

Special Interest Group meeting

Anaerobic Fungi: Genomics and Biotechnological potential

Chair: Jason Stajich (UC Riverside)

Tuesday July 17th. 7:30 to 9:00 PM (Room204 2Floor)

1) Kerstin Voigt (Jena): The evolution of basal fungi: lessons from anaerobic fungi

The kingdom Fungi represents a monophyletic group within the Opisthokonta. At a higher taxon level, the Fungi can be discriminated from the nucleariids, choanoflagellates and multicellular animals by their primarily heterotrophic-osmotrophic life style and the presence of chitin and its derivatives in their cell wall. Below-kingdom level, the Fungi split into two groups, the basal and the derived fungi. The basal fungi exhibit a monokaryotic organization of their thalli, whereas the derived fungi implement dikaryotic phases during their thallic development. From an evolutionary point of view the derived fungi (Dikarya) are younger than the basal lineages of the fungi. Unlike the Dikarya, the basal fungal lineages split into the several phyla comprising the zoosporic fungi including the anaerobic fungi, which are either paraphyletic or polyphyletic to each other. The limits and utilities of phylogenetic analyses will be discussed with respect to the recent proposals to introduce new phyla.

2) Gareth Griffith (Aberystwyth), Phylogenetics and Taxonomy of Neocallimastigomycota

The past decade have seen a doubling in the number of genera of anaerobic fungi and use of phylogenetic markers beyond ITS has clarified the relationship between the different genera. We have recently undertaken analyses using the RPB2 locus which are helpful in clarifying these relationship. One problem that persists in the persistence of several invalid names and also lack of living cultures or DNA that related to type specimens (many of which are no longer extant)

3) Yan Wang (UC Riverside): Phylogenomics and dating the divergence of the anaerobic gut fungi

The Neocallimastigomycota anaerobic gut fungi (AGF) are a monophyletic group which we estimate emerged ~74 Mya coinciding with origins of herbivory in mammals (70-95 Ma) based the BEAST analyses of 426 conserved orthologs. We examined 20+ AGF lineages using transcriptome and genome sequencing projects. Neocallimastigomycota genomes contain unique genetic elements that likely contribute to their distinct differences from sister zoosporic fungi in the Chytridiomycota. Comparative genomic exploration of Neocallimastigomycota fungi have provided more insight into the tripartite symbiosis system in the rumen environment. Our analyses suggest that AGF lineages have acquired functional Pfam domains of "Rhamnagal_lyase", "Gal_lectin", and "Cthe_2159" from plants, animals, and bacteria respectively which could be important for their ability to metabolize recalcitrant plant material and thrive in the low pH and low oxygen rumen.

4) Mostafa Elshahed, M (Oklahoma): Ecology/genomics of the Neocallimastigomycota

Recent genomic analysis provides valuable insights into the role played by horizontal gene transfer in facilitating the evolution of anaerobic gut fungi into a distinct gut dwelling lineage. Culture dependent and independent approaches strongly suggests that wild, non-domesticated animals represent an important source of hitherto unknown novel anaerobic fungal genera; and that mammalian domestication was associated by a loss of fungal diversity. Finally the utility of utilizing SMRT sequencing for PCR-based diversity surveys for assessment of anaerobic fungal diversity will be discussed.

5) Adrian Tsang (Concordia): Comparison of the transcriptomes four anaerobic fungi: *Neocallimastix frontalis*, *Piromyces rhizinflatus*, *Orpinomyces joyonii* and *Anaeromyces mucronatus*