

FUNGAL GENETICS

Determining the sequence of history

Sex-determination mechanisms are famous for their extraordinary diversity and the sequencing revolution promises to untangle the evolutionary events that have fashioned them. Joseph Heitman and colleagues do just this in a recent paper that describes the evolutionary history of the mating-type (*MAT*) locus of a human fungal pathogen, *Cryptococcus neoformans*. They also uncover some intriguing parallels between the *C. neoformans* *MAT* locus and the human Y chromosome.

In fungi, sex only occurs between compatible cell-mating types. Unusually, the *C. neoformans* *MAT* locus resembles that of both the Ascomycotina group of fungi — to which *Saccharomyces cerevisiae* belongs — and members of its own group, the Basidiomycotina. Like *S. cerevisiae*, *C. neoformans* has a bipolar mating system with a single *MAT* locus that contains two alleles, a and α . However, this locus is larger than that of *S. cerevisiae* and contains gene types that resemble the two unlinked sex-determination loci of some tetrapolar Basidiomycotina fungi. To explore how a complex sex-determining region evolved from simpler loci, the researchers compared the sequences of the *MAT* loci of two variants of *C. neoformans* and a sibling species, *Cryptococcus gattii*.

Based on the number of synonymous mutations that have accumulated over time, the researchers found that the genes within the

C. neoformans *MAT* locus could be classified as ‘ancient’, ‘intermediate’ or ‘recent’, according to when they were acquired by the *MAT* locus during evolution. They suggest that the ancient class represents the two ancestral unlinked sex determination regions — one containing pheromone and pheromone-receptor genes and one containing homeodomain genes. They hypothesize that the pheromone locus expanded to acquire other ancient components of the pheromone-signalling cascade together with some intermediate genes, and that the homeodomain locus acquired other intermediate genes thought to function during meiosis. In one of the two mating types, chromosomal translocation then fused the pheromone and homeodomain clusters together, entrapping the recent category of genes. The resulting tripolar mating system — consisting of the pheromone cluster, the homeodomain cluster and the fused cluster — then collapsed by gene con-

version into the bipolar system we see in *C. neoformans* today.

Not only does the *C. neoformans* *MAT* locus resemble other fungal sex-determination loci, but Heitman and colleagues also provide tantalizing evidence that it has similar features to the sex chromosomes of animals and plants. Curiously, the human Y chromosome also has four temporal clusters that represent the sequential acquisition of genes. The authors draw on this and other intriguing similarities — such as the palindromic orientation of the pheromone genes — and discuss the future of *C. neoformans* as a model for understanding sex-chromosome dynamics.

Jenny Bangham, Assistant Editor,
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References and links

ORIGINAL RESEARCH PAPER Fraser, J. A. *et al.* Convergent evolution of chromosomal sex-determining regions in the animal and fungal kingdoms. *PLoS Biol.* **2**, e384 (2004)

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