



Plant-Microbe Interactions

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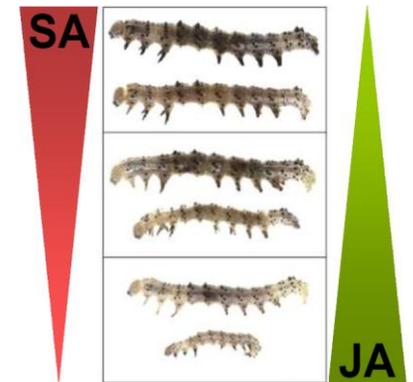
Exploring and exploiting the plant immune system

During your master's program you have the possibility to work in our group on an interesting research project for your major or minor. We offer a broad diversity of research projects. Depending on your interest you may learn techniques from the disciplines of microbial ecology, phytopathology, molecular biology, genetics, genomics, or microbiology. For a tailor-made research project please contact Corné Pieterse (C.M.J.Pieterse@uu.nl), Guido van den Ackerveken (G.vandenAckerveken@uu.nl), Peter Bakker (P.A.H.M.Bakker@uu.nl), or Saskia van Wees (S.vanWees@uu.nl).

Hormonal modulation of plant defense against pathogens and insects

In nature plants have to deal with many different biotic and abiotic stresses. Plants have sophisticated defensive strategies to perceive attack by pathogens and insects. They are capable of integrating pathogen- and insect-induced signals into defenses that are specifically directed against the attacker. The plant-produced alarm signals salicylic acid (SA), jasmonic acid (JA), and ethylene (ET) play a major role in this defense response. SA, JA, and ET signaling pathways cross-communicate, providing the plant with a regulatory potential to fine-tune its defense reaction. We discovered several regulatory proteins that function as modulators in cross-talk between SA and JA, thereby prioritizing the SA pathway over the JA pathway. By using state-of-the-art computational biology and whole genome expression profiling (RNA seq) we aim to build a gene regulatory network model of the antagonistic SA-JA signal interaction in the model plant *Arabidopsis thaliana*. This will provide a detailed understanding of the complexity of the dynamics of the plant immune system upon pathogen and insect attack.

Techniques: Gene expression studies (quantitative RT-PCR, RNA seq analysis), mutant analyses, molecular cloning, western blotting, chromatin immunoprecipitation, pathogen and insect bioassays. *Corné Pieterse and Saskia van Wees.*



Functional analysis of downy mildew resistance in *Arabidopsis* and crops

Downy mildew is a devastating and economically important plant disease. We have identified a number of genes in *Arabidopsis* that are required for susceptibility to the downy mildew pathogen. When mutated, these genes lead to resistance that can be applied in crops. To understand the molecular mechanisms of resistance we undertake a genetic, genomic and molecular approaches. Candidate genes will be identified that increase our understanding of how disease resistance is being established in the mutants. Two of the downy mildew resistance genes (DMR1 and DMR6) have been cloned and encode metabolic enzymes. A second focus in our research is on the metabolomic analysis of these mutants. Our current data indicate that novel, so far unknown, mechanisms govern resistance in our mutants. Our knowledge is being translated to economically important crops.

Techniques: Genetics, metabolite analysis, gene expression studies (qPCR), mutant analyses, molecular cloning, pathogen bioassays. *Guido van den Ackerveken.*

Mining the genome of the downy mildew pathogen for gene families involved in infection and disease

The genome sequence of *Hyaloperonospora arabidopsidis* has recently been obtained and we are studying gene families that are potentially involved in the infection process. Various assays have been developed to analyze the role of these genes in enhancing plant disease susceptibility or in suppressing plant defense responses. A particularly interesting class of proteins includes the so-called RXLR proteins that are actively transported into the plant cells and which are likely to suppress host defenses. We intend to unravel the molecular mechanism and host targets of these effector proteins. The availability of the genomes of several oomycete plant pathogen species now opens up the possibility to perform comparative genomic studies to identify gene families that have a potential function in the infection process.

Techniques: Bioinformatics, gene cloning, generation of transgenic plants, transient expression assays, gene expression studies (qPCR), defense suppression assays, pathogen bioassays. *Guido van den Ackerveken.*



Plant responses to plant growth-promoting rhizosphere bacteria

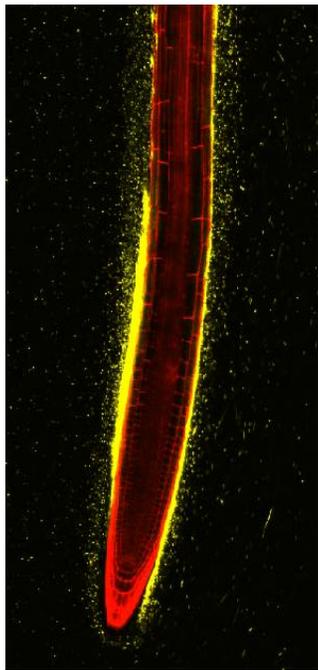
Non-pathogenic, plant growth-promoting rhizobacteria are able to help the plant to defend itself by activating a systemic, broad-spectrum resistance called rhizobacteria-induced systemic resistance (ISR). In the past years we investigated the molecular mechanisms of how beneficial soil-borne rhizobacteria are able to stimulate the plant's immune system, thereby protecting the plant against a broad spectrum of plant pathogens and even insect herbivores. We unraveled many molecular details of the ISR signaling pathway. Microarrays have shown that ISR is based on priming for enhanced defense-related gene expression, rather than on direct activation of defense. Ecological studies revealed that priming for enhanced defense has significant fitness benefits when plants are grown under pathogen pressure.

Techniques: Microbiology, mutant analysis, disease bioassays, gene expression studies (qPCR). *Corné Pieterse & Peter Bakker.*

The plant microbiome and plant health

The diversity of microbes associated with plant roots is enormous, in the order of tens of thousands of species. This complex plant-associated microbial community, also referred to as the second genome of the plant, is crucial for plant health. Recent advances in plant-microbe interactions research revealed that plants are able to shape their rhizosphere microbiome, as evidenced by the fact that different plant species host specific microbial communities when grown on the same soil. Upon pathogen or insect attack, plants are able to recruit protective microorganisms, and enhance microbial activity to suppress pathogens in the rhizosphere. Research is focused on obtaining a comprehensive understanding of the mechanisms that govern selection and activity of microbial communities by plant roots. This will provide new opportunities to increase crop production.

Techniques: Microbial ecology, microbiology, mutant analysis, disease bioassays, gene expression studies (qPCR). *Peter Bakker.*



Mycorrhizal ecology

Almost all plants form intimate symbiotic associations with mycorrhizal fungi. Mycorrhizal fungi form extensive mycelial networks in the soil and forage effectively for minerals such as nitrogen and phosphorus that are delivered to the plant roots. Plants often benefit from infection by these fungi and show enhanced growth. Plants can obtain up to 80% of nitrogen and up to 90% of their phosphorus demand from mycorrhizal fungi. Mycorrhizal fungi in turn receive photosynthates from the plant and the result is an association between two completely different organisms. Our research focuses on arbuscular mycorrhizal fungi (AMF), the most common group of mycorrhizal fungi. In particular we investigate the agricultural and ecological significance of mycorrhizal fungi and mycorrhizal fungal diversity.

Techniques: Plant and microbial ecology, microbiology, bioassays. *Marcel van der Heijden (Switzerland).*

