

Transcriptome analysis reveals the underlying mechanism of nanocomposite packaging in delaying quality deterioration of *Flammulina velutipes*

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Abstract

To expound the molecular mechanism of nanocomposite packaging material (Nano-PM) in delaying quality deterioration of *Flammulina velutipes* during storage, transcriptome analysis was conducted to observe the changes of gene expression in *F. velutipes* that was packaged in Nano-PM, polyethylene packaging material (Normal-PM) and no packaging material (No-PM). In comparison with Normal-PM, 379 differentially expressed genes (DEGs) were identified in Nano-PM packaged *F. velutipes*, comprising of 161 up-regulated genes and 218 down-regulated genes. Gene Ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG) enrichment analysis indicated that Nano-PM improved the stress resistance of *F. velutipes* by up-regulating *RBOHF* and *msp2*, which were related to reactive oxygen species (ROS) metabolism. Nano-PM also ensured sufficient energy supply by regulating oxidative phosphorylation and glycolysis/gluconeogenesis. Moreover, the regulation of gene expression also delayed programmed cell death (PCD) and lignification. Furthermore, the quantitative real-time PCR (qRT-PCR) results were also in accordance with transcriptome analysis. Therefore, Nano-PM could regulate the expression of specific genes, which in turn alleviated quality deterioration of *F. velutipes* during storage.