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Diversity of yeasts and lactic acid bacteria occurring during spontaneous fermentation of mawè, a cereal dough produced in West Africa

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Introduction

Mawè is a West African cereal-based spontaneously fermented dough. The fermentation of mawè is dominated by yeasts and lactic acid bacteria (LAB) (Hounhouigan et al., 1994). However, the diversity of yeasts and LAB involved in maize mawè fermentation have only been investigated in urban processing units.

Aim

To identify yeasts and LAB occurring during spontaneous fermentation of mawè in diverse urban and rural maize or sorghum mawè processing units in Benin.

Conclusion

The yeasts associated with mawè fermentation were ***Pichia kudriavzevii*** (**66%** of the total isolated yeasts) at all stages of the fermentation; ***Kluyveromyces marxianus*** (**25%** of the total isolated yeasts) mostly from the intermediate stage till the end stage; ***Saccharomyces cerevisiae*** (**5%** of the total isolated yeasts) mostly identified only at the end stage. Additionally, ***Ogataea polymorpha***, ***Candida glabrata*** and ***Wickerhamomyces anomalus***, were isolated constituting a minor part, together comprising **4%** of the total isolated yeasts.

The LAB associated with mawè fermentation were ***Lactobacillus fermentum*** (**87%** of the total isolated LAB) at all stages of the fermentation; ***Pediococcus acidilactici*** (**5%** of the total isolated LAB) mostly from the intermediate stage till the end stage, ***Lactobacillus plantarum*** (**4%** of the total isolated LAB) identified at all stages, ***Weissella confusa*** (**3%** of the total isolated LAB) mainly detected at the onset of the fermentation and ***Pediococcus pentosaceus*** (**1%** of the total isolated LAB).

Materials & Methods

Four kinds of mawè including commercial maize and sorghum mawè, home mawè and mawè for come were sampled at different fermentation times from **eight production sites** in **urban and rural area in southern Benin, West Africa**. Samples were produced following the flow diagram Fig.1 and picture 1 shows a mawè production site.

Isolated **yeasts (n = 334)** and **LAB (n = 344)** were grouped by **$(GTG)_5$-based repetitive PCR followed by sequencing** of the 26S rRNA gene for yeasts and the 16S rRNA gene for LAB. *Kluyveromyces* spp. were unambiguously identified to species level by restriction fragment length polymorphism (RFLP) of internal transcribed spacer region followed by sequencing.

Fig. 1. Flow diagram of mawè production. The grits is not washed in home mawè processing. In come mawè processing, the cleaned maize is directly soaked in boiled water without grinding.

Picture 1. Mawè production site of St Michel market, Cotonou, Benin

Results & discussion

For the four kinds of mawè, yeast counts increased continuously from 0 to 36h (Fig. 2a). LAB counts increased between 0 and 24h and thereafter decreased (Fig. 2b). The average value of pH decreased over time to 4.1±0.30.

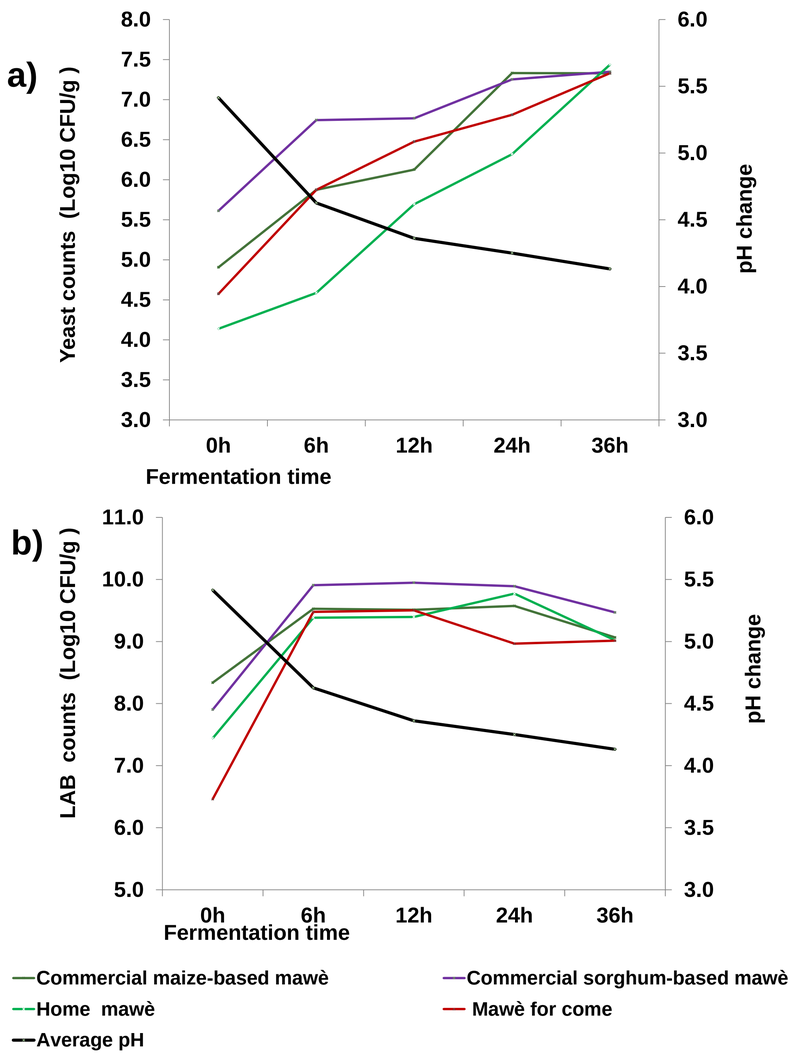

Fig. 2. Microbial count and pH change during mawè fermentation

The Rep-PCR profile and cluster analysis followed by gene sequencing showed that six different species of yeast (Fig. 3) and five different species of LAB (Fig. 4) are responsible for the spontaneous fermentation of mawè.

This study confirms the findings of Hounhouigan et al. (1994) and Greppi et al. (2013). However ***O. polymorpha*** and ***L. plantarum*** have never been detected in mawè by the previous studies.

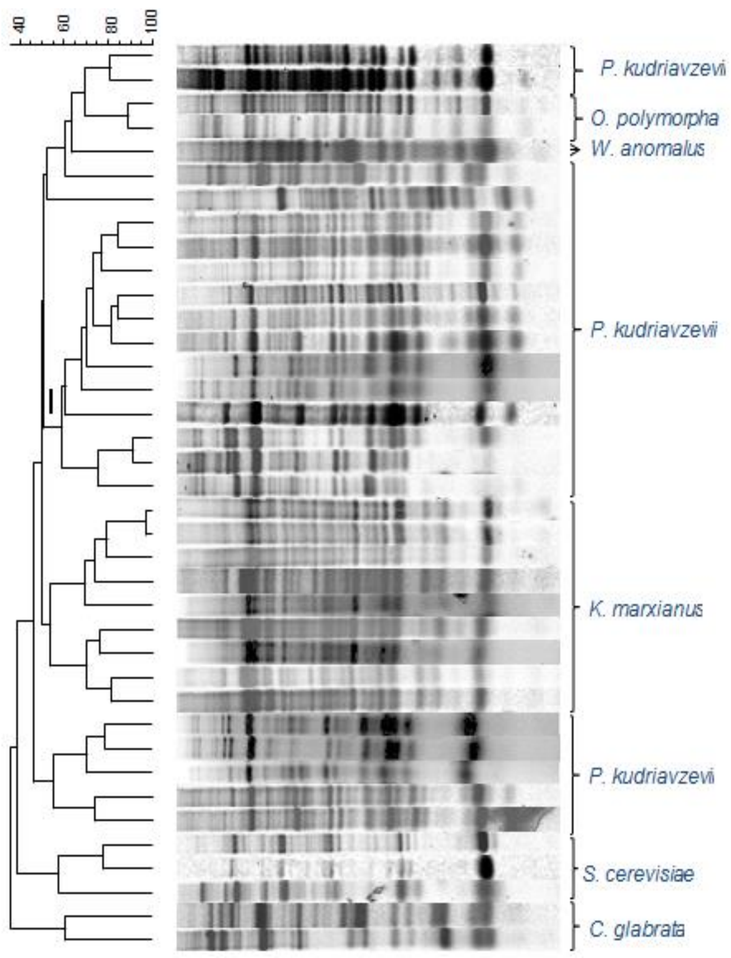

Fig. 3. Dendrogram obtained by cluster analysis of (GTG)5-based rep-PCR fingerprints of yeasts isolated during spontaneous fermentation of mawè. The Dendrogram is based on Dice's coefficient of similarity with the unweighted pair group method with arithmetic average clustering algorithm (UPGMA). Only a representative sub-sample of sequenced isolates is shown. Isolates were subsequently identified by sequencing of 26S rRNA gene.

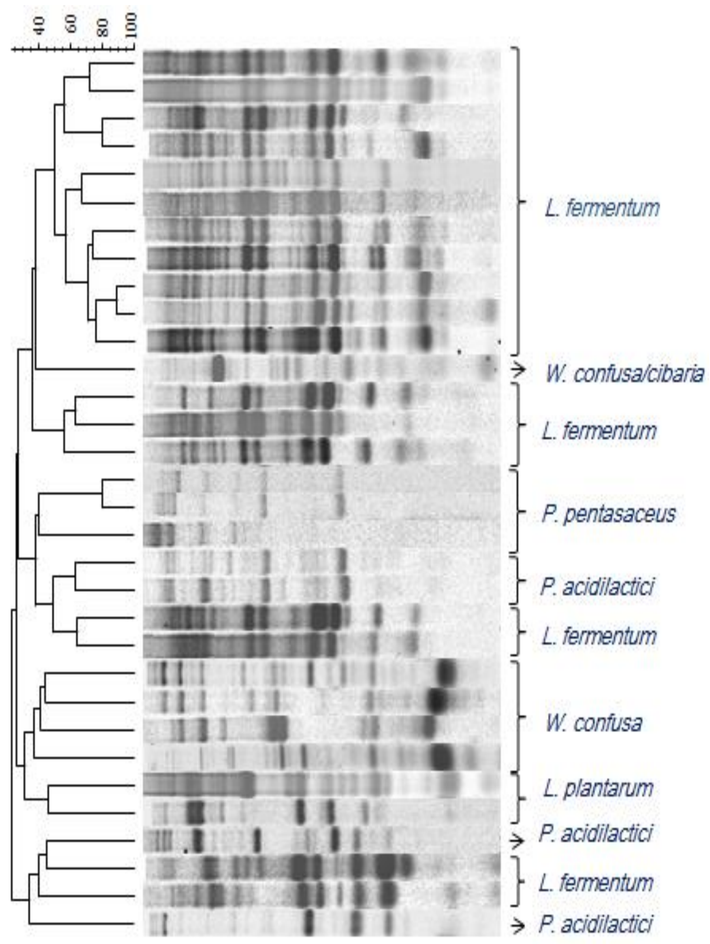

Fig. 4. Dendrogram obtained by cluster analysis of (GTG)5-based rep-PCR fingerprints of lactic acid bacteria isolated during spontaneous fermentation of mawè. The Dendrogram is based on Dice's coefficient of similarity with the unweighted pair group method with arithmetic average clustering algorithm (UPGMA). Only a representative sub-sample of sequenced isolates is shown. Isolates were subsequently identified by sequencing of the 16S rRNA gene.

Main references: 1) Greppi, A., Rantisou, K., Padonou, W., Hounhouigan, J., Jespersen, L., Jakobsen, M., Cocolin, L., 2013. International Journal of Food Microbiology 165(2), 200–207.

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