Integrated decoys and aphid recognition in wheat

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The plant response to aphid feeding is similar to when a pathogen infects. One such economically important aphid is *Diuraphis noxia* that is a highly specialised aphid pest on a limited number of grasses. When it feeds on wheat, phenotypic responses similar to pathogen infection are observed in the wheat plants. Although this interaction have been studied, we are only starting to understand the molecular interaction and have yet to identify any of the wheat resistance genes. From wheat harbouring the *Dn1*-resistance gene we have identified a WRKY integrated domain nucleotide-binding leucine-rich repeat (NLR-ID) protein (TaADNR1) that plays an extensive role in *D. noxia* detection. Knockdown studies of resistant cultivars show that the loss of this protein result in increased aphid fitness and a highly susceptible wheat phenotype. This was observed for four different biotypes of *D. noxia* indicating that biotypification is not based on the loss of recognition by TaADNR1. The integration of the WRKY domain onto the NLR core protein is a very recent *Triticum* specific event as this WRKY domain only occurs in *T. aestivum* and none of the hexaploid precursors. This indicates that WRKY domain integration happened in the last ten thousand years. The integration of a WRKY domain onto TaADNR1 and one of its two homoeologs highlights the possible significance of these NLR-IDs. This significance is reinforced as the *TaAdnr1* transcript is targeted by a miRNA during this interaction.

Towards the characterisation of a novel resistance gene to control the rice root-knot nematode

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The rice root-knot nematode, *Meloidogyne graminicola*, is considered a major threat to rice agriculture, particularly in Asia where changes in agricultural practices in response to environmental and socioeconomic conditions have led to a dramatic increase in the nematode disease pressure. Development of resistant rice varieties is essential to mitigate the spread of the disease and to promote sustainable control. Resistance to *M. graminicola* was identified in the Chinese tropical *Oryza sativa japonica* cultivar Zhonghua 11 (Zh11). Histological characterisation of the infection indicated that the resistance kicks in shortly after penetration and impairs the development of the nematode feeding site. Notably, phenolic compounds accumulate in the nematodes' neighbouring root cells during migration and a hypersensitive reaction occurs, leading to necrosis. Genetic characterisation of crosses between Zh11 and the susceptible *indica* cultivar IR64 suggested the presence of a major dominant resistance gene. As Zh11 demonstrated the hallmarks of a typical NB-LRR-type of resistance, a targeted resistance gene-enrichment sequencing (RenSeq) approach was developed in rice, which combined with bulk-segregant analysis of the F2 plants, identified one major resistance locus at the bottom of the rice chromosome 11. KASP markers are in development to screen the recombinants and identify resistance candidate genes.

Root-knot nematode effectors and their role in the tomato root interactome during infection

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Tomato (*Solanum lycopersicum*) is one of the widely consumed vegetable crops all over the world, as well as an important source of nutrition in the human diet. Tomato roots interact with beneficial or pathogenic organisms such as Root-Knot Nematodes (RKN). These interacting organisms manipulate the host cell metabolism by secreting different proteins, called effectors, in order to suppress the plant's immune response. The average tomato yield loss due to *Meloidogyne* spp. is 10%, hence it is important to develop new strategies to investigate this plant-pathogen relationship. Despite this remarkable co-evolution, a molecular understanding of the nature of both, effectors, as well as the mechanism of their action is still missing. Based on literature and unpublished results, 20 RKN effectors, shown to be important for successful parasitism, were selected for further investigation. Although many RKN effectors have been partially characterized, to date only five host targets of RKN effectors have been identified. For the selected effectors, we have started to identify tomato proteins as interaction partners and aim to elucidate the network of protein-protein interactions, and unravel the connection between the effectors, the plant immune system and defense related JA and/or SA pathways. Studying the interactome in tomato roots will also provide an insight into important biological questions that remained unexplored so far.

Resistance-gene independent variation in susceptibility to the root-knot nematode Meloidogyne incognita in Solanum lycopersicum

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Root-knot nematodes (*Meloidogyne spp.*) are among the most devastating plant parasites in global food production. For example, *M. incognita* control is important in tomato production, yet depends on a few resistance (R-) genes. Hence, the rise of resistance breaking (virulent) *M. incognita* populations is an ever-increasing concern, incentivizing the search for novel natural variation for virulence control. Here, we investigated susceptibility to *M. incognita* in tomato accessions without R-genes. Initially, 179 tomato accessions were screened for *M. incognita* susceptibility by challenging at least 10 plants per accession with 100 infective juveniles. We found large, accession-dependent, variation in susceptibility. To uncover underlying mechanisms, a high-resolution time-series RNAseq experiment on 10 accessions differing in susceptibility was performed. By isolating galls and corresponding tissue in mock-infected plants at 1, 2, 3, 4, 7, and 10 days post-inoculation, feeding-site establishment was followed. We found >700 genes differential expressed related to feeding-site establishment and >100 genes correlating with accession susceptibility (Bonferroni-corrected $p < 0.05$). In conclusion, we found R-gene independent variation in susceptibility to *M. incognita* in tomato. This can help to identify genes associated with feeding site formation and loss-of-susceptibility. Furthermore, it opens the possibility to study the role of natural variation on feeding-site establishment.