

# Evolutionary relationships between the laccase genes of Polyporales

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Laccase (benzenediol:oxygen oxidoreductases, EC 1.10.3.2) is one of the oldest studied enzymes. Over the years, countless number of reviews and original articles were devoted to different structural, functional, biological, ecological and biotechnological aspects of laccases. Nevertheless, much remains to be discovered about this enzyme. As it was already pointed out: “laccases are a never-ending story”. Here we present our recent discoveries regarding evolutionary history of laccases of Polyporales fungi. These discoveries were previously published in: Savinova OS et al. (2019) *Front Microbiol* 10, 152; and to some extent were previously published in: Moiseenko KV et al. (2019) *Microorganisms* 7(11), 527. Fungal genomes almost always contain several non-allelic copies of laccase genes - laccase multigene families; however, evolutionary history of these families and their relationships among them are mostly unknown. In the presented work, a gene-tree/species-tree reconciliation analysis for the laccase multigene families from 28 wood-decaying fungal species from the Polyporales order was performed. The sample included representative fungi from all four main Polyporales clades: the Core Poliporoid, the Antrodia, the Phlebioid, and the Residual Polyporoid. The results of the analysis suggest that all Polyporales laccases derived from a single ancestral gene. Extensive duplications of this gene began almost immediately after the splitting of the Polyporales order into its four main clades, and continued with the evolution of the angiosperms, which may be a consequence of the conquest of new ecological niches by the fungi. This work was partially funded by the Russian Foundation for Basic Research, Grant No. 19-04-01183.