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RESEARCH AREA

During my work I focus on the genetic background of the evolution of complex multicellularity in fruiting body forming fungi. In the kingdom of Fungi, complex multicellularity emerged 8-11 times indenpendently. In fungi, the highest manifestation of complex multicellulratiy is the formation of their sexual reproductive structure, the fruiting body. Some fruting body consits of more than 30 different cell type. The molecular background of the differentiation of these cell types is ,mostly unkown. The main focus of my work are the gene regulatory networks underlying the differentiation of certain cell types along with the cytoskeletal changes that determine the shape of these cells. Using comparative genomics and transcriptomics we identified several conserved regulators, that – based on their expression pattern – might play a role in fruiting body formation. I participate in the identification and functional chatracterization of these regulatrors. Furthermore, using molecular biology, histology and fluorescent microscopy I investigate the shape and the cytoskeleton of certain fruiting body cells with a special focus on the septin cytoskeleton.

TECHNIQUES AVAILABLE IN THE LAB

Molecular cloning (PCR, bacterial transformation, restriction enzyme based cloning, Gibson assembly), genetic manipulation of fungi, protein expression and purification (SDS-PAGE, Western blot), fluorescent microscopy, histological section preparation from fruiting bodies, bioinformatics (statistics in R, functional genomics, transcriptomic analysis).

SELECTED PUBLICATIONS

Merényi, Zs., **Virágh, M.**, Gluck-Thaler, E., Slot, JC., Kiss, B., Varga, T., Geösel, A., Hegedüs, B., Bálint, B., Nagy, LG. (2022) *Gene age shapes the transcriptional landscape of sexual morphogenesis in mushroom forming fungi (Agaricomycetes).* **Elife. 11:** e71348.

Virágh, M., Merényi, Zs., Csernetics, Á., Földi, Cs., Sahu, N., Liu, XB., Hibbett, DS., Nagy, LG. (2022) *Evolutionary Morphogenesis of Sexual Fruiting Bodies in Basidiomycota: Toward a New Evo-Devo Synthesis.* **Microbilol Mol Boil Rev. 86:** e00019-21.

Hage, H., Miyauchi, S., **Virágh, M.**, Drula, E., Min, B., Chaduli, D., Navarro, D., Favel, A., Norest, M., Lesage-Meessen, L., Bálint, B., Merényi, Zs., Eugenio de, L., Morin, E., Martínez, TA., Baldrian, P., Štursová, M., Martynez, MJ., Novotny, C., Magnuson, JK., Spatafora, JW., Maurica, S., Pangilinan, J., Andreopoulos W., LaButti, K., Hundley, H., Na, H., Kuo, A., Barry, K., Lipzen, A., Henrissat, B., Riley, R., Ahrendt, S., Nagy, GL., Grigoriev, IV., Martin, F., Rosso, MN. (2021) *Gene family expansions and transcriptome signatures uncover fungal adaptations to wood decay.* **Environ Microbiol. 23:** 5716-5732.

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

Kiss, E., Hegedüs, B., **Virágh, M.**, Varga, T., Merényi, Zs., Kószó, T., Bálint, B., Prasanna, AN., Krizsán, K., Kocsubé, S., Riquelme, M., Takeshita, N., Nagy GL. (2019) *Comparative genomics reveals the origin of fungal hyphae and multicellularity.* **Nat Commun. 10:** 4080.

Krizsán, K., Almási, É., Merényi, Zs., Sahu, N., **Virágh, M.**, Kószó, T., Mondo, S., Kiss, B., Bálint, B., Kües, U., Barry, K., Cseklye, J., Hegedüs, B., Henrissat, B., Johnson, J., Lipzen, A., Ohm, RA., Nagy, I., Pangilinan, J., Yan, J., Xiong, Y., Grigoriev, IV., Hibbett, DS., Nagy, LG. (2019) *Transcriptomic atlas of mushroom development reveals conserved genes behind complex multicellularity in fungi.* **Proc Natl Acad Sci U S A. 116:** 7409-7418.