Fungi are a diverse kingdom of organisms which can be found in nearly every ecological niche from rainforests to deserts, oceans to prairies. Identifying and classifying members of the diverse phyla has required morphological and molecular phylogenetic approaches which have benefited from the dropping costs in sequencing genomes and transcriptomes. Phylogenomic approaches, which apply whole genome data to resolve phylogenies by identifying shared genomic content and the use of molecular phylogenetics has further improved confidence and resolution. The fungal tree of life has benefited from the myriad of efforts including the 1000 Genomes project (1KFG) which have produced more than 1500 reference quality genome sequences. I will discuss progress in understanding fungal evolution using this high-quality resource of fungal genomes and examine how some biological characteristics have been linked to genomic changes. This includes examination of the evolution of multicellularity in fungi and comparisons of genomes of extremophile fungi isolated from arid, frozen, or highly salt environments.

Rapid and inexpensive genome sequencing has also enabled approaches that generate skim-sequencing or low coverage genome sequences as opposed to single barcode marker sequencing for identification and classification. I will present new methodological results on how the ZyGoLife project (http://zygolife.org) has sequenced and assembled low coverage genomes of more than 500 strains of zygomycete fungi to examine the genetic diversity, cryptic species, and phylogenetic relationships.