

Label-free proteomic quantification of packaged *Flammulina filiformis* during commercial storage

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Abstract

Fresh *Flammulina filiformis* is perishable and undergoes dynamic postharvest changes in physiological metabolism and biochemistry. In this study, we use label-free quantitative proteomics to elucidate the mechanisms of *F. filiformis* responses to cold storage and internal packaging stimuli. External quality including weight, browning, stipe elongation and cap opening were characterized during 21 d of commercial storage at 4 °C. Among the 291 proteins identified from fresh and stored *F. filiformis*, we detected 39 upregulated and 73 downregulated differentially expressed proteins (DEPs). After 9 d of storage, 19 % of the upregulated DEPs were involved in the tricarboxylic acid (TCA) cycle, whereas 32 % of the downregulated DEPs were associated with translation. At the end of the storage period, the Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway analysis indicated that most DEPs were involved in antibiotics biosynthesis, carbon metabolism and amino acid metabolites. Our results illuminate the biological processes occurring in *F. filiformis* under commercial storage conditions and provide a theoretical basis for the quality control of fresh *F. filiformis*.