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Genomics, transcriptomics, proteomics, and biochemistry of white-rot basidiomycete *Trametes hirsuta* 072

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Wood-rotting fungi are organisms with the highest natural capacity to degrade lignocellulose substrates, which is enabled by complex systems of extracellular enzymes, whose expression and secretion depend on the nature of the environment. We sequenced and assembled the complete genome of the white rot saprotrophic fungus *Trametes hirsuta* 072 (Basidiomycota, Polyporales) providing a framework for studies of gene transcription, translation, and secretion of essential fungal proteins. The genome sequence is assembled in 13 chromosomes and a circular mitochondrion, and it is partially annotated. Our transcriptomic and proteomic studies are focused primarily on ligninolytic oxidases and enzymes providing degradation of cellulose and hemicellulose. Our results identified seven laccase genes containing exons and introns, including the respective promoter regions. We found 18 ligninolytic peroxidase genes encoding nine putative lignin peroxidases, seven putative short manganese peroxidases, and two putative versatile peroxidases. The expression of the genes at various conditions of the fungal growth was studied on the transcriptomic and proteomic levels. Only a few genes encoding ligninolytic, cellulolytic, and hemicellulolytic enzymes were expressed in large quantities providing specific response of the fungus to the particular conditions of growth.

Biography

Andrey R Pavlov is currently working as a Research Scientist in Fidelity Systems, Inc., Gaithersburg, Maryland, USA.

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