Using Virulence Mutants to Identify Avr Genes in the wheat stem rust fungus, *Puccinia graminis* f. sp. *tritici*

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The wheat stem rust fungus *Puccinia graminis* f. sp. *tritici* (*Pgt*) is one of the most destructive pathogens of wheat. Resistance of host lines is often governed by recognition of fungal effector proteins (avirulence/virulence proteins) by plant resistance proteins (R proteins). We have taken a mutational genomics approach to identify *Avr* genes in *Pgt*. We isolated spontaneous mutants with virulence for *Sr50*, *Sr5, Sr27, Sr21* or *Sr45* by selection on resistant host lines. Sequence analysis of the *Sr50* virulent mutant revealed that virulence resulted from the exchange of a whole chromosome between the two haploid nuclei of this dikaryotic organism, resulting in loss of the avirulence allele. This confirms the important role of somatic exchange events in virulence evolution in *Pgt*. The *AvrSr50* gene was identified from the 25 candidate effector genes from this chromosome by transient co-expression with the cloned *Sr50* gene in *N. benthamiana*. *AvrSr50* recognition was confirmed in wheat by viral expression. *AvrSr50* is expressed early during infection and is highly expressed in haustoria. Three mutants with virulence for *Sr27* contain overlapping deletions and a single candidate gene for *AvrSr27* has been identified. Likewise, *AvrSr5* mutants contain large deletions spanning several candidate effector genes. New expression assays are being developed for confirmation of avirulence gene function in wheat.