

## LÁSZLÓ NAGY



**Biological Research Centre  
Institute of Biochemistry**

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## RESEARCH AREA

We are interested in the general principles of genomes evolution, that of the evolution of organismal complexity, fungal development and their biotechnological applications. Fungi are the most ubiquitous microbes in modern biotechnology which, despite centuries of research, offer huge unharnessed potentials. Our research focuses on gene regulatory networks underlying fungal morphogenesis and the degradation of complex plant polysaccharides (e.g. lignocellulose). Complex plant polysaccharides, such as lignin and cellulose, are the most abundant repositories of sequestered carbon on Earth. Fungi can most efficiently reintroduce this sequestered carbon into the carbon cycle, contributing a key step to ecosystem functioning worldwide. However, the genes and gene regulatory networks that underlie the fungal decomposition of complex plant biomass are unknown. Gene regulatory networks are finely tuned circuits that regulate precise spatial and temporal expression of genes. We use modern -omics, genetic, phylogenetic and bioinformatic approaches to uncover the evolutionary origins and genetic bases of fungal morphogenesis, multicellularity and to translate basic research results into biotechnological applications.

## TECHNIQUES AVAILABLE IN THE LAB

Students applying to our research group can learn diverse techniques in the field of bioinformatics, modern high-throughput-omics, molecular and microbiology. We employ a wide repertoire of molecular biology methods, including polymerase chain reaction (PCR), gene knockout, CRISPR-Cas9, vector construction, protein and gene expression visualisation and various microscopy techniques. Of '-omics' methods, we employ genomics, genome-sequencing, transcriptome sequencing and perform bioinformatic analyses of data generated by these approaches. We employ state of the art long-read technologies (NanoPore). We use diverse bioinformatic pipelines for data-analysis, phylogenetic reconstruction, molecular clock, comparative genomic questions as well as develop novel algorithms and routines.

## SELECTED PUBLICATIONS

Varga, T., et al., **Nagy, G.L.** (2019) Megaphylogeny resolves global patterns of mushroom evolution. **Nat Ecol Evol** **3**: 668-678.

Krizsán, K., et al., **Nagy, G.L.** (2019) A transcriptomic atlas of mushroom development highlights an independent origin of complex multicellularity. **Proc Natl Acad Sci USA** **116**: 7409-7418.

Kiss, E., Hegedus, B., Varga, T., Merenyi, Z., Koszo, T., Balint, B., Prasanna, A.N., Krizsan K., Riquelme, M., Takeshita, N., **Nagy, L.G.** (2019) Comparative genomics reveals the origin of fungal hyphae and multicellularity. **Nat Commun** **10**: 4080.

**Nagy, G.L.**, Kovács, G.M., Krizsán, K. (2018) Complex multicellularity in fungi: evolutionary convergence, single origin, or both? **Biol Rev Camb Philos Soc** **93**: 1778-1794.

Sipos, G., et al., **Nagy, G.L.** (2017) Genome expansion and lineage-specific genetic innovations in the forest pathogenic fungi *Armillaria*. **Nat Ecol Evol** **1**: 1931-1941.