ÁRPÁD CSERNETICS

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RESEARCH AREA

Transition from simple to complex multicellularity was a giant evolutionary innovation in the history of life. Mushroom-forming fungi are ideal model organisms of complex multicellularity: they start their lifecycle as unicellular spores thus developing multicellular filaments followed by formation of a complex fruiting body structures with various fungal tissues in the sexual cycle. Complex multicellularity appeared multiple times independently (convergent origins) in the fungal kingdom via unique mechanisms. In contrast, yeasts are secondarily simplified organisms with multicellular ancestors. They spend most of their life cycle as unicellular organisms but retain the genes for multicellular complexity. The potential for yeast-like growth (i.e. genetic toolkit) evolved early in fungal evolution but the transitions to yeast-like lifestyle happened much later multiple times and yeast-like growth became dominant independently in distantly related clades. To gain deeper insight into such evolutionary innovations we examine genome-evolution, differences in gene expression and reconstruct gene regulatory networks with comparative genomics and -transcriptomics and lab experiments. Investigating the genetic and molecular background of fungal plant cell wall degradation is also among our research interests. Lignocellulose decomposition is one of the most industrially exploited fungal traits (e.g. in bioethanol production). Our goal is to reconstruct gene regulatory networks that underlie plant biomass degrading fungal extracellular enzyme biosynthesis.

TECHNIQUES AVAILABLE IN THE LAB

Coprinopsis cinerea is our primary model system, however, several members of Basidiomycota and Ascomycota are also involved in these experiments. In addition to basic microbiological techniques, we also use state-of-the-art methods of genetics, molecular biology and bioinformatics. Of those I would like to highlight the followings: cultivation of fungi and induction of fruiting body formation, microscopy imaging techniques, DNA and RNA isolation, genome- and transcriptome (RNA-Seq) sequencing and data-analysis, protein-DNA interaction assays (identification of DNA binding sites of transcription factors with Chip-Seq, DAP-Seq and CUT&RUN), gene cloning, CRISPR/Cas9-based genome editing, heterologous protein expression, protein purification and Western-blot, phylogenetic reconstruction.

SELECTED PUBLICATIONS

Nagy, L.G., Varga, T., **Csernetics, Á.**, Virágh, M. (2020) Fungi took a unique evolutionary route to multicellularity: Seven key challenges for fungal multicellular life. **Fungal Biol Rev 34:** 151-169.

Nagy, G., Vaz, A.G., Szebenyi, Cs., Takó, M., Tóth, E.J., **Csernetics, Á.**, Bencsik, O., Szekeres, A., Homa, M., Ayaydin, F., Galgóczy, L., Vágvölgyi, Cs., Papp, T. (2019) CRISPR-Cas9-mediated disruption of the HMG-CoA reductase genes of Mucor circinelloides and subcellular localization of the encoded enzymes. **Fungal Genet Biol 129:** 30-39.

Homa, M., Galgóczy, L., Manikandan, P., Narendran, V., Sinka, R., **Csernetics, Á.**, Vágvölgyi, Cs., Kredics, L., Papp, T. (2018) South Indian isolates of the Fusarium solani species complex from clinical and environmental samples: identification, antifungal susceptibilities, and virulence. **Front Microbiol 9:** 1052.

Nagy, G., Szebenyi, Cs., **Csernetics, Á.**, Vaz, A.G., Tóth, E.J., Vágvölgyi, Cs., Papp, T. (2017) Development of a plasmid free CRISPR-Cas9 system for the genetic modification of Mucor circinelloides. **Sci Rep 7:** 16800.

Csernetics, Á., Nagy, G., Iturriaga, E.A., Szekeres, A., Eslava, A.P., Vágvölgyi, Cs. and Papp, T. (2011) Expression of three isoprenoid biosynthesis genes and their effects on the carotenoid production of the zygomycete Mucor circinelloides. **Fungal Genet Biol 48:** 696-703.