

Ancestral traits and genomic innovations in early diverging fungi - implications for mucormycosis

We live in the genomic era which means that the whole genetic information of many species has been read. The genomic content is shaped by various factors including the way how an organism lives, reproduces and gets food. The adaptation of the organism to a particular lifestyle can shape the composition of genes. Fungi, as a very diverse group of organisms, are not only interesting for specialists but also important for the health and human economy as pathogens of crops, fermenting organisms, with additional use in bioreactors. Some fungi cause severe infections with fatal outcomes because of inefficient diagnosis and treatment. Invasive fungal infections are a growing problem in the developed countries and in COVID-19 patients. In the COVID-19 pandemic, new types of mucormycosis infection were reported and require individual consideration.

The main idea of our project is to describe how different groups of fungi cope with their environments and find the genomic features which separate one type of fungi from the other. We will navigate the fungal tree of life keeping in mind that different branches of the tree group organisms living in different ways. During this journey, we will look for genes and groups of genes which are specific for ancient fungi. We will describe which genes are present in evolutionarily old fungi (Mucorales) and which are absent in modern fungi and mammals.

This will result in a big dataset spanning many traits for each organism which will be analysed simultaneously with statistical tools. All this data together may shed new light on how we understand the relationship between organisms lifestyle and genome organisation. On the practical side, we may find new genes which may facilitate the diagnosis of invasive fungal infections or treat this disease with more efficacy than currently available drugs.