

Abstract

Moisture absorption and bacterial growth are critical factors for quality deterioration of freeze-dried *Agaricus bisporus*. In order to explore the bacterial composition and the resultant odor changes in freeze-dried *A. bisporus* during storage under three typical conditions (RT: 25°C, 55% RH; HT: 37°C, 85% RH; AT: ambient temperature), bacterial diversity and communities were analyzed using metagenomics. Moreover, volatile compounds were determined using SPME-GC-MS. The results demonstrated that the bacterial composition in freeze-dried *A. bisporus* was dominated by *Pseudomonas*, followed by *Rhizobium* and *Pedobacter*. In addition, *Mucilaginibacter*, *Flavobacterium*, and *Thermus* were a few other genera more dominant in HT samples, *Chryseobacterium* was the other genera more dominant in AT samples, while, *Sphingobacterium* and *Chryseobacterium* were a few other genera more dominant in RT samples. Furthermore, the increase of benzaldehyde content in HT samples may have been induced by the growth of Pseudomonads and the esters production in RT and AT samples might have been induced by *Chryseobacterium*. This study provided comprehensive information on exogenous bacterial composition and the resultant odor in freeze-dried *A. bisporus*. These results may be a theoretical basis for quality control and quick quality detection based on volatiles of freeze-dried *A. bisporus*.