

## Metagenetic analysis of the bacterial community composition and dynamics in fermenting Enset (Ensete ventricosum)

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**Background and objective** 

sequencing.

**Materials and methods** 

Enset (*Ensete ventricosum*) provides staple food for over 15 million people in Ethiopia after fermentation into kocho [1]. Traditional methods of enset fermentation are time consuming and labor intensive. The fermentation is by far the slowest step, as fermentation time varies from a month to a year, depending on incubation temperature, which is partly dependent on the altitude of the production site [2]. An accurate understanding of the microbial dynamics during the fermentation can help to optimize and standardize the process. The aim of this study was to assess the bacterial community composition and its dynamics during enset fermentation using Illumina Miseq

In order to assess the bacterial community composition and its dynamics during fermentation, twelve matured enset plants (Gena, Maze and Ketishe varieties) were processed and allowed to ferment in a bamboo basket, called 'erosa', for 2 months.

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 [3].





Fig. 2. Enset plant (A), Enset processing (B), Fermenting enset inside storage device 'erosa' (C) two month fermented enset (D) baked kocho bread (E)

Fig. 1 Relative abundance (%) of the bacterial community during enset fermentation of variety Gena, Maze and Ketishe for 60 days.

## Discussion

• The most important similarities in the bacterial community of the three varieties on day 1 were the presence of a bacterium assigned to the family of

Enterobacteriaceae (22.9, 28.2 and 17.7%) and Leuconostoc mesenteroides (29.7, 9.5 and 13.9%), for Gena, Maze and Ketishe, respectively.

- Prevotella paludivivens, Lactobacillus sp. and Bifidobacterium minimum dominated the later stages of the fermentation.
- Clostridium spp. were also present throughout the fermentation, evoking questions on the food safety and spoilage.
- The bacterial community differed at the start, but it converged towards a more uniform community towards the end of the fermentation.  $\bullet$

## References

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