

 FUNGAL EVOLUTION

Amphibious selection

The skin disease chytridiomycosis, which is caused by the chytrid fungal pathogen *Batrachochytrium dendrobatidis*, has devastated amphibian populations worldwide. Writing in *mBio*, Abryamyan and Stajich describe how they used an *in silico* phylogenomic approach to identify a potential key player in *B. dendrobatidis* pathogenicity.

The phylum Chytridiomycota comprises saprophytes and parasites that infect many animals, but only one member of the phylum — *B. dendrobatidis* — is specific for

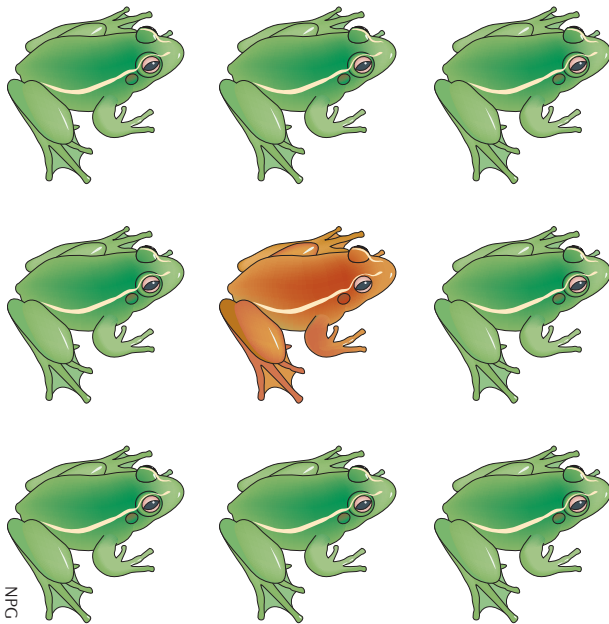
amphibians. Abryamyan and Stajich were interested in the genomic modifications that were necessary for *B. dendrobatidis* to adapt to its amphibian hosts. Lineage-specific expansion (LSE) of whole gene families or domains within genes can allow the evolution of novel functions that promote survival in new environments or in those that are subject to fluctuating conditions. On examination of the complete genome sequence of *B. dendrobatidis* isolate JEL423, the authors noted a huge expansion of a gene family containing a particular domain, carbohydrate-binding module 18 (CBM18), which is thought to bind chitin. A Pfam search found 67 copies of CBM18 in 18 different genes, with one locus containing 11 copies. This is compared with just ten copies in the entire genome of the related non-pathogenic chytrid fungus *Homolaphlyctis polyrhiza* and three copies in the genome of the saprotrophic chytrid *Spizellomyces punctatus*.

Analysis of the 67 copies of CBM18 in the *B. dendrobatidis* genome revealed that the domain is present in three main categories of genes: those carrying only CBM18 domains (designated lectin-like (LL) genes), those carrying an additional tyrosinase-like domain (TL genes) and those carrying an additional deacetylase-like domain (DL genes). Bayesian analysis allowed the authors to construct a phylogenetic tree of the domains, which supported the existence

of three monophyletic clades comprising the LL, TL and DL groups and suggested that the evolutionary trajectory of each domain is independent of the gene it is located in, indicating that these domains may be under positive selection. Phylogenetic analysis also revealed that the domain has been duplicated many times through intragenic and intergenic duplications. Analysis of the rates of synonymous and non-synonymous substitutions using both site and branch models allowed the authors to look for a signature of adaptive selection both at individual sites in the gene sequence and at specific branches in the phylogenetic tree of the domains, revealing that specific amino acids in the CBM18 domains of the LL clade are under positive selection.

Although *B. dendrobatidis* was first identified more than 10 years ago, as yet few details of the molecular mechanisms involved in its pathogenicity have been revealed. This *in silico* analysis pinpoints the expansion of the CBM18 domain as one key event in the evolution of *B. dendrobatidis* pathogenicity. Functional analysis of the CBM18-containing proteins is a top priority for future experimental research.

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