35-4 - Cross-Kingdom Kommunikation in Pflanzen: Vergleich von mikrobiellen Krankheitserregern und Mutualisten

Cross-kingdom communication in plants: Comparative study of pathogenic and mutualist interactions

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Communication strategies between plants and eukaryotic microbes based on small (s)RNA exchange have been detected in several plants with fungal pathogens (Cai et al., 2018) and indicated in arbuscular mycorrhiza (Silvestri et al., 2019) and nodulating bacteria (Ren et al., 2019). Bidirectional cross-kingdom communication between plants and microbes is based on RNA interference (RNAi) silencing of gene transcripts whose degradation in turn affects the course of the plant-microbe interaction.

While some of the specific proteins and mechanisms within this silencing pathway are known (like ARGONAUTE proteins and DICER-like endonucleases) and can thus be predicted in organisms in which RNAi hasn't been studied in detail (Šečić et al., 2019), the questions of general function and conservation of targeted genes remain open. Current understanding is that microbe-derived sRNAs function as virulence or colonization factors and plant-derived sRNAs target microbial genes, either in order to prevent a successful infection or aid establishment of colonization with a mutualist.

We investigated the level of conservation and differences between the target hubs and pathways in cross-kingdom interaction of plant hosts with pathogens and mutualists. In a comparative analysis we utilized sRNA sequencing datasets and established bioinformatic pipelines (Zanini et al., 2018; Zanini et al., 2021) to detect and validate putative sRNA effectors exchanged between organisms and their target transcripts. Grasping the complexity, abundance and mechanisms specific to these interactions is essential in order to develop detection strategies of sRNA exchange and further improve the application of RNA-based protection strategies.

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35-5 - Calcium-mediated signalling events orchestrate plant-nematode interactions

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Plant-parasitic nematodes (PPNs) are among the most damaging plant pathogens that threaten current and future global food security. Most of the damage caused by PPNs is due to a small group of root-infecting sedentary endoparasitic nematodes (SEPs) that includes cyst nematodes and root-knot nematodes. Infection is initiated by an infective second-stage juvenile that invades the host root, migrates towards the vascular cylinder and subsequently induces the formation of an elaborative feeding cell(s), which nourishes the nematodes throughout its parasitic stages. Very little is explored on the cross-talk between signalling molecules and downstream targets during early events in plant-nematode interactions. Accumulating evidence suggests that calcium (Ca^{2+}) as a central second messenger connects the perception of microbial signals via plasma membrane-localized pattern recognition receptors to establish appropriate immune responses in plants. Each recognition event is encoded into Ca^{2+} signatures that are ultimately sensed and decoded to distinct downstream responses through transcriptional reprogramming of the defense-related genes by diverse intracellular Ca^{2+} binding proteins. Our previous work suggested that many of these calcium-regulated genes are significantly upregulated in Arabidopsis roots at the early stage of nematode infection. In the present work, analysis of genetically encoded biosensors revealed a cytosolic Ca^{2+} burst during the early nematode infection process. We found that the amplitude and duration of the Ca^{2+} signatures vary depending on the infection stage, the migration and feeding behaviour of the parasites. This is the first example of nematode-induced Ca^{2+} signatures recorded for nematode parasitism. Functional analysis of key genes associated with calcium signalling network during early events has begun to reveal how calcium mediates the molecular dialogue in orchestrating plant-nematode interactions.

Keywords: Arabidopsis, sedentary endoparasitic nematodes, Ca2+ signatures, immune response

35-6 - Tricky parasites: How nematodes take their vitamins from plants

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Heterodera schachtii is a plant-parasitic nematode with an economically important impact on sugar beet production. The second-stage juveniles invade the root of their host and move intracellularly towards the vascular cylinder, where they induce the formation of a plant derived syncytium and become sedentary. The hypertrophic and hypermetabolic syncytium serves as the sole nutritional source for the developing juveniles. Due to this dependency, it is crucial for *H. schachtii* to successfully initiate and maintain the syncytium in order to complete its lifecycle and produce progeny. Transcriptome data of *Arabidopsis thaliana* derived syncytia compared to uninfected root tissues revealed an increase in expression of genes involved in metabolic processes, including the biosynthetic pathways of several vitamin Bs (VBs). These water-soluble vitamins are essential nutrients, as they cannot be stored or synthesized by humans and, presumably, all other animals. The important function of the increase in transcript abundance of VB biosynthetic genes during cyst nematode infection was confirmed for VB 5, the precursor of co-enzyme A. The first enzymatic step in the *de-novo* VB 5 biosynthesis is encoded by *AtPANB1*, which is significantly up regulated in the syncytium. *AtPANB1* knock out mutants were less susceptible to infection by *H. schachtii*. The last enzymatic step is performed by AtPANC, which is not differentially expressed in the syncytium, and the loss-of-function mutation had no effect on the parasitism of *H. schachtii*. Notably, our