⁺ into further downstream signalling events. CDPKs participate in abiotic stress responses in ABA-signalling and in the control of the stomatal aperture. In innate immune signalling, CDPKs have been identified as positive and as negative regulators for both local early and late systemic defence responses in PTI and ETI. Our current research focuses on the primary biochemical enzyme activation mechanism as well as on the identification of biological processes and genuine *in vivo* phosphorylation substrates for distinct CDPK isoforms. In particular, we aim for biochemical mechanisms how CDPKs mediate calcium specificity, and how calcium signals are decoded by CDPK isoforms into different signalling outputs.

„Hide and seek“: Interactions between parasitic *Cuscuta* and its hosts.

Kirsten Krause

Dept. of Arctic and Marine Biology, The Arctic University of Norway

Discrimination between “self” and “non-self” in plants is a fundamental but enigmatic process that has a profound impact on plant productivity. Parasitic plants that infect other plants have perfected strategies to overcome non-self-recognition in plants and may help us to understand this important mechanism.

Species of the parasitic plant genus *Cuscuta* infect the stems of other plants and retrieve all their nutrients from them. Every infection starts with a coiling of the parasite around the host stem and the development of an infection organ, known as haustorium. Host surfaces are breached by using enzymes as well as mechanical force. Mature haustoria are nested deeply within the host tissue and produce lateral and apical finger-like scavenging cells called “feeding hyphae” that differentiate into the cell type with which they connect. The seamless connection between the two partners is accentuated by the development of cytoplasmic connections known as plasmodesmata.

In an attempt to understand the actions and reactions at the host-parasite interface we develop approaches to unravel how *Cuscuta* is able to infect many different host species indiscriminately, how some few resistant hosts are able to detect and fend off the parasite, and why susceptible hosts fail to notice the intruder.

Ex situ genebanks: transition from seed repositories to bio-digital resource centres

Andreas Graner

Dept. of Genebank, IPK Gatersleben

Ex-situ conservation of plant genetic resources represents the major backbone to maintain the intraspecific diversity of many important crop plant species. At present about 7 million seed samples are stored in far more than 1000 *ex-situ* collections worldwide. Arguably, the vast diversity resting on the shelves of genebanks has been remained untouched yet by scientists and plant breeders. Benefitting from genomics technologies, the conservation management of individual collections can be optimized (i) to monitor the authenticity of a given accession and (ii) to activate a collection to provide informed access to genetically defined material.

Technical advances in several key areas including (i) structural and functional genomics, (ii) phenotypic cataloging of accessions using automated imaging and (iii) novel biotechnological approaches need to be exploited to better understand and utilize genetic diversity for crop improvement. While the application of novel technology opens up a wealth of entry points for genetic analyses, it also entails a tremendous amount of data. Therefore, integrated concepts of data management and analysis are instrumental when aiming at the exploitation of novel technologies for the systematic phenotypic and genotypic characterization of genebank collections. In this context, free access to digital information needs to be secured at a global scale to ensure innovation in a sustainable way.

Ein Blick unter Wasser: physiology, evolution and ecoanthropology of algae-pathogen interactions

Claire Gachon

Scottish Marine Institute, The Scottish Association for Marine Science

Collectively, algae account for roughly half of the global primary production. Land and marine ecosystems differ in some of their key drivers, such as biomass turn-over and the velocity of climate change. Marine biota also host higher levels of less well characterised biodiversity than terrestrial ones, and algal cultivation is developing exponentially worldwide. All these factors are profoundly changing the marine environment and our dependence from it. In this talk, I will present some of my group's work on the diseases of brown algae, red algae and diatoms, at the crossroad between ecology, comparative genomics and aquaculture. Firstly, I will cover the discovery of novel pathogens relevant for the dynamics of phytoplankton blooms and algal aquaculture, and how this yields novel models for oomycete comparative genomics. Secondly, I will how we established three pathosystems with biotrophic, intracellular pathogens to interrogate the cellular mechanisms resulting in innate or induced disease resistance in brown algae. Based on preliminary results on the heritability of disease resistance, we are now deploying GWAS on the sugar kelp *Saccharina latissima*, with the view to inform future breeding programmes. Finally, I will briefly present the networking and structuring efforts undertaken in the GlobalSeaweed and GlobalSEaweed-STAR initiatives to develop an appropriate biosecurity framework for seaweeds globally.

Root system adaptation to flooding

Margret Sauter

Plant Developmental Biology and Physiology, Kiel University

Plants have to cope with environmental changes on site as their mobility is rather limited. Soil water logging and flooding are encountered by plants at an increasing frequency due to globally increasing weather extremes. Roots are the first plant organs that suffer from oxygen shortage as a result of too much water in the soil. Hypoxia, in turn, limits respiration which leads to a shortage in ATP. Roots are essential for all autotrophic plants and it is therefore crucial that a functional root system is maintained during flooding. We study root development under hypoxic conditions in the model plant *Arabidopsis thaliana* L. and in the crop *Oryza sativa* L. (rice). Our results reveal that plants adapt their root system architecture despite of energy limitations to ultimately avoid or ameliorate oxygen shortage. The avoidance responses include changes in root growth direction as well as restructuring of the whole root system. In flooded rice, the original crown system in the anoxic soil is partially or fully replaced by an adventitious root system that is located in the oxygenated flood water and more easily supplied with oxygen from the atmosphere. Our research focus is on the molecular mechanisms that control root development under low oxygen conditions.

Resistance mechanisms in plants against UV radiation

Wolfgang Bilger, Frauke Pescheck
Plant ecophysiology, Kiel University

UV-A (315-400 nm) and UV-B (280-315 nm) radiation are part of the solar spectrum and, hence, an omni-present stress factor for light-dependent photosynthesizing organisms. UV-B can damage DNA, inhibit protein synthesis and cause mutations. The function of proteins or protein complexes, among them photosystem II and RubisCO, can be inhibited directly by absorption of UV-A and UV-B radiation or indirectly by UV-induced formation of reactive oxygen species. Since this stress factor was always present during evolution, all organisms possess resistance mechanisms either preventing or repairing damage. Although DNA and proteins can be repaired or newly synthesized, this can be expensive and avoidance of damage using screening pigments is a common strategy. In higher plants screening pigments such as hydroxycinnamic acid derivatives or flavonoids are located preferentially in the epidermis. Using a non-destructive method based on chlorophyll fluorescence we investigated the influence of environmental conditions on the accumulation of screening pigments in leaves. Besides UV radiation, also photosynthetically active radiation (PAR), low temperature and nitrogen limitation were inducing UV screening. Field experiments demonstrated that the interaction of climatic factors led to the paradoxical situation that UV protection by screening pigments was highest in wintertime, when UV-B irradiance was lowest. We conclude that higher plants are using different UV protection strategies simultaneously and that they can shift the balance between these mechanisms according to environmental conditions.

Surface-based host-microbe interactions in seaweed and seagrasses: Untargeted and spatial metabolomics coupled with microbiome and bioassay analyses

Deniz Tasdemir

Marine Natural Products Chemistry, GEOMAR Kiel

The surfaces are crucial in biotic interactions of marine organisms and prone to microbial colonization leading to biofilm formation and fouling. However, our understanding on surface metabolome and surface-based host-microbe interactions is very limited. We studied the surface chemistry of the brown seaweed *Fucus vesiculosus* (FV) and the eelgrass *Zostera marina* (ZM) in conjunction with their surface microbiome and antifouling activities. Untargeted metabolomics analyses proved their surface metabolome to be chemically diverse and different from those of the whole organisms. For the first time, many bacterial or fungal metabolites were annotated from FV surfaces, prompting epibiome analyses by amplicon sequencing and CARD-FISH imaging. Untargeted spatial metabolomics by DESI-Imaging Mass Spectrometry localised various primary and secondary metabolites on FV surface imprints and in cross-sections, pointing out their ecological functions. The surface metabolome of ZM was dominated by sulfated flavonoids (SFs) and fatty acids (FAs). DESI-IMS showed that FAs were distributed evenly on the ZM leaf surface, while SFs were localized centrally with a high accumulation at the apex. The individual metabolites demonstrated differential inhibitory/anti-settlement activities against epiphytic yeasts. This is the first study combining in-depth untargeted and spatial metabolomic approaches with microbiome and ecological function analyses on marine plant/seaweed surfaces.

Investigation of the secondary plant substances profile affected by microorganisms in various environments using different analytical approaches

Tobias Demetrowitsch, Heike Seybold, Julia Jensen-Kroll, Eva Stukenbrock, Karin Schwarz
Division of Food Technology, Kiel University

The profile of secondary plant compounds (SPS) in plants is sometimes very complex and individual components are characteristic for the plant family. The analytical detection is a considerable challenge and requires a platform with different analyses techniques including mass spectrometry and, for high throughput, ultra-high resolution mass spectrometry such as FT-ICR MS.

The interest in SPS is very high in many areas because they have a wide range of different bioactivities and can be associated with positive effects on animal and human health as well as undesired or toxic effects.

Microorganisms can influence the spectrum of SPS by triggering stress or non-specific immune responses in plants. In addition, SPS may be subject to degradation or post-harvest transformation by microbial activity. There are also interactions between secondary plant compounds that affect the growth of microorganisms and their composition in the microbiota.

Three different examples will be presented. A targeted approach to analyze the degradation and transformation of glucosinolates from *Brassica oleracea* by microorganisms in spontaneous fermentation. A suspected-targeted approach for the degradation products of quercetin in intestinal microbiota. Moreover, using wheat as an example, the effect of microorganisms on SPS and the entire metabolome was analyzed using a non-targeted approach.

Arabinogalactan-proteins: Signalling molecules of plant cell wall

Birgit Classen, Lukas Pfeifer

Dept. Pharmaceutical Biology, Kiel University

Arabinogalactan-proteins (AGPs) are complex branched glycoproteins of the plant cell wall and highly glycosylated members of the family of hydroxyproline-rich glycoproteins (HRGPs). They are characterised by large arabinogalactan moieties linked to a small protein core rich in hydroxyproline and seem to be ubiquitous in cell walls of angiosperm land plants.

One focus of our recent research are investigations on AGPs in the evolutionary context. On the one hand, we search for AGPs in spore-producing land plants and their fresh-water algae ancestors, on the other hand, we are interested whether AGPs are present in seagrasses, which evolved from early monocotyledonous land plants and returned to the marine habitat. In both cases, we identified interesting new structural features not known from angiosperm AGPs, probably due to deviating functions.

AGPs are implicated in many processes of cell development and have also been described as important molecules for adaption to biotic and abiotic stress. In a model for biotic stress we investigated presence of AGPs in barley plants either resistant to or susceptible for infection with nematodes. The results show an increase of HRGPs after infection, being more pronounced in the resistant plants. In seagrasses, AGPs are highly charged which could be an adaptation to abiotic stress caused by high salinity.

Exploring the mechanisms of chemical communication for application in sustainable agriculture

Jürgen Gross

Julius Kühn Institute, Dossenheim

In the light of insect decline and biodiversity loss, chemical plant protection products are under pressure. Sustainable alternatives to chemical pesticides or the quantitative reduction of pesticide application are necessary to empower agriculture for global food and nutrition security.

Key aspects of my research are chemically mediated multitrophic interactions between plants, phytopathogens, herbivorous vector organisms and their natural enemies. Our current research in the field of Applied Chemical Ecology will be showcased. This involves the use of infochemicals for the development of innovative applications in plant protection. Newly identified chemical compounds, blends and antagonists are used for the development of biotechnical control methods covering the full spectrum of methods and materials available for application. Attractive and repellent compounds were identified and tested in laboratory studies and field surveys. Additionally, a new entomopathogenic fungus was isolated from an insect host and is under development for application as biocontrol agent. Traps and dispensers, microencapsulated volatiles, and also nanotechnology are used for the development of appropriate formulations for field applications of infochemicals. These applications include the development of specific chemical lures for monitoring, mass trapping or deterring of pests, as well as complex push-and-pull strategies, attract-and-kill systems and new push-pull-kill strategies. By exploring these innovative pest control measures we are breaking ground for a more sustainable agriculture.

Use of microorganisms and nematodes in crop production

Ralf-Udo Ehlers

*Gesellschaft für Biotechnologie und biologischen Pflanzenschutz,
Schwentinental*

Defence de-escalation as answer to adapted herbivores

Elisabeth Kaltenegger, Tatyana Livshultz, Chelsea R. Smith,
Dietrich Ober

Biochemische Ökologie und Molekulare Evolution, Kiel University

Plants produce a huge diversity of secondary metabolites. Many of them are involved in the defense against herbivores. An important driving force of the evolution of this huge diversity is the ongoing adaptation of the herbivore community to the plants defense compounds. With an increasing feeding pressure, selection will favor the biosynthesis of a modified or new compound. Adapted herbivores however often store the ingested defense compound for their own protection. Thereby, the plants former defense compound become an attractant. In this case, an alternative route to escape the feeding pressure of adapted specialists is to reduce the biosynthesis of the compound. To test such a scenario of de-escalation, pyrrolizidine alkaloids (PAs) in the Apocynaceae have proven to be an interesting model system.

Apocynaceae show a striking interaction with milkweed and clearwing butterflies. The butterflies use PAs not only for their own defense, they also synthesize mating pheromones from PAs. However, only few extant Apocynaceae produce PAs. We hypothesize, that in the evolutionary past, PAs were widespread in Apocynaceae species but due to the interaction with the milkweed PAs were reduced. We tested this scenario of de-escalation by reconstruction the evolution of an key enzyme of PA biosynthesis.

List of Participants

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