FUNGAL PATHOGENESIS

The advantages of keeping your offspring quiet

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Plants can counteract infections with plant pathogens in part by expressing resistance (*R*) genes that target pathogen avirulence (*Avr*) effector proteins. Gijzen and colleagues now show that the oomycete *Phytophthora sojae*, the causative agent of root and stem rot in soybean plants, uses an epigenetic silencing mechanism to

escape this effector-mediated immune detection.

The *P. sojae* avirulence gene *Avr3a* is encoded

in a highly polymorphic region of the genome. Four *Avr3a* haplotypes have been identified, each of which expresses virulent or avirulent alleles of *Avr3a*. To investigate the inheritance of the different haplotypes, Gijzen and colleagues outcrossed the avirulent *P. sojae* str. P7076 (*Avr3a*^{P7076}/*Avr3a*^{P7076}) with the virulent *P. sojae* str. ACR10 (*Avr3a*^{ACR10}/*Avr3a*^{ACR10}). As expected, the parental ACR10 strain caused disease in all plants, and the parental P7076 strain infected only soybeans without the corresponding *R* gene, *Rps3a*. The outcross revealed an unexpected pattern that did not match the previously described dominance of avirulent *Avr* genes: all the *Avr3a*^{P7076}/*Avr3a*^{ACR10} F₁ progeny could infect soybean plants irrespective of the presence of the host *R* gene. According to Mendelian genetics, further crossing should produce a mixture of virulent and avirulent progeny strains; however, all F₂ and F₃ progeny were virulent, even those that were homozygous for the avirulent *Avr3a*^{P7076} allele.

Why were all the progeny strains able to cause disease even though

some had an avirulent genotype? To answer this question, the authors looked at the mRNA levels of *Avr3a*. *P. sojae* str. ACR10 lacks *Avr3a* transcripts and therefore cannot be targeted by the corresponding plant resistance gene, whereas *P. sojae* str. P7076 expresses *Avr3a* mRNA, which is targeted by the host *Rps3a* gene. Surprisingly, all of the progeny, even the F₂ and F₃ generations, inherited *Avr3a* silencing. Furthermore, the parental ACR10 strain and the progeny from the crosses harboured a pool of 24–26-nucleotide small RNAs (sRNAs) covering *Avr3a*. Previous studies have shown that such sRNAs are involved in DNA methylation and gene silencing in plants. Thus, the results suggest that *P. sojae* uses sRNA-mediated epigenetic modification of avirulence genes to evade host immune detection over multiple generations.

Transgenerational gene silencing has the potential to spread rapidly in a pathogen population, but as the gene sequence remains intact, the adaptation is potentially reversible. This gene silencing thus offers a potent and flexible mechanism of adapting to host immunity and could be present in other pathogens.

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ORIGINAL RESEARCH PAPER Qutob, D. et al. Transgenerational gene silencing causes gain of virulence in a plant pathogen. *Nature Commun.* 4, 1349 (2013)

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