

## FUNGAL GENETICS

## Expanding horizons through chromosome exchange

Members of the ascomycete fungi genus *Fusarium* range from plant pathogens to soil dwellers. The publication of a genomic comparison of several *Fusarium* species sheds light on the differences between these species and shows that horizontal transfer of entire chromosomes between species has important consequences for the lifestyle and host range of these pathogens.

Ma and colleagues sequenced the genomes of *Fusarium verticillioides* and *Fusarium oxysporum* f. sp. *lycopersici*; a third genome, that of *Fusarium graminearum*, had been sequenced previously. The host ranges of *F. graminearum* and *F. verticillioides* are narrow compared with that of *F. oxysporum*, which infects a wide range of plants, although each strain has a specific and narrow host range. Using comparative genomics, the authors identified a core genome shared by the three sequenced organisms. Interestingly, the genome of *F. oxysporum* f. sp. *lycopersici* is notably larger than that of the other two species and contains many strain-specific genes. Each genome has a different number of chromosomes: 4 in *F. graminearum*, 11 in *F. verticillioides* and 14 in *F. oxysporum* f. sp.

*lycopersici*. Further analysis showed that *F. oxysporum* f. sp. *lycopersici* is more closely related to *F. verticillioides* than to *F. graminearum*.

To understand the interactions of *F. oxysporum* f. sp. *lycopersici* with its host, the tomato plant, the authors then focused on the genomic regions detected only in this strain. Analysis of codon usage indicated that the *F. oxysporum* f. sp. *lycopersici*-specific genes are likely to have been acquired through horizontal gene transfer, and phylogenetic analysis of these genes across seven ascomycete genomes indicated that this is likely to have involved horizontal transfer of whole chromosomes from other *Fusarium* species, although the identity of these species is unknown. To determine whether the horizontal transfer of chromosomes can influence the host range of the fungus, the authors focused on chromosome 14 of *F. oxysporum* f. sp. *lycopersici*, which encodes multiple proteins involved in host-specific interactions. The authors mixed *F. oxysporum* f. sp. *lycopersici* in which chromosome 14 encoded an antibiotic marker with other strains of *F. oxysporum* that are pathogenic for different plants and that contained a different antibiotic

cassette. Selecting for fungi with both resistances, the authors found that chromosome 14 was transferred from *F. oxysporum* f. sp. *lycopersici* to the other strains at a rate of 0.1 to 10 per million spores. Recombination was not detected for other regions of the genome, so the chromosome must have been horizontally transferred. Acquisition of the *F. oxysporum* f. sp. *lycopersici* chromosome 14 increased the ability of some recipient strains to colonize tomato plants, indicating that the transfer of chromosomes can alter the host range.

Not all strains that acquired chromosome 14 could grow on tomato plants, and those that could were not as pathogenic as *F. oxysporum* f. sp. *lycopersici*. Therefore, loci on other chromosomes also have a role in full adaptation to a particular host. Nonetheless, this is a powerful demonstration that these pathogenic fungi can exchange entire chromosomes and that this can lead to the changes in their host range.

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*F. oxysporum* f. sp. *lycopersici*-specific genes are likely to have been acquired through horizontal gene transfer



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