

Dynamics of microbial community during tempeh fermentation

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Abstrak

Tempeh is sliceable soybean-cake fermented by *Rhizopus oligosporus*. Various bacteria were detected in tempeh employing cultivation technique with limited information about their origin or sources. The present study aimed to examine the source/s of bacterial community in tempeh by combining metagenomics analysis and cultivation technique. Samples were obtained from a number of steps in tempeh production employing two-times boiling of soybean (WJB tempeh production). All samples were plated on Enterobacteriaceae and Lactic Acid Bacteria medium. Total DNA were extracted directly from tempeh for metagenomics analysis, employing High-Throughput Sequencing (HTS) and cloned 16S rRNA genes. Firmicutes and Proteobacteria were the predominant and second dominant bacteria existed in fresh tempeh (FT) obtained by metagenomics analysis. In contrast, cultivation technique showed that Proteobacteria was the predominant phylum, suggested that most of the Firmicutes were not culturable. FT was dominated by *Lactobacillus* and *Acetobacter*. Both FT and soaking water (SW) were dominated by same species of *Lactobacillus*, i.e. *L. delbreuckii* and *L. mucosae*, indicated that SW was probably the source of bacterial community established in the final product of fermentation. Predominant bacteria in starter culture (SC), *Acinetobacter*, was not detected in FT, indicating that bacteria in SC might not play significant role in bacterial community development in FT.