**Oral Session 3**  
[Diversity, Phylogeny & Ecology of Agaricomycotina]

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A transcriptomic atlas of mushroom development reveals conserved genes behind fruiting body development

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**Purpose:** Mushroom formation is one of the most spectacular and complex processes in the fungal world, comparable to the development of higher plants and animals in terms of its complexity. Yet, its genetic bases, in particular, conserved developmental genetic events are hardly known. Here we identify conserved developmentally regulated genes in fruiting body transcriptomes of six Agaricomycetes, *Coprinopsis cinerea, Rickenella mellea, Phanerochaete chrysosporium, Armillaria ostoyae, Schizophyllum commune* and *Lentinus tigrinus.*

**Methods:** We obtained developmental transcriptome data for the entire course of fruiting body development of these species and inferred the phylogenetic history of developmentally regulated genes in a dataset of 202 genomes.

**Results:** We find that 10-40% of the genes are differentially regulated during fruiting body development in the examined species, comprising functions related to cell wall synthesis and modification, mRNA stability, cell growth and regulation of transcription, among others. By studying the conservation of developmentally genes and their evolution through a comparative analysis of 202 fungal genomes, we aim to understand the origins of fruiting body-related genes and to understand the minimal gene set required to initiate and develop agaricomycete fruiting bodies.

**Conclusion:** This is the first systematic comparative analysis of developmentally regulated genes in mushroom-forming fungi, and illuminates some of the conserved functionalities that fungi deploy during fruiting body development.