

Preliminary screening of bacterial and fungal communities from spontaneous fermentation of Durian pulps (*tempoyak*) using high-throughput amplicon sequencing

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ABSTRACT

Fermentation is a method used to prolong the shelf-life and taste of fruit. Tempoyak is a fermented food made from durian pulps. Accumulating works were conducted to isolate and characterize the microbial communities using culture-dependent methods, with little effort in identifying the diversity using culture-independent approaches like next-generation sequencing (NGS) in tempoyak. The culture-dependent method showed several limitations such as tedious technique in plating, biasness in morphological identification and incompatibility of media selection for microbial growth. To date, the NGS allowed identification of the unculturable microbes up to species level. The purpose of this study is to screen the microbial communities in tempoyak using amplicon sequencing by targeting 16S rRNA and ITS2 for determining the diversity of bacterial and fungal communities respectively. On the other hand, this study also compared the complex microbial structure from the first day, T₀ to day 14, T₁₄ of the fermentation process. Here, we observed that sample T₁₄ showed more diverse in both bacterial and fungal populations as compared to sample T₀. Overall, genus *Lactobacillus* are the most abundant microbes representing the bacterial community. This study highlighted the importance of the NGS in characterizing the complex microbial communities in fermented food, for which could be useful to screen for potential unculturable microbial communities hindered by the limitation of culture-dependent approach.

KEYWORDS

Microorganisms; Amplicons; Fermentation process; Food

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