

Connectivity - Plant Interactions Reloaded

Invited Speaker & Flash Talk Abstract
in speaking order



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Invited Speakers

Auxin canalization in self-organizing plant development

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The plant hormone auxin is a versatile intercellular signal influencing virtually all aspects of plant life. It has a unique ability to be directionally transported within tissues forming local auxin maxima or gradients that are central to many developmental processes mediated by auxin. The key components of this polar auxin flow are plant-specific, auxin exporters from the PIN family showing typically polar, subcellular localization at the plasma membrane. PINs have been shown to mediate auxin export from cells in many homologous and heterologous systems but their structure and mechanism of their action are still unknown. The important but mechanistically not well-understood property of PIN-dependent polar auxin transport is its ability to self-organize and form polarized auxin-transporting channels. This, so called, auxin canalization mechanism provides a positional cue for formation of vasculature during organogenesis, leaf venation or regeneration around the wound.

Recently we have provided new molecular insights into the feedback mechanisms between auxin signaling and PIN polarity - a crucial component of canalization. We identified CAMEL/CANAR receptor-like kinase complex that is required for auxin-mediated PIN repolarization. Here we will also present how this signaling system cooperatively with different auxin signaling pathways regulate PIN-dependent auxin transport contributing to the self-organizing nature of plant development.

Getting to the roots of plant resilience to salinity stress

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Salt stress is one of the major threats for agriculture, and exposure to salt alters root architecture. Yet the mechanisms underlying salinity-induced changes in Root System Architecture (RSA) remain to be identified. We examined natural variation in root development among *Arabidopsis* accessions and identified genetic loci associated with salt induced changes using genome-wide association studies (GWAS).

Validation of selected genetic loci has revealed novel-stress induced pathways that are activated locally in response to salt, allowing finetuning of RSA for optimal performance of plants in saline soils. We continue to investigate these pathways for their salt-specificity and dependence on hormonal signalling as well as the consequences of RSA modulations for stress resilience.

Plants as pathogens

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Parasitism is a successful way of life, one that is ubiquitous to all domains of life. In plants, the transition from a free-living organism to being a parasite that steals water and nutrients from another plant provides a significant ecological-evolutionary advantage in highly competitive and resource-poor environments. The transition of plants to a parasitic lifestyle brings about extreme morphological changes and massive genetic reconfigurations. By applying -omics-enabled genetics and phylo-statistical hypothesis testing, the work of my group could demonstrate that the establishment of parasitic specializations, where parasites can no longer conclude their lifecycle without a host, trigger genomic reconfigurations that proceed with rapid functional and physical reductions in the parasites' genomes, accompanied by a gradual acceleration of molecular evolutionary rates. The transition to obligate parasitism starts an eco-evolutionary feedback loop that affects all genomic compartments, thereby furthering trophic specialization. As this happens, we observe that diversification patterns change. It can be assumed that parasite specialization and diversification is co-shaped by an increasing dependency on their hosts, which creates an isolating barrier absent from ordinary plants. Population-genomic analyses show notable local adaptations associated with host preferences and life history switches. Moreover, likelihood-based inferences suggest that several weedy parasites have arisen from populations that prefer non-crop hosts, perhaps as a result of invading the parasites' natural ecosystems. Together with ongoing functional-genetic studies regarding the molecular level of interactions between parasites and hosts, the eco-evolutionary knowledge of parasitic plants' diversification constraints (and facilitators) might eventually help to improve predictions of the weed potential of selected species.

Microbiome-induced epigenetic mechanism of heat stress tolerance in plants

Heribert Hirt

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In response to recurrent stresses, plants are able to memorize and induce a set of genes for survival to overcome otherwise lethal conditions. Plant stress memory has been shown to have an epigenetic basis in stress genes. We study the contribution of the microbiome of desert plants to the extraordinary capacity of desert plants to survive under extreme conditions of heat, drought or salt stress. We show that *Enterobacter* sp. SA187, a microbial strain of endophytic microbiome the indigenous desert legume *Indigofera argentea*, can confer multi-stress tolerance to non-host plants and important crops. Using *Arabidopsis thaliana* as a genetic model system, we uncovered that microbial-induced plant heat stress tolerance is an epigenetic mechanism. Importantly, microbiome-induced stress protection of crops is not linked to any penalty on plant growth or yield. These findings have important implications for crop production not only on arid lands but also for global food safety strategies of developing sustainable agricultural systems under conditions of global warming.

What determines the diversity of pathogenic microbial communities in nature?

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Pathogens are prevalent across all ecosystems and they may have strong negative effects on their hosts. Hence, there is a pressing need to understand determinants of risks of infection and how these evolve. To date, host-pathogen interactions have been largely viewed within the ‘one host-one parasite’ framework although in reality the same host may be attacked by a myriad of pathogenic microbes. As molecular tools have become increasingly available for the study of parasites, we now know that a single host individual can support a highly diverse pathogen community. However, remarkably little is known about the factors that determine which pathogens co-occur within the same host individual, how they interact and what this diversity means for disease ecology. In my talk I will present case studies of within host pathogen strain and species diversity, and what we know to date of the determinants of this diversity.

On Growth and Form in Petals

Vivian Irish

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Petals are important for pollinator attraction, by providing visual, tactile, olfactory, and other cues. These cues in part rely on the function of petal epidermal cells; these epidermal cells have a distinctive morphology that is widely conserved across angiosperm species. To explore the molecular basis of how petal epidermal cell form is regulated, we have identified mutations that disrupt shape, size, and chirality. We have focused on one gene, *RHMI*, mutations of which cause a dramatic left-handed helical growth of individual cells, resulting in left-handed twisted petals. *RHMI* encodes a UDP-L-rhamnose synthase, and *rhm1* mutations affect synthesis of the pectic polysaccharide rhamnogalacturonan-I. Unlike other mutants that exhibit helical growth of fixed handedness, the orientation of cortical microtubule arrays is unaltered in *rhm1* mutants. Our findings reveal a novel source of left-handed plant growth caused by changes in cell wall composition that is independent of microtubule orientation. We propose that an important function of rhamnose-containing cell wall polysaccharides is to suppress helical twisting of expanding plant cells via modulating the inherent chirality of cellulose. These biophysical interactions between different polysaccharides in the cell wall in turn affects cell morphology, petal morphology, and ultimately the ability of pollinators to successfully ensure plant reproductive success.

The role of floral traits in pollination and plant defense

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Biological communities are formed from complex webs of interactions among species. While antagonistic and mutualistic species interactions have historically been studied independently, with their own theoretical developments and bodies of literature, there is now widespread recognition that these interactions interact to affect host ecology and evolution. For example, plants are often under simultaneous and conflicting selection pressures exerted by both herbivores and pollinators. This seminar will focus on the degree to which plants may experience tradeoffs in pollinator attraction vs. plant defense against herbivores, and the role that community context plays in these multispecies interactions. Tradeoffs that plants experience may be high when both mutualists and antagonists are feeding on the same plant resource, such as floral nectar. I will focus on the role of floral nectar secondary chemistry in mediating multi-species interactions and the ecological contexts in which nectar secondary chemistry as well as other floral traits may be detrimental vs. beneficial to plant fitness.

Flash talks

Temporal differentiation of nutrient uptake and biomass growth as a driver of yield advantages in intercropping

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Intercropping, i.e. the simultaneous cultivation of different crops on the same field, has demonstrated yield advantages compared to monoculture cropping. These yield advantages have often been attributed to complementary resource use, but few studies quantified the temporal complementarity of nutrient acquisition and biomass production as a driver for yield benefits. Our understanding of how nutrient uptake rates of nitrogen (N) and phosphorus (P), and their dependence on above and belowground complementary processes, change throughout the growing season and between different neighbors is limited. Here, we conducted weekly destructive harvests to measure temporal trajectories of N and P uptake and biomass production by three crop species (oat, lupin and *camelina*) growing either as isolated single plants, in monocultures or in intercropping systems. Additionally, we quantified organic acid exudation in the rhizosphere and symbiotic N₂-fixation of the lupin throughout the growing season. Logistic models were fitted to characterize nutrient acquisition and biomass production trajectories. We found that oat intercropped with *camelina* accumulated more biomass, N and P than when intercropped with lupin. As this was not due to temporal differentiation of nutrient uptake or biomass growth between intercropped oat and *camelina*, we suspect that root exudation of *camelina* could have improved performance of oat. Comparing isolated singles and crops grown in community revealed that lupin entered competition up to 6 weeks later than oat and *camelina*, giving intercropped oat an advantage early in the growing season, which levelled off quickly and did not result in a yield advantage of the oat. This study demonstrates temporal shifts in nutrient uptake rates and biomass production between crop species grown with or without competition and with intra- vs interspecific competition. This not only contributes to our understanding of the temporal dynamics in competitive plant-plant interactions but has also relevance for improving nutrient-use efficiency and designing species mixtures in sustainable intercropping systems.

Plant immune component shapes leaf microbiota

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NADPH oxidase RBOHD is required for microbiota homeostasis in leaves. The plant microbiota consists of a multitude of microorganisms that affect plant health and fitness. However, it is currently unclear how the plant shapes its leaf microbiota and what role the plant immune system plays in this process. Here, we tested *Arabidopsis thaliana* immunity mutants for an altered bacterial community assembly using a gnotobiotic system. Absence of the NADPH oxidase RBOHD caused strong changes in community composition due to an enrichment of selected bacteria. Specifically, we identified opportunistic pathogens that colonized wild-type plants asymptotically but caused disease in *rbohD* plants. Strain dropout experiments revealed that the lack of RBOHD unlocks the pathogenicity of single microbiota members driving dysbiosis in *rbohD*. For full protection, healthy plants require both a functional immune system and a microbial community. Our results show that the NADPH oxidase RBOHD is essential for microbiota homeostasis, emphasizing the importance of the plant immune system in controlling the leaf microbiota.

Reduced pollination services contribute to stabilize southern species range limit

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Climate factors have attracted a lot of attention in the study of species distribution limits, while little is known about the role of biotic interactions. Biotic factors may also contribute to range limits as they may change together with climate over space, or may interact together in affecting species distributions. Here, we monitored insect pollination using time-lapse cameras in populations of the North American plant *Arabidopsis lyrata* over a transect spanning from the southern to the northern range limit. With approximately 4,500 hours of observation, we tested whether pollinator services declined from the core to the edge of species distribution and what the driving factors were: low plant census size, low flower density, less attractive flowers due to marginal conditions, fewer flowering plants species, and/or unfavourable temperature conditions. Overall, we spotted 67 pollinating insect taxa, supporting the idea that the plant-pollinator network is a generalist system. Pollination services declined from the core to the southern range edge but not to the northern range edge. None of the hypothesized mechanisms for declining pollination service was supported. However, we found that the chance of a flower being visited by a pollinator generally increased with plant census size, and that visitation rate per flower decreased within high density patches. Although mechanisms remain elusive, the strong decline in pollination service toward the southern range limit suggests that for a herbaceous plant of the temperate zone, low pollination services could be involved in the contribution of the southern range limits.