Comparative analysis of transcriptomes of different morphological structures of the basidiomycete *Lentinus edodes*

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Key message. A comparative analysis of transcriptomes at the vegetative and generative stages of the development of *Lentinus edodes* basidiomycetes was carried out. The nature of differential gene expression was described, and the activated/repressed metabolic pathways were visualized.

Keywords: Basidiomycetes morphogenesis, sequencing, analysis of transcriptome profiles, differential gene expression

The xylotrophic basidiomycete *L. edodes* (shiitake) is an important and popular culture in terms of biotechnological use. However, many questions remain unclear regarding the molecular-physiological aspects of the morphogenetic development of basidiomycetes. The purposes of this study are to comparatively analyze the transcriptomes of morphological structures that are sequentially formed during the ontogenesis of this type of macromycete and to characterize the differences in the physiological processes occurring at these stages. We carried out a comparative analysis of the transcriptomes of *L. edodes* nonpigmented vegetative mycelium, brown mycelial mat, primordia, and fruit bodies, describing the nature of differential gene expression (DEG). The analysis used high-throughput sequencing methods and the Illumina HiSeq 2500 platform. DEG was classified by functional category by using information from the KEGG and Gene Ontology databases (Blast2Go), as well as the BioCyc web resource. It was found that in a brown mycelial mat, 10216 genes were differentially expressed, as compared with the nonpigmented mycelium. The expression of 5166 genes was activated, and that of 5050 genes was repressed. At the generative stages of development relative to the vegetative mycelium, 5395 genes were differentially expressed in primordia. Of these, 2775 genes were activated and 2620 genes were repressed. In fruit bodies, 5567 genes were activated and 5634 were repressed (11201 DEG in total). At the stage of the mycelial mat, preceding fruiting, as in the basidiomas themselves (relative to the vegetative mycelium), there was activation of the categories associated with G-proteins (Rho protein signal transduction, heterotrimeric G-protein complex, G-protein coupled receptor activity, Rho guanylnucleotide exchange factor activity), which are important components of signaling pathways, also including MAP-kinases (MAPK signaling pathway, AMPK signaling pathway, and sphingolipid signaling pathway). The activated pathways also included metabolic pathways associated with lipid and pigment biosynthesis (fatty acid metabolism, biosynthesis of unsaturated fatty acids, melanogenesis), cysteine, lysine, tryptophan (cysteine biosynthesis, lysine biosynthesis, tryptophan biosynthesis), phenolic compounds (chorismate biosynthesis, tryptophan biosynthesis), as well as with ion transport, including metal ion transport, copper ion binding, iron ion transmembrane transporter activity, and calcium ion transmembrane transporter activity. The activated categories were those responsible for programmed cell death (phagosome, ubiquitin-mediated proteolysis, mitophagy, apoptosis), intercellular contacts and the cytoskeleton (gap junction, regulation of actin cytoskeleton, focal adhesion, carbohydrate-binding glycoproteins), and cell differentiation of walls and biogenesis of cell wall (cell wall biogenesis, chitin biosynthetic process, phenol oxidase, glucanase, chitinase and chitin synthase). The functional categories related to the storage, transmission, and realization of genetic information (DNA replication, purine metabolism, mismatch repair, nucleotide excision repair, RNA polymerase, ribosome biogenesis in eukaryotes, spliceosome, ribosome, non-homologous end-joining) at the stage of the mycelial mat and in primordia were saturated with repressed genes. However, in the fruit bodies, the genes of these categories were activated, as were the groups of genes associated with intercellular transport of substances (protein export, SNARE interactions in vesicular transport, endocytosis). The categories saturated with repressed genes at the stage of the mycelial mat and activated in the basidiomas included those related to cell division (mitotic cell cycle cytoskeleton-dependent cytokinesis, regulation of the cell cycle, mitotic cytokinesis) and to the proteasome-dependent degradation of biopolymers (proteasome accessory complex, proteome complex, proteasome regulatory particle). Thus, the analysis of the transcriptomes and the visualization of the activated/repressed metabolic pathways in different morphological structures of the fungus made it possible to identify the physiological peculiarities of *L. edodes* during ontogenesis.