HOST-JUMPS DROVE RUST EVOLUTION

Rust fungi. Left: *Hamaspora acutissima*; Middle: *Phragmidium mucronatum*; Right: *Uromyces scaevolae*. Photos by Alistair McTaggart.

Rust fungi are one of the most diverse groups of plant pathogens and their divergence was thought thought to mirror the evolution of their hosts. Recently ancestral rusts were hypothesized to have angiosperm hosts, which altered the long-held view of rust evolution. Estimates on the age of rust fungi range from 150–300 million years ago (Ma), however, this had not been tested with a molecular clock.

In the study by McTaggart *et al.* (2015), a molecular clock was calibrated to the evolution of rust fungi on species of *Acacia* (~20 Mya), which have a rich fossil record in Australia. The ancestral *Pucciniales* were calibrated to the ages of divergence for either angiosperms (up to 194 Ma), or to the hosts of the most ancestral species of rust on gymnosperms in the cupressophytes (up to 256 Mya). Two ribosomal DNA genes (LSU and SSU) and a mitochondrial gene (CO3) were used for phylogenetic reconstruction with Bayesian evolutionary analyses.

Rust fungi were recovered with a much younger age than previously hypothesized, with a mean age between 113–115 Ma (full range between 70–161 Ma), when calibrated to angiosperms or cupressophytes. This new estimate of age provides evidence that host jumps, rather than coevolution, were the main speciation events that drove the evolution of rust fungi. Genera of rust fungi likely arose from host jump events and then diversified by co-speciation or taxonomically small host-shifts. Perhaps there is more plasticity in the host range of rust fungi, and host expansions on novel host populations that have not developed resistance will be common; this has already occurred with taxa such as *Cronartium ribicola*, *Puccinia lagenophorae,* and *P. psidii*.

McTaggart AR, Shivas RG, van der Nest MA, Roux J, Wingfield BD, Wingfield MJ (2015) Host jumps shaped the diversity of extant rust fungi (*Pucciniales*). *New Phytologist*: DOI 10.1111/nph.13686.

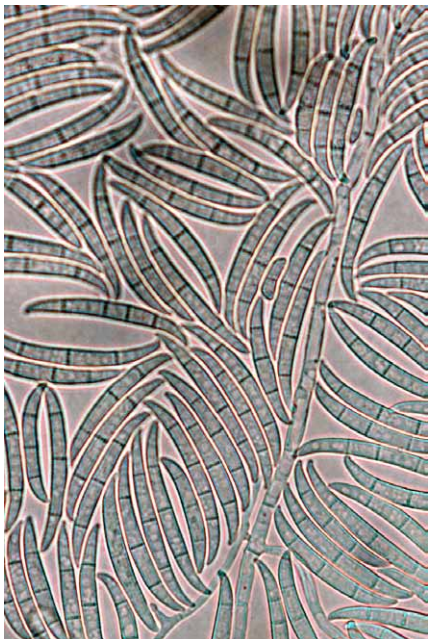
SENSING HOST PLANT SIGNALS: A NEW ROLE FOR PHEROMONE-SENSING MACHINERY?

Just how plant pathogenic and root-infecting fungi are able to respond and grow towards chemical stimuli from plants has remained obscure. Now David Turrà and colleagues from the Universidad de Córdoba in Spain have been able to elucidate this phenomenon in the case of *Fusarium oxysporum* and the roots of *Solanum lycopersicum* (Turrà *et al.* 2015). They studied the germination of microconidia in the presence of a range of compounds, and elegantly demonstrated that the fungus was able to grow towards the roots as a result of a response triggered by class III peroxidases secreted by the plant roots. This involved a mitogen-activated protein kinase (MAPK) and a transmembrane protein Ste2 in the fungal cell well. Intriguingly, the Ste2 protein is a functional homologue of the sex pheromone α-receptor in *Saccharomyces cerevisiae* .

In addition, the group went on to demonstrate that hyphal growth towards nutrients, including sugars and amino acids, is controlled by a particular MAPK cascade.

While it is unclear how widespread the phenomenon is in root-infecting fungi, the genes involved would appear to be conserved and they interpret plant-sensing in complex environments such as soil as an unexpected alternative role for the fungal pheromone machinery.

Turrà D, El Ghalid M, Rossi F, Di Pietro A (2015) Fungal pathogen uses sex pheromone receptor for chemotropic sensing of host plant signals. *Nature* **527**: 521–524.



Fusarium oxysporum.

FIFTY KEY EVENTS IN FUNGAL SYSTEMATICS

Taxonomy	Year	Nomenclature (and organization)
	1753	Starting point for "botanical" nomenclature
Fungi recognized as a separate kingdom	1783	
Treatment of the known fungi started	1821	
Pleomorphism in fungi recognized	1851	
Asexual fungi classified separately	1870	
	1910	Category of special forms introduced
	1912	Separate naming of morphs permitted
Incompatibility as a species criterion	1927	
Keys to all known fungal genera	1931	
	1935	Latin diagnosis or description mandatory
	1940	Index of Fungi initiated
Ascomycete ontogeny linked to ascus types	1951	
Categories of conidiogenesis	1953	
	1954	Registration of fungal names proposed
Parasexual cycle discovered	1956	
	1958	Type designations mandatory
Numerical taxonomy of fungi	1964	
Scanning electron microscope	1965	
Taxonomy of Fungi Imperfecti conference	1969	
	1971	International Mycological Association founded
Sexual-asexual synthesis conference	1977	
	1981	Later starting points for fungal nomenclature ended
	1981	Rules on naming pleomorphic fungi revised
	1982	International Commission on the Taxonomy of Fungi founded
	1986	Systema Ascomycetum launched
Cladistics used in mycology	1988	
rDNA fungal primers introduced	1990	Specification of location of types mandatory
	1991	Abandonment of dual nomenclature proposed
Ascomycete Systematics international workshop	1993	Metabolically inactive cultures permitted as types
	1993	Epitype concept introduced
Amplified fragment-length polymorphisms introduced	1995	
Saccharomyces cerevisiae genome sequenced	1996	
Phylogenetic species recognition	2000	Index Fungorum available online
Oomycota placed in kingdom Straminipila	2001	
	2004	MycoBank registration system launched
Phylogenomics	2006	
Assembling the Fungal Tree of Life project	2006	
Molecularly based ordinal classification of Fungi	2007	
Next-generation sequencing	2008	
DNA Barcode primers for Fungi proposed	2011	Amsterdam Declaration on fungal nomenclature
1000 fungal genomes project launched	2011	Separate naming of morphs of pleomorphic fungi ended
	2012	English allowed as an alternative to Latin for diagnoses
	2012	Electronic publication permitted for new names
	2013	Registration mandatory for new fungal names
Reference Sequences for higher fungal taxa issued	2014	

Reproduced from; Crous PW, Hawksworth DL, Wingfield MJ (2015) Identifying and naming plant-pathogenic fungi: past, present, and future. *Annual Review of Phytopathology* **53**: 246–267.