

New results on fungal genetics

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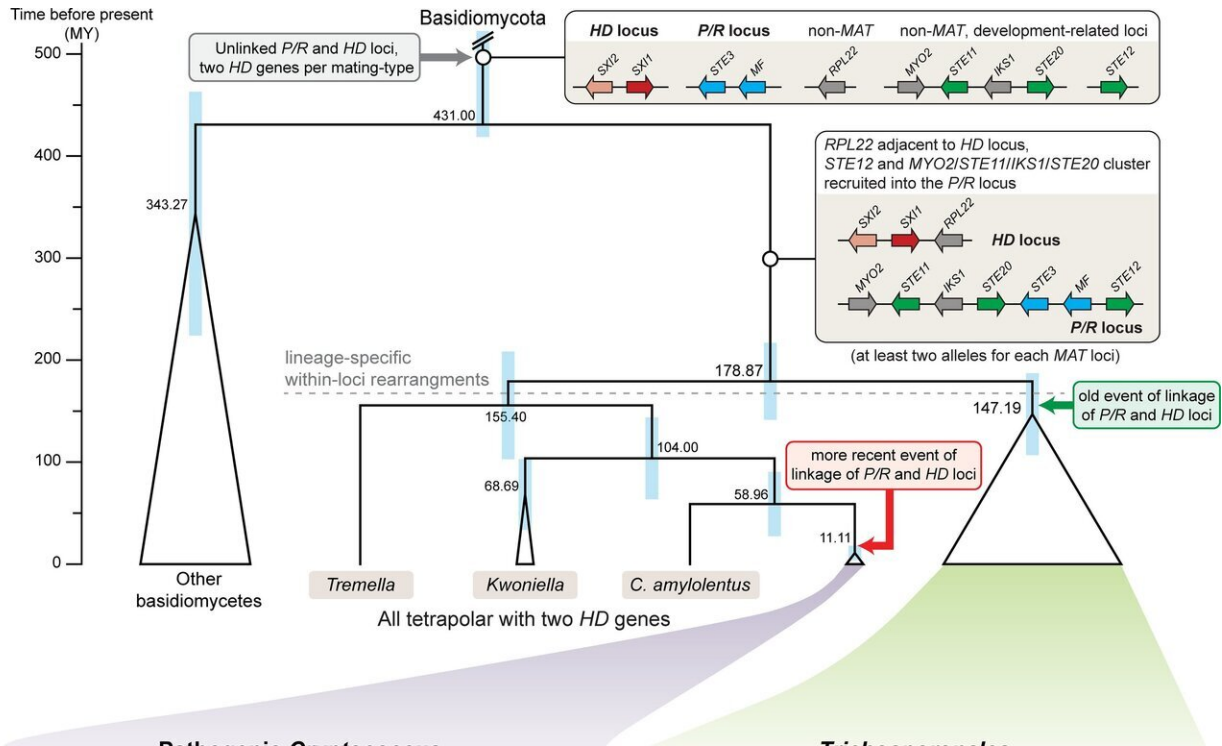


Fig 5. Model for the evolution of the MAT loci in Tremellomycetes. Genes at the core MAT loci include the homeodomain transcription factor genes (HD locus, shown in red/pink) and the pheromone and receptor genes (P/R locus, shown in blue). Genes involved in sexual development, but not originally part of a MAT locus are shown in green, other genes are shown in grey. Only genes from the *C. neoformans* MAT locus that are also linked to the core MAT genes (STE3, HD genes) in the Trichosporonales are shown (STE11, STE12, STE20, IKS1, MYO2, RPL22). Other genes present at the MAT loci are left out for clarity. A trend towards integrating other developmental genes into the MAT loci is reflected in the recruitment of the STE12 gene and an ancestral STE11/STE20 cluster into the P/R locus. This resulted in a tetrapolar arrangement with (at least)

two alleles for each MAT locus. In the Tremellales, tetrapolarity is retained in the extant Tremella, Kwoniella, and non-pathogenic Cryptococcus lineages, whereas in the pathogenic Cryptococci, the MAT loci fused and one HD gene was lost from each MAT allele. Fusion of the MAT loci occurred independently and earlier in the ancestor of the Trichosporonales, also with loss of one HD gene, resulting in two known MAT alleles with combinations STE3a-SXI1 and STE3 α -SXI2 that differ from those in the known Cryptococcus alleles. The STE12 gene is shown in outline only to indicate that it is not part of the MAT locus in all species; STE12 may have been recruited to the P/R locus in the Tremellales-Trichosporonales common ancestor and eventually evicted from the MAT locus in the Trichosporonales possibly associated with the fusion event of P/R and HD loci, or instead STE12 was recruited to MAT only in the Tremellales. The phylogenetic relationships and inferred dates of speciation (numbers in black on tree nodes) are depicted according to [S7 Fig](#). The blue bars correspond to 95% confidence intervals.

<https://journals.plos.org/plosgenetics/article?id=10.1371/journal.pgen.1008365>

An international team of researchers has found unusual genetic features in fungi of the order Trichosporonales.

Several [fungal species](#) from the order Trichosporonales are of interest for industrial applications because they might be used for the production of biofuels. However, to explore their biotechnological potential it is necessary to learn more about their biology. An team of researchers led by Associate Professor Minou Nowrousian from the Department of Molecular and Cellular Botany of the Ruhr-University Bochum (RUB) has now analyzed 24 genomes of Trichosporonales fungi with a focus on [genes](#) that are important for sexual development. The study was performed in collaboration with the laboratory of Prof. Dr. Joseph Heitman from Duke University, U.S., who has an ongoing collaboration with the RUB and has been a visiting professor with the RUB Research School

The researchers published their results in the journal *Plos Genetics* on 6 September 2019.

The genes that regulate sexual development in fungi are called [mating](#) type genes. They must differ between mating partners to allow successful cell fusion. In fungi of the basidiomycetes, which comprise the Trichosporonales, but also well-known mushrooms like the button mushroom, the mating type genes are often located at two different positions within the genome, which are called mating type loci. However, there are species with fused mating type loci, where both loci are physically linked on the same chromosome. The chromosomes that contain the mating type loci often have functions similar to sex chromosomes in animals and plants.

Discovery of novel features



Minou Nowrousian is a molecular botany expert. Credit: RUB, Kramer

The team from Germany and the U.S. has analyzed the mating type genes in 24 species of the order Trichosporonales, and discovered physically linked mating type loci with previously unknown features.

The results showed that all analyzed Trichosporonales species have fused mating type loci with properties that are different than the properties of previously analyzed fused mating type loci in other basidiomycetes. Both the order of the genes within the fused loci as well as the sequences of the genes are highly conserved, in contrast to fused mating type loci in other basidiomycetes. This is unusual, because mating type as well as sex chromosomes tend to degenerate during evolution. The mechanisms that stabilize the Trichosporonales mating type loci will be analyzed in future studies.

More information: Ruhr-Universitaet-Bochum Sheng Sun et al. Convergent evolution of linked mating-type loci in basidiomycete fungi, *PLOS Genetics* (2019). [DOI: 10.1371/journal.pgen.1008365](https://doi.org/10.1371/journal.pgen.1008365)

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