Yeast community of Indonesian tempeh based on ITS-PCR T-RFLP analysis

Abstract
Tempeh is the most highly consumed traditional fermented food in Indonesia. It is a product of a mixed microbial fermentation which harbors various types of molds, yeasts, and bacteria. Previous studies indicated that tempeh production methods might affect yeast population. However, studies of yeast community structure and population dynamics during tempeh production using DNA directly extracted from tempeh has not been reported. This research aimed to study the effect of two different tempeh production methods (method A and B) on yeast community phylotypes at five stages of tempeh production. The yeast community was estimated by PCR amplification of ITS1-5.8S rRNA-ITS2 DNA sequence, followed by T-RFLP analyses. Boiled soybean and tempeh at different stages of fermentation was used as a source of metagenomic DNA. The result indicated that many yeast phylotypes were found in all stages of both tempeh production methods. There are two groups of yeast community phylotypes in tempeh produced by method A, and three groups of yeast community phylotypes in tempeh produced by method B. Nine phylotypes were found to be common and two of them predominant in both tempeh samples. Some phylotypes might be specific in one of the stages or in the tempeh production methods.

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