

Microbiota community structure in traditional fermented milk dadiah in Indonesia: Insights from high-throughput 16S rRNA gene sequencing

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Abstract

Dadiah is an Indonesian traditional fermented milk and is neither pasteurized nor boiled, but no food poisoning has been reported to date. Microbiota inhabiting dadiah has never been fully explored. In this study, we performed deep sequencing of 16S ribosomal RNA genes extracted from 11 dadiah samples and analyzed the dadiah microbiota at the genus level. We found that *Lactococcus*, *Lactobacillus*, and *Leuconostoc* were predominant among the dadiah microbiota. Unexpectedly, *Klebsiella* and *Chryseobacterium*, potential pathogens, were also found in some of the dadiah samples. There was little difference in the microbiota among samples taken from the same bamboo tube. In contrast, there were differences between the dadiah microbiota from different bamboo tubes, even those collected from the same sampling area. Furthermore, the composition of the dadiah microbiota showed large differences between sampling areas. We believe that our findings will lead to further improvement in the preparation of dadiah.

Key words: Dadiah, fermented buffalo milk, deep sequencing, 16S ribosomal RNA, microbiota