

ABSTRACT

TATI BARUS. Role of Bacterial Community in Tempe Bitter Taste Formation: Microbiological and Terminal Restriction Fragment Length Polymorphism (T-RFLP) Analysis. Under direction of ANTONIUS SUWANTO, ARIS TRI WAHYUDI, and C. HANNY WIJAYA.

Soybean tempe, referred to as tempe, is an indigenous fermented food of Indonesia. It has a variety of tastes, sometimes with a hint of bitterness, which may differ in intensity. The cause of bitterness in tempe has never been reported previously. Thus, the aim of this study is to investigate the role of bacteria community in the formation of bitter taste in tempe. Sensory test was carried out in order to determine the scores of bitterness intensity in tempe. Sensory test on EMP, WJB, CLR, DRG, and MLB tempe showed that EMP tempe had the highest score of bitterness (2.3) and WJB had the lowest (1.3). The intensity of bitterness in EMP and WJB was significantly different, which was not directly caused by the processing method. It was also revealed that the mould had no impact on the difference of bitterness intensity in EMP and WJB. *Rhizopus oligosporus* and *Mucor* sp. were isolated from both EMP and WJB tempe with abundance, i.e 3.4×10^5 and 3.5×10^3 CFU g^{-1} in EMP; and 3.8×10^5 and 4.8×10^3 CFU g^{-1} in WJB. The difference in the abundance and the types of bacteria found in EMP and WJB tempe may result in the difference of bitterness intensity. Plating analysis showed that soaking water and fresh tempe of EMP contained a higher number of bacteria than WJB. Soaking water of EMP tempe contained a higher number of *Enterobacteria*, approximately 5×10^3 fold, and spore-forming bacteria groups 3×10^2 fold compared to WJB. Similarly, the number of total mesophilic bacteria, *Enterobacteria*, and spore-forming bacteria in fresh EMP tempe are 5×10^2 , 2×10^2 and 2×10^1 fold, respectively, higher than those in fresh WJB tempe. Based on the sequencing of 16S rRNA gene, the dominant mesophilic bacteria grown on PCA media in EMP tempe were *Acetobacter indonesiensis*, *Bacillus subtilis*, *Klebsiella* sp., and *Flavobacterium* sp. while those in WJB tempe were *Klebsiella* sp., *Bacillus pumilus*, *Brevundimonas* sp., *Acinetobacter* sp. and *Pseudomonas putida*. *Bacillus*, a group of proteolytic bacteria, was found at 9×10^4 fold higher in the soaking water of EMP compared to the one of WJB. Based on bacterial community analysis using T-RFLP, it was also shown that bacterial abundance in soaking water of EMP tempe is 40%-119% higher. The major difference (119%) was found after 7 hours soaking. Similarly, bacterial abundance in fresh EMP tempe was 62% higher than the one in fresh WJB tempe. Bacterial communities in EMP and WJB tempe were also dominated by different types of bacteria. T-RFLP results also demonstrated that the types of bacteria involved during tempe processing consisted of both culturable and unculturable bacteria. The latter group was more dominant compared to the former.

Keywords: tempe, bitter taste, bacteria community analysis, T-RFLP