1960ies into commercial potato cultivars and has been highly effective in managing two pathotypes of *G. rostochiensis* for decades. In the past, we generated two nematode inbred lines that are either fully virulent or avirulent with regard to *H1*. For both lines, high-quality genome assemblies were created using PacBio sequencing. By comparing the effector gene families in both inbred lines, we aim to discover effector variants that are responsible for gain of virulence. Ultimately, insights on effector variants are essential in our understanding why host plant resistance proteins loose resistance against certain potato cyst nematode populations. This understanding may provide ways to develop new breeding strategies and hence reduce the damages caused by these pathogens in a specific and environmentally sound manner.

Salicylic acid biosynthesis in rice and nematode interference
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Salicylic acid (SA) is an important plant hormone that mediates host responses upon pathogen infection. While it is widely accepted that this hormone is synthesized by either the phenylalanine ammonia-lyase (PAL) or the isochorismate synthase (ICS) pathway, some of the enzymes involved have not yet been identified. Furthermore, the importance of each of these pathways in pathogen-induced SA accumulation differs between plants. In *Arabidopsis thaliana*, it is the ICS pathway that is mainly induced upon pathogen infection, while in potato (*Solanum tuberosum*) there seems to only be PAL pathway upregulation under similar circumstances. In rice (*Oryza sativa*) there is no clear consensus on whether the ICS or PAL pathway is the most important or whether they work in tandem, as is the case in soybean (*Glycine max*). Using CRISPR/Cas9 methods, we are creating stable knock-out rice plants for our genes of interest and will analyze those mutants for transcription levels of relevant genes and SA accumulation upon pathogen infection. We have also identified a chorismate mutase and isochorismatase in nematodes that could interfere with the biosynthesis of SA. Therefore, we will also perform infection experiments with nematodes on these plants, to elucidate how they can alter the biosynthetic pathway. Using enzyme activity assays, we are elucidating the role and function of known and unknown genes to map the mechanisms of the two biosynthesis pathways in detail.

Silencing of an integrated domain nucleotide-binding leucine-rich repeat (NLR-ID) gene, Adnr1, indicates that it underlies Diuraphis noxia resistance in Dn7-mediated resistance in wheat
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The Russian wheat aphid (*Diuraphis noxia* Kurdjumov, RWA) is a major pest of bread wheat (*Triticum aestivum* L.) that has contributed to the major crop losses of susceptible cultivars over the past three decades. However, plants have a continuously evolving innate immune systems to counter various evolving pathogens and pest virulence strategies. Wheat cultivars carrying inbred resistance genes provided resistance against *D. noxia* until the recent development of at least three resistance breaking biotypes (RWASA1-4). *TaAdnr1*, a nucleotide-binding leucine-rich repeat gene (NLR) carrying an integrated WRKY-domain, was identified to play a crucial role in the *Dn1*-resistance gene-based wheat response against the RWA. The aim of this research was to ascertain the role of *TaAdnr1* in imparting resistance to the three resistance-breaking RWASA biotypes. Virus induced gene silencing (VIGS) of *TaAdnr1* resulted in the *Dn7*-mediated resistance response becoming a susceptible phenotype. This was quantified through determining the silencing efficiency as reduced transcript abundance, increased aphid reproduction rates, decrease in dry weights of the plants and the loss of the oxidative response. These results indicated that the NLR-ID underlies aphid recognition in wheat cultivars harbouring different resistance genes. Furthermore, ADNR1 is suggested to recognise effectors from all four biotypes indicating that these effectors are not changed during biotypification of *D. noxia*.

RanGAP1 and RanGAP2 are common virulence targets of two independently evolved effectors from the potato cyst nematode Globodera pallida and Potato Virus X
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The closely related potato resistance genes *Gpa2* and *Rx1* encode canonical intracellular CC-NB-LRR immune receptors. They belong to the same *R* gene cluster but evolved to defend against two unrelated pathogens. Gpa2 detects specific GpRbp-1 effector variants secreted by the potato cyst nematode *Globodera pallida*, whereas Rx1 recognizes the viral coat protein (CP) of Potato Virus X. How effector recognition by these receptors occurs has yet to be demonstrated. However, artificial tethering studies suggest that recognition may occur indirectly through the shared co-factor, Ran GTPase Activating Protein 2 (RanGAP2). Using a combination of Co-IP and cellular imaging studies, we could show that both the eliciting and non-eliciting variants of GpRbp-1 and PVX-CP can interact with RanGAP2 in planta through its WPP domain. Moreover, we could show that the RanGAP1 homolog can also associate with these effectors in the cell. From these data, we conclude that RanGAP1 and RanGAP2 are a common host target for two distinct pathogen effectors with a possible role in virulence. Interestingly, infection assays on mutants and TRV-VIGS silenced plants could show that RanGAP2 and RanGAP1 contribute to the pathogenicity of both cyst nematodes in *Arabidopsis* and PVX in *N. benthamiana*. From these data, a picture emerges that RanGAP1 and RanGAP2 are shared virulence targets of two evolutionary distinct pathogens, which are guarded by two closely related CC-NB-LRR immune receptors in potato.

Identification, cloning and RNAi silencing of selected genes for management of pigeon pea pod borer, Maruca vitrata
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Pigeon pea (*Cajanus cajan*) is a widely cultivated perennial legume crop in tropical and sub-tropical regions of the world. Pod borer, *Maruca vitrata*, is one of the major biotic stress in pigeon pea. Due to the emergence of resistance to chemical pesticides, new management methods are required. Based on transcriptome analysis of *M. vitrata*, 12 genes responsible for growth and development, and six genes expressed in midgut were selected, cloned and used for both in vitro and host delivered RNAi. *In vitro* RNAi via feeding of dsRNA of selected nine genes resulted in phenotypic and behavioural changes such as sluggishness, nonfeeding and discoloration of *M. vitrata* larvae. Quantitative RT-PCR confirmed the silencing of two of the growth and development related genes (*chymotrypsin-like serine protease* and *serine protease S3 subunit)* and three