

Evolutionary transition to the ectomycorrhizal habit in the genomes of a hyperdiverse lineage of mushroom-forming fungi

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Abstract

The ectomycorrhizal (ECM) symbiosis has independently evolved from diverse types of saprotrophic ancestors. In this study, we seek to identify genomic signatures of the transition to the ECM habit within the hyperdiverse Russulaceae. We present comparative analyses of the genomic architecture and the total and secreted gene repertoires of 18 species across the order Russulales, of which 13 are newly sequenced, including a representative of a saprotrophic member of Russulaceae, *Gloeopeniophorella convolvens*. The genomes of ECM Russulaceae are characterized by a loss of genes for plant cell wall-degrading enzymes (PCWDEs), an expansion of genome size through increased transposable element (TE) content, a reduction in secondary metabolism clusters, and an association of small secreted proteins (SSPs) with TE 'nests', or dense aggregations of TEs. Some