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OOMYCETES

Adaptation after jumping ship

The oomycete *Phytophthora* spp. are important plant pathogens that have a specific host range, but the molecular mechanisms responsible for host specialization are poorly understood. Kamoun and colleagues now show that an effector protein of *Phytophthora infestans* (which infects *Solanum* plants) evolved to function in its sister species *Phytophthora mirabilis* (which infects the plant *Mirabilis jalapa*) as a result of amino acid substitutions in the effector and corresponding mutations in its target protease, which together drive adaptation to a new host.

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P. mirabilis diverged from *P. infestans* following a host jump more than 1,000 years ago, and since the split, 82 effector genes have been undergoing positive selection in the two species, which suggests that these genes contribute to host specialization. The authors selected the *P. infestans* cystatin-like protease inhibitor EpiC1 for further study; this effector targets defence proteases in *Solanum* plants to promote infection. Phylogenetic reconstruction of the EPIC1 gene family revealed that the EpiC1 orthologue in *P. mirabilis* (PmEpiC1) has undergone positive selection, consistent with the hypothesis that effector proteins are important for adaptation to a new host.

PmEpiC1 showed considerably lower inhibitory activity compared with EpiC1 when challenged with a range of RCR3 proteases from *Solanum* spp.; however, compared with EpiC1, PmEpiC1 showed stronger activity against its own target protease MRP2 (*Mirabilis* RCR3-like protease 2). This indicates that PmEpiC1 had lost the ability to efficiently inhibit the EpiC1 target protease as it evolved to target a homologous protease in its own host. Furthermore, by synthesizing and purifying the ancestral EpiC1 protein, the authors found that its protease specificity matched that of *P. infestans* EpiC1, which indicates that the altered target specificity of PmEpiC1 was a novel adaptation that evolved over time after the host jump.

The authors found that EpiC1 and PmEpiC1 adopt a similar fold and probably use three domains to interact with their target proteases, two of which are polymorphic between the two effectors. Protease inhibition assays using chimeric proteins and single-site mutants revealed that the Gln to Arg mutation at position 111 in PmEpiC1 is crucial for determining target specificity, and sequencing of nine *P. mirabilis* isolates showed that the mutation is fixed in this species. Furthermore, mutations in a stretch of seven amino acids in the proteases were also required for specificity; replacing this region of RCR3 with the corresponding region of MRP2 resulted in efficient targeting of RCR3 by PmEpiC1.

These findings highlight the importance of effector and target specialization in shaping the adaptation of a pathogen to a new host and offer crucial insights into the evolutionary dynamics that follow a host jump.

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ORIGINAL RESEARCH PAPER Dong, S. *et al.* Effector specialization in a lineage of the Irish potato famine pathogen. *Science* **343**, 552–555 (2014)
FURTHER READING Raffaele S. & Kamoun, S. Genome evolution in filamentous plant pathogens: why bigger can be better. *Nature Rev. Microbiol.* **10,** 417–430 (2012)