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## Metagenetic Analysis of the Bacterial Community Composition and Dynamics in Fermenting Enset (*Ensete ventricosum*)

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### Abstract

Enset (*Ensete ventricosum*) provides staple food for over 15 million people in Ethiopia after fermentation into kocho. The fermentation has hardly been investigated and is prone to optimisation. The aim of this study was to assess the bacterial community composition and its dynamics during enset fermentation using Illumina Miseq sequencing. To this end, three predominantly used enset varieties (Gena, Maze and Ketishe) were processed and allowed to ferment for two month in a bamboo basket, also called ‘erosa’. For each variety, fermenting enset samples from days 1, 7, 17, 31 and 60 were subjected to high-throughput 16S ribosomal RNA gene sequencing via the Illumina MiSeq platform. A visual comparison between bacterial community compositions from different fermentation days (non-metric multidimensional scaling) showed that samples were highly dissimilar on day 1, both between and within different varieties. During fermentation, samples evolved to a more similar bacterial community composition and as from day 31 and continuing until day 60, samples from all varieties had reached a comparable bacterial community composition. The most important similarities on day 1 were the presence of a bacterium assigned to the family Enterobacteriaceae with a relative abundance of 22.9 %, 28.2 % and 17.7 % and the lactic acid bacterium *Leuconostoc mesenteroides* (29.7 %, 9.5 % and 13.9 %) for Gena, Maze and Ketishe, respectively. In addition, the varieties Gena and Ketishe harbored the aerobic bacterium *Nocardiopsis* sp. (14.2 % and 24.6 % respectively) but this bacterium was absent in Maze. Another unequivocal observation from the metagenetic profiles was that the genera *Dysgonomonas* and *Clostridium* as well as *Prevotella paludivivens* were found in a very low abundance, but in a consistent way. *Dysgonomonas* is reported to cause gastroenteritis in immunocompromised persons. As the genus *Clostridium* contains pathogenic species as well as spoilage organisms, further research is necessary to elucidate the safety of fermented enset. Overall, *Leuconostoc mesenteroides*, initiated the fermentation. Later on, *Prevotella paludivivens*, *Lactobacillus* sp. and *Bifidobacterium minimum* dominated. These three species are potential candidates for the development of a starter culture to optimise enset fermentation.

**Keywords:** Enset, fermentation, kocho, metagenetics, starter culture