Volume 59(1):91-101, 2015
Acta Biologica Szegediensis
http://www2.sci.u-szeged.hu/ABS

Unitary GABAergic volume transmission from individual interneurons to astrocytes in the cerebral cortex

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Communication between individual GABAergic cells and their target neurons is mediated by synapses and, in the case of neurogliaform cells by a unitary form of volume transmission. Effects of non-synaptic volume transmission might involve non-neuronal targets and astrocytes not receiving GABAergic synapses but expressing GABA receptors are suitable for evaluating this hypothesis. Testing several cortical interneuron types in slices of the rat cerebral cortex, we show selective unitary coupling from neurogliaform cells to astrocytes with a fast, $GABA_A$ receptor and GABA transporter mediated component and a slow component that results from the activation of $GABA_B$ receptors on neurons. Unitary GABAergic responses failed to produce Ca^{2+} influx in astrocytes but were able to significantly hyperpolarize the reversal of nearby $GABA_A$ receptor mediated synapses. Our experiments identify a presynaptic cell type specific, GABA mediated communication pathway from individual neurons to astrocytes suggesting a role for unitary volume transmission in the control of ionic and neurotransmitter homeostasis.

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Macroevolutionary investigations on fungal models: The origins of taxonomic diversification in the order Agaricales

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One of the hot topics of current evolutionary biology is macroevolution. Macroevolution basically constitutes the study of the mechanisms behind speciation, diversification and adaptation processes, which are thought to have shaped the biological diversity as we see today and its history presented by fossils. One of the central concepts is adaptive radiation, i.e. when explosive speciation takes place in a geologically short time. These processes have been extensively studied in plants and animals yet we have limited knowledge as to what were the key contributing factors to the functional, life-history, and ecological diversity displayed by fungi today. Therefore our research project targets one group of fungi, the order Agaricales based on previous results at our department to address these questions. The Agaricales is the most species-rich group of the Basidiomycota, numbering ca. 480 genera and 14,000 described species. However, the forces driving speciation and evolutionary diversification in these mushrooms are poorly known. Understanding why and how certain lineages became extremely species-rich, while others are only represented by a few species and determining the timing of major lineage expansions are questions of utmost importance in basic research with important implications in conservation and classification.

To address these questions, we use statistical models of lineage diversification in a phylogenetic framework. Modelling of diversification relies on a new two-gene dataset (referred to as diversity dataset) for ca. 3,000 species. We selected the nLSU and RPB2 loci, which are known to provide sufficient phylogenetic information for relationships at the infrageneric level. In addition to the diversity dataset, a phylogenomic dataset is also being produced from the accessible whole genomes of basidiomycetous fungi, meaning about 60 to 100 species. We will use these two datasets to examine general patterns of speciation and extinction, to identify shifts in diversification rates and whether transitions between different fruit body types have an effect on speciation and extinction rates. We compiled a taxon database for all accepted genera in the Agaricales, which we used to estimate the appropriate species number per genus for a balanced sampling strategy scaled to 3,000 species. Preliminary analyses highlighted the patchy distribution of LSU and RPB2 in GenBank, which makes balanced sampling and dataset-assembly for large-scale investigations difficult. To overcome this, during the ADiv we are generating multiple LSU and RPB2 sequences using standardized protocols, resulting in universally applicable sequences that can be later leveraged for other projects too, including barcoding. In the first two years, we isolated DNA from 2,200 species, and sequenced the first ca. 1.5 kb of the LSU gene in 1,400 of these. In the third year, we continue with sequencing and commence diversification analyses using our datasets.

This study was supported by the Hungarian Scientific Research Fund (OTKA NN 106394).

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