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Microbial interactions and quorum sensing mechanisms of importance for sustainable cereal-based food fermentation: the case of *mawè* and *mawè* based foods

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Introduction

Mawè is an African uncooked fermented dough from local cereals, used for the preparation of traditional cooked dishes including cooked dough, steam-cooked bread, porridge, beverage, fritters and couscous. *Mawè* is obtained by spontaneous fermentation which may be supported by backslopping of microorganisms. Hence, *mawè* is dominated by many strains of heterofermentative lactic acid bacteria (LAB) and yeasts. In this study LAB and yeast strains suitable for safe and nutritious *mawè* production are identified and microbial interactions and quorum sensing mechanisms during *mawè* fermentation are studied.

Fig. 1 . Preparation method and uses of mawè

Methodology

Four kinds of *mawè* including *commercial maize-* and *sorghum-based mawè*, *home mawè* and *come mawè* were sampled from eight production sites in both urban and rural areas in southern Benin.

For each *mawè*, microbial count was performed at 0, 6, 12, 24 and 36 hours.

For each sampling time, isolates were randomly picked, purified and identified to species level by $(GTG)_5$-based rep-PCR in addition to 16S and 26S rRNA gene sequencing.

Results

❖ Change in microbial count (Log_{10} CFU/g of wet *mawe*) and pH during *mawè* fermentation

For the four kinds of *mawè*, LAB count increased from 7.54±1.0 to 9.55±0.45 between 0 and 24h and there after decreased to 9.14±0.37 at 36h (Fig. 2a) whereas yeast count increased continually from 4.81±0.77 to 7.36±0.42 between 0 and 36h (Fig. 2b).

The highest count of LAB and yeast are found in *sorghum-based mawè* (Fig. 2a), while *come mawè* and *home mawè* undergo the lowest LAB and yeast population, respectively (Fig. 2a and 2b).

The average value of pH decreased from 5.41±0.55 at 0h to 4.13±0.31 at 36h.

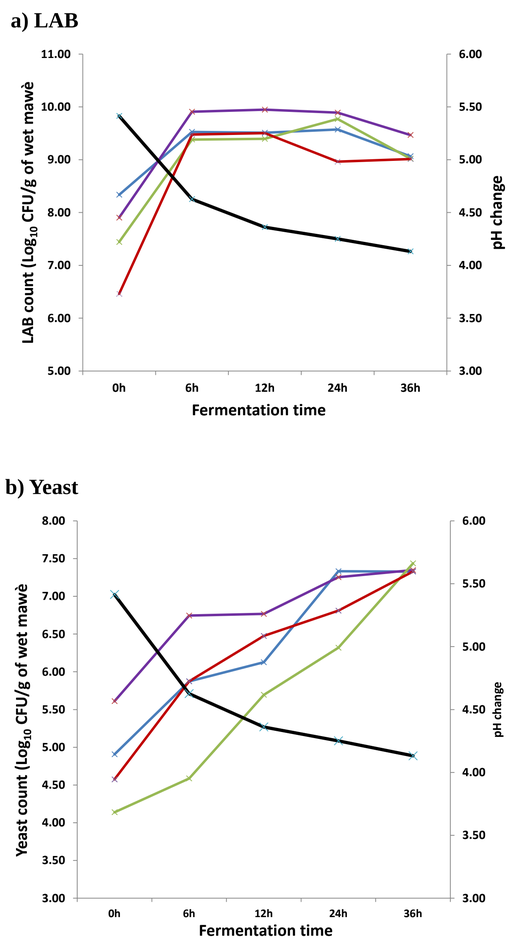

Fig. 2 . Change in microbial count and pH during *mawè* fermentation

❖ Microbial diversity

The cluster analysis (Fig. 3) showed a large microbial diversity involving spontaneous fermentation of *mawè*.

Cluster analysis resulted in identification of 18 different groups for LAB (Fig. 3a) and 14 different groups for yeasts (Fig. 3b).

The LAB population was dominated by isolates of group 14 (34.8 %) followed by those of group 11 (29.6 %). The most predominant isolate of yeast represent 48.5 % (group 5) followed by group 9 (19.5 %).

Contrary to previous finding of Hounhouigan et al (1994) and Greppi et al (2013) on *commercial maize-based mawè*, our results revealed a more diverse microbiota of the four different kinds of mawè studied (including *commercial maize-* and *sorghum-based mawè*, *home mawè* and *come mawè*).

❖ Upcoming work

The identity of the isolates will be determined using16S and 26S rRNA gene sequencing.

On the selected isolates, quorum sensing mechanisms and the effect of the quorum sensing molecules on pathogenic bacteria and spoilage organisms will be investigated.

Additionally, environmental conditions in *mawè* stimulating production of quorum sensing molecules and -inhibitors will be studied. This will lead to development of multifunctional starter cultures specially targeted at *mawè* production for better and safer *mawè* with optimized fermentation.

Conclusions and implications

The spontaneous fermentation of *mawè* involves a great diversity of microorganisms.

Understanding of microbial interactions are key for development of multifunctional starter cultures for better and safer *mawè* fermentation.

Besides, implementation of starter cultures could, in turn, positively impact the preparation of traditional cereal-based African foods product from house-hold to semi-industrial scale.

Acknowledgements

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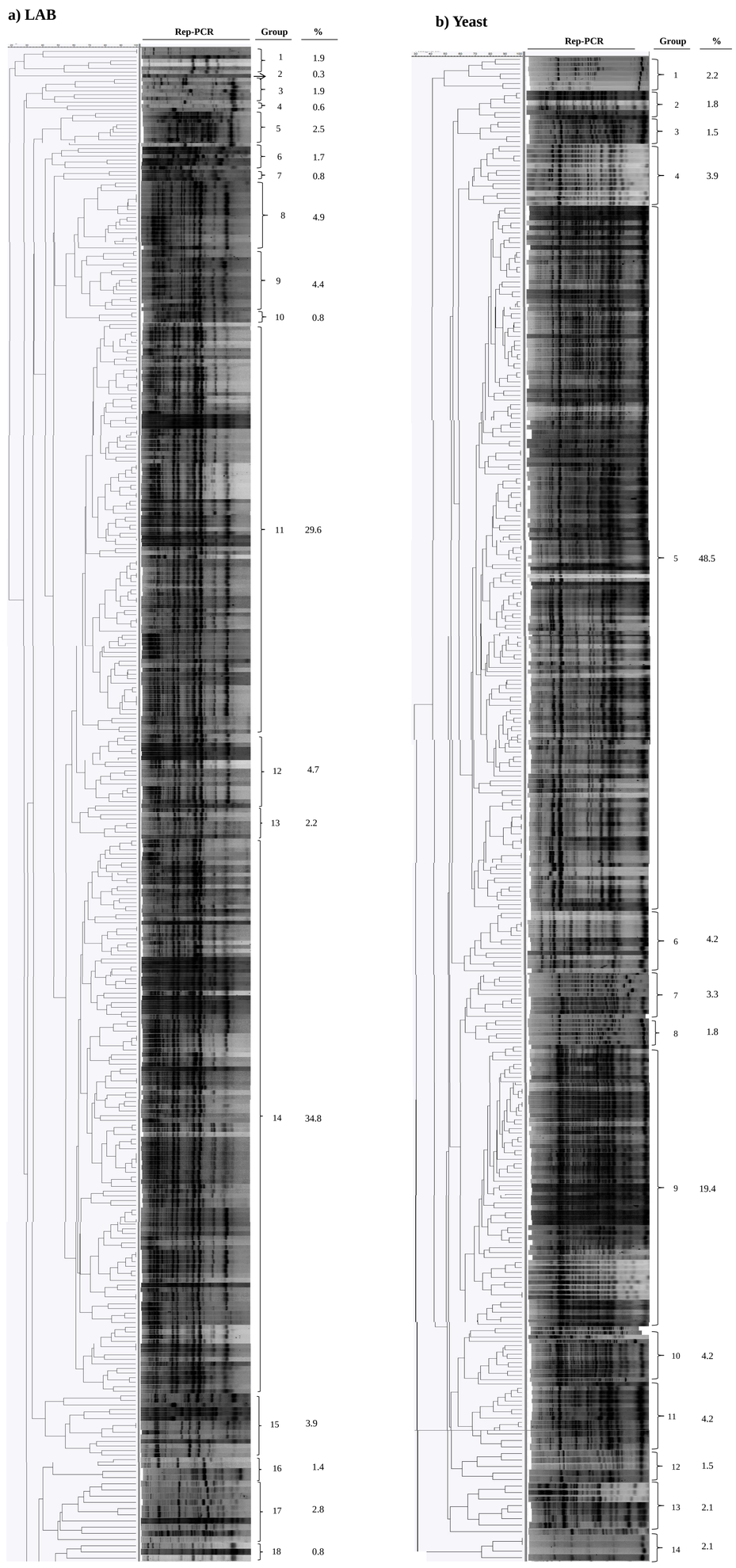

Fig. 3 . Dendrograms obtained by cluster analysis of rep-PCR (GTG5) fingerprints. The dendrograms are based on Dice's Coefficient of similarity with the unweighted pair group method with arithmetic averages clustering algorithm (UPGMA).