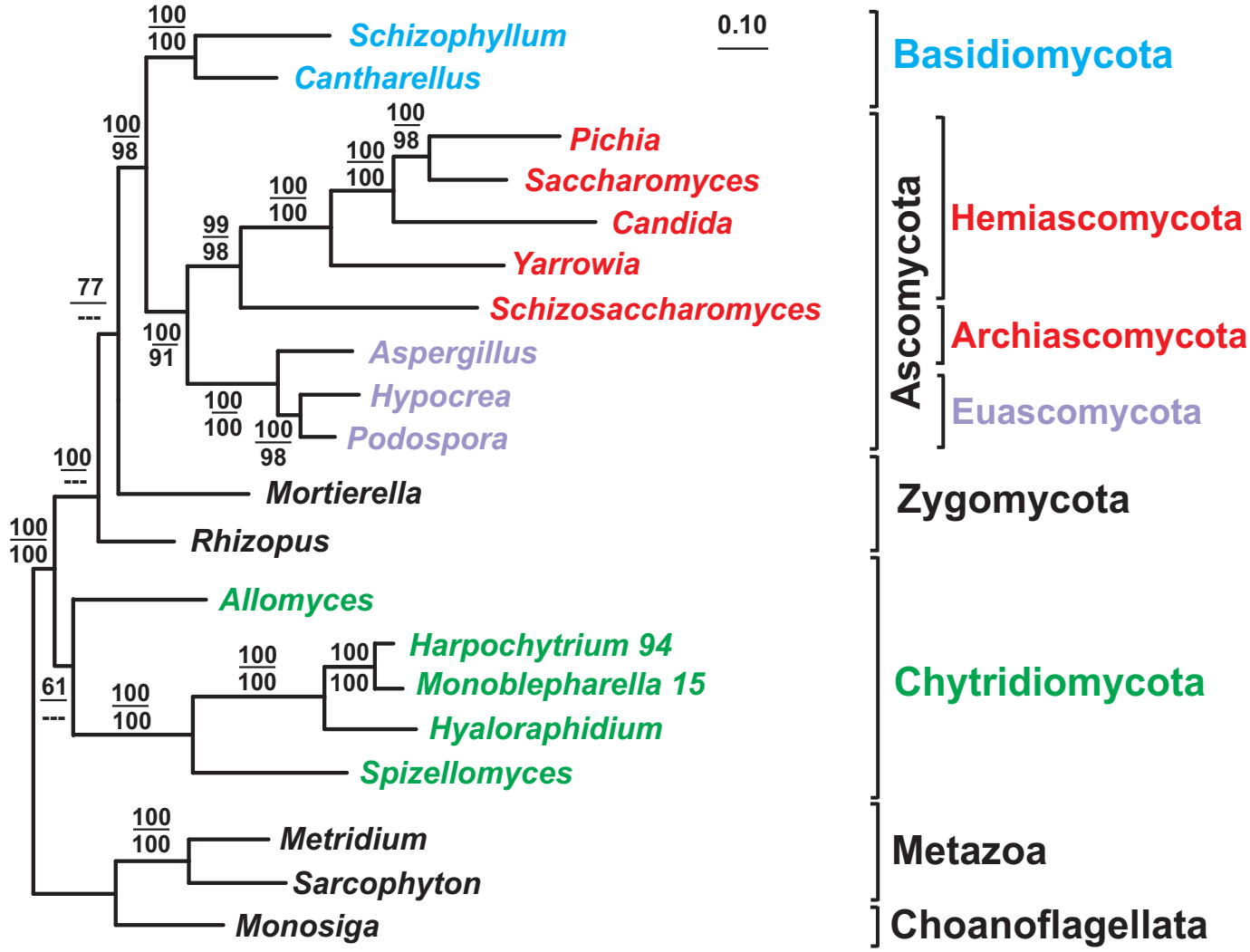
Phylogenetic analysis based on mitochondrial protein sequences



The concatenated 11 proteins (Cox1,2,3,atp6,9,Nad1,2,3,4,4L,5; except Schizosaccharomyces which has no Nad genes) were used for an ML analysis with PROML, among-site variation and the PMB model of amino acid evolution (Tillier, 2002). The upper value represents % bootstrap support with the ML method, the lower value is bootstrap support with a distance approach (PUZZLEBOOT; ML distances calculated with PUZZLE). Note that despite the high bootstrap support for Schizosaccharomyces associating with yeasts, there is no significant support for this topology with the Shimodaira/Hasegawa AU test. It needs more data to resolve this issue … Note also, that Allomyces has moved into a now monophyletic chytrid assemblage, although only with marginal support.