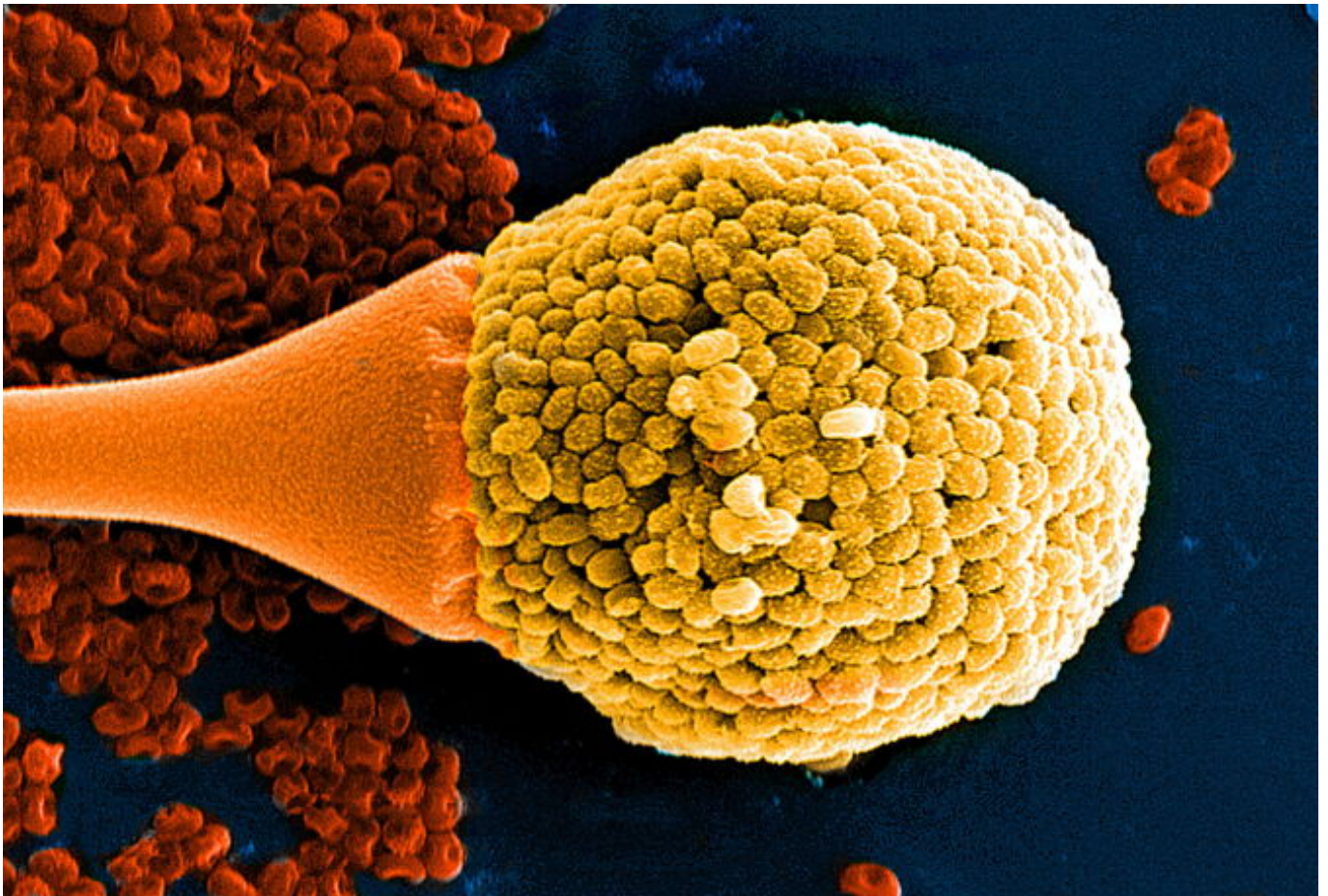


Functional genome analysis and virulence-related gene expression



Basal-lineage terrestrial fungi (formerly „Zygomycota“) exhibit a wide variety of life styles ranging from saprophytic species to pathogens of other fungi, plants and animals. Several species are known to cause infections in humans. Dependent on the causative agents the infections are classified as Mucormycosis or Entomophthoromycosis caused by members of the Mucorales and Entomophthorales, respectively. To date little is known about the molecular mechanisms involved in the infection processes of these fungal pathogens. Although regarded as uncommon fungal infections, the incidence of the mucormycosis has increased over the past few years. Out of a total of 26 species capable of causing systemic infections, *Rhizopus* spp. is the most common causative agent. However, *Lichtheimia* species are the 2nd and 3rd most serious cause of mucormycosis in Europe and the USA, respectively. We have sequenced the genomes of the two clinically most important species *L. corymbifera* and *L. ramosa*. The genomes are highly dissimilar from other mucoralean pathogens. Comparative analyses and functional characterization of the genes revealed potential virulence factors in iron-uptake and hydrolytic enzymes. Transcriptome analyses under infection-associated conditions are used to identify genes, which are necessary for the adaptation to the host environment. The insect-pathogenic fungus *Conidiobolus coronatus* is

representative for one of the most common causes of Entomophthoromycosis in humans. This species belongs to the most-basal lineage of terrestrial fungi providing an evolutionary link between terrestrial fungi and their aquatic ancestors. This project is carried out in collaboration with the department of [Molecular and Applied Microbiology](#) and the research group [Systems Biology and Bioinformatics](#).