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Albugo Genomics to Investigate Pathogen Virulence Mechanisms and Host Specificity

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Successful pathogens need to suppress host defences. In plants, conserved microbial molecules activate pattern triggered immunity (PTI) via receptor kinases, and pathogen effectors can activate (directly or indirectly) effector-triggered immunity (ETI) via NB-LRR/NLR cytoplasmic receptors (1).

Albugo sp. (white rusts, Oomycetes) provide a very interesting system to analyse defence suppression. After infection of *Arabidopsis thaliana* (*At*) by a compatible (virulent) *Albugo laibachii* strain, the plant becomes susceptible to formerly incompatible downy mildew pathogens (2) as well as powdery mildews. This indicates a suppression of resistance.

To identify these powerful suppressors of host defence, genomes of two *Albugo laibachii* strains were sequenced using the Illumina genome analyser. We used VELVET (3) assemblies combined with MINIMUS to assemble the whole gene space and estimate the genome size to be ~38Mb. The assemblies together with expression data were used to computationally analyse for effectors. Two major effector classes could be identified: CRNs and CHXC. CRNs have previously been described for other oomycete pathogens like *Phytophthora infestans* (4), while CHXCs are hitherto undescribed. CRNs and CHXCs show a high degree of gene duplication as well as heterozygosity and SNPs between the two strains. This might be due to the fast evolution of effector genes arising from an evolutionary arms race between pathogen and host (5).

To manipulate their host cell, effectors need to cross the host plasma membrane. Using *P. capsici* as a heterologous test system (Huitema, unpublished), we could show that the N-terminal domain carrying the CHXC motif is able to deliver a known avirulence protein (Avr3a) into the host cell. To verify effector function, candidate effectors are currently tested for their functionality to repress resistance using the effector detector vector system which uses type III secretion to deliver an Albugo effector, assaying for increased virulence in *Pseudomonas syringae* (6). Both CHXC and CRN effector candidates can enhance *P syringae* virulence.

Further *Albugo* strains are currently being sequenced to address evolutionary aspects of effectors within this pathogen clade with a main focus on the CHXC effector class.

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