

GENOME PHYLOGENY OF GENUS RHIZOPUS

Andrii Gryganskyi

Lambert Spawn Co, Coatesville, USA

andriig@lambertspawn.com

Phylogenomic approach has the tremendous potential to resolve the inter-relationships of the fungal taxons in the order *Mucorales* within the tree of life. Species of genus *Rhizopus* are especially important as animal and plant pathogens and industrial fermenters for food and metabolite production. They are ubiquitous soil dwellers and their spores can be found literally in any soil, plant or aerial environmental sample. A dataset of 192 orthologous genes (single copy genes) was used to construct a phylogenetic tree of 21 *Rhizopus* strains, classified into four species isolated from habitats of industrial, medical and environmental importance. The phylogeny indicates that the genus *Rhizopus* consists of three major clades, with *R. microsporus* as the basal species and the sister lineage to *R. stolonifer* and two closely related species *R. arrhizus* and *R. delemar*. A comparative analysis of the mating type locus across *Rhizopus* reveals that its structure is flexible even between different species in the same genus but shows similarities between *Rhizopus* and other mucoralean fungi. The topology of single-gene phylogenies built for two genes involved in mating is similar to the phylogenomic tree. Comparison of the total length of the genome assemblies showed that genome size varies by as much as threefold within a species and is driven by changes in transposable element copy numbers, genome duplications and possibly hybridization.

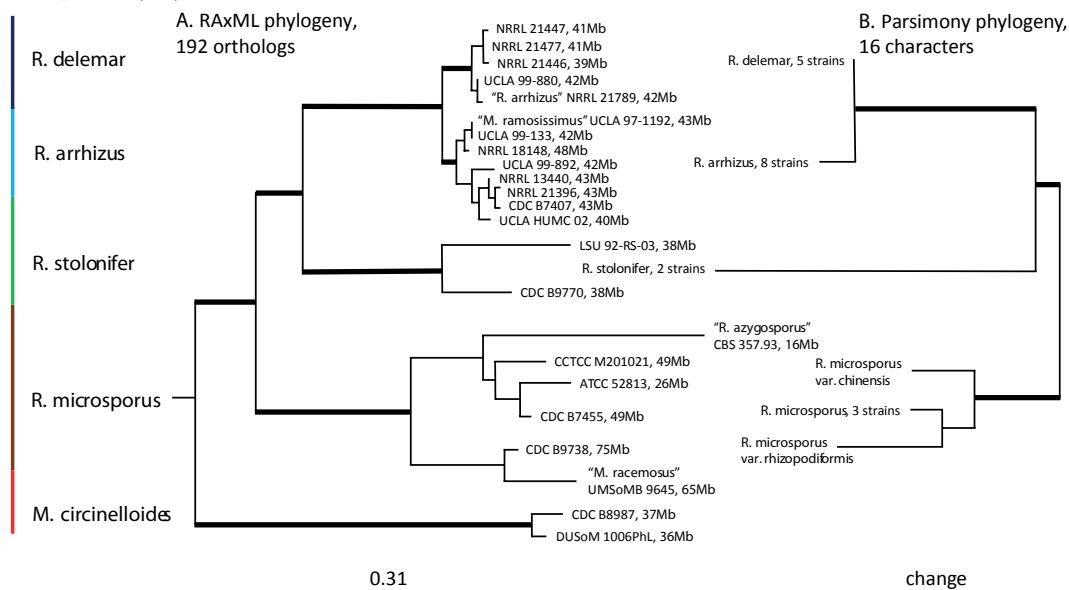


Fig. Genome-based maximum likelihood phylogeny and parsimony phylogeny based on non-molecular characters. (A) Rooted maximum likelihood tree of the genus *Rhizopus* based on 192 orthologous genes. Misidentified strains are indicated in quotes: "*Mucor racemosus*" B9645 = *R. microsporus* B9645 and "*Mucor ramosissimus*" 97-1192 = *R. arrhizus* 97-1192. Genome size is indicated in bold after the strain name. (B) Unrooted parsimony tree of 16 non-molecular (14 micromorphological and two ecological) characters. Morphological and physiological data for different strains of the same species are consolidated in the tree except for those strains that differ in at least one character. Thick branches denote statistically significant bootstrap values.