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Bacterial Community Dynamics during the Production of Ogi from Millet 'A Nigerian Fermented Food' Using Culture-Dependent Approach

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Abstract: *Analysis of bacterial community dynamics in malted and fermented millet during ogi production was investigated. Malted millet were wet milled using a sterilized blender and kept on conical flasks for 72 hours to allow spontaneous fermentation from which bacterial analysis were performed at 12 hourly interval. Nine bacterial strains were isolated and identified as Lactobacillus sp. Escherichia coli, Streptococcus sp., Staphylococcus sp. Bacillus sp., Enterobacter sp., Leuconostoc sp., Pediococcus sp., and Flavobacterium sp. Changes in bacterial community revealed that Lactobacillus sp., Streptococcus sp., and Pediococcus sp. predominate in all the days during millet fermentation. Flavobacterium sp., Escherichia coli were isolated in the first 48 hours of fermentation after which their population declined, while Bacillus sp. was presence in the first, second and third days respectively. The highest aerobic bacterial and lactic acid bacteria count were recorded as 3.9logcfu/g (48h) and 11.2logcfu/g (60h) respectively.*

INTRODUCTION

The majority of traditional cereal based foods consumed in Africa are processed by natural fermentation. Here fermented foods are produced primarily at household and village level where they find wide consumer acceptance (Inang and Idoko, 2006). Traditional fermentation processes used in the production of these foods are uncontrolled and dependent on microorganism from the environment or the fermentation process. Ogi is an acid fermented cereal gruel or porridge prepared from fermented millet, maize or guinea corn in West Africa (Omemu, 2011). It is a stable food that serves as a weaning food for infants and an important source of carbohydrate among the cereal crops (Owusu-Kwarteng et al., 2010). It has been indicated that some of the microorganism responsible for ogi fermentation, such as *L. plantarum* use some of the amino acid for growth (Okorie et al., 2013). The important microorganisms of ogi fermentation have been recorded. The following mould are implicated *Cephalosporium* sp., *Fusarium* sp., *Aspergillus* sp. and *Penicillium* sp.; yeast: *Saccharomyces cerevisiae* and *Candida mycoderma*. For bacteria species there were indications of *Lactobacillus plantarum*, *Corynebacterium* sp. and *Aerobacter cloacae* with *Lactobacillus plantarum* mainly responsible for the production of lactic acid, the main flavor base of ogi (Omemu, 2011). Many work have been carried out on the production of ogi and fermentation of millet but information on the bacterial community dynamic during the malting and fermentation of millet for ogi production is scanty. We therefore seek to analyze the dynamics of bacteria community during malting and fermentation processes of millet for ogi production.

MATERIALS AND METHODS

Sample processing/malting

The millet grains were picked cleaned separated and 150g each were weighed. The weighed grains were washed with distilled water, steeped in 500ml sterile distilled water in a cleaned sterile Erlenmeyer flask for 24 hours at room temperature. After 24 hours, the water was drained and the soaked grains spread on a sterile jute bag for fermentation at room temperature (28 ± 2^0C) for 48 hours and wetted twice daily.

Fermentation and isolation of bacteria from sample

Rootlet from germinated/malted millet were removed, wet milled with 300ml sterile distilled water using a sterilized blender (sterilize with 70% ethanol). The milled samples were kept in sterile conical flasks covered with clean aluminum foil to allow spontaneous fermentation for 72 hours at room temperature. Samplings were carried out at 12 hourly intervals (12h, 24h, 36h, 48h, 60h and 72h) for bacteriological analysis following the procedures as described (Henshaw and Ikpoh, 2009), plated on Nutrient agar, de Mann Rogosa and Sharpe agar.

RESULTS AND DISCUSSION

Analysis of bacterial community dynamics in malted and fermented millet during ogi production was investigated. Results obtained showed that total aerobic bacteria counts during the 72h fermentation period increase sharply in the first 36h of fermentation (Fig. 1) and decrease gradually in the remaining hours of fermentation. These results agreed with earlier report by Mbata et al., (2009) while studying fermented maize fortified with groundnut. The highest aerobic bacterial count was recorded at 48hours (3.9 log cfu/g) followed by 36 hour (3.7 log cfu/g) of fermentation periods figure1. Lactic acid bacteria counts showed a gradually increase from 0hour to 60hours of fermentation after which a decrease was observed at 72 hours. Highest LAB count was recorded at 60hours (11.2log cfu/g) and the least at 0hr (3.5log cfu/g) figure 2. Similar report was made by Wakil and Onilude (2010) during the monitoring of the effect of fortification on bacterial population in maize-cowpea blend and maize-cowpea-groundnut blend.

Nine genera of bacteria were isolated from malted and fermented millet. These are; *Flavobacterium* sp., *Escherichia coli*, *Staphylococcus* sp., *Bacillus* sp., *Streptococcus* sp., *Leuconostoc* sp., *Lactobacillus* sp., *Enterobacter* sp. And *Pediococcus* sp. Many of these microorganisms have been isolated from cereal-based fermented foods. These microorganisms and other was isolated by Omemu while studying fermentation dynamics of ogi. *Bacillus subtilis* and *B. pumilus* have been implicated in the fermentation of seed legumes. The presence of *Staphylococcus* sp., *Escherichia coli* could be attributed to the raw material, the environment and the processing equipment (Naphil and Daodu, 2011) or any milling process (Omemu, 2011).

The bacterial community dynamics results showed that *Lactobacillus* sp., predominate from 24-72 hours of fermentation period as the counts increases within this time frame. This observation agrees with the report of Holzapfel, 2002. *Staphylococcus* sp., *Enterobacter* and *Escherichia coli* were observed in the first 36 hours of fermentation. This could be from the environment, processing equipments (Naphil and Daodu, 2011). As the retting juice tends towards acidic pH range their population disappeared with increase in the presence of LAB. This observation is in agreement with earlier report by Vieira-Dalode et al., (2007). The present of *Leuconostoc* sp. was observed at 48-60 hours of fermentation while *Pediococcus* sp. from 60-72 hours of fermentation period.

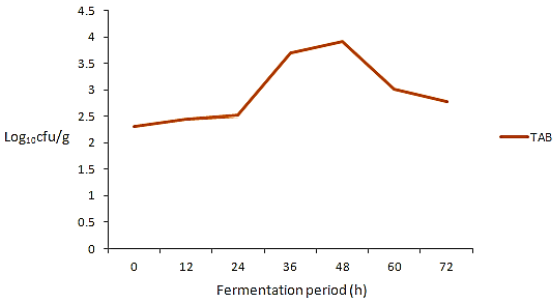

Figure 1; total aerobic bacterial (TAB) count following days of fermentation of millet for ogi production

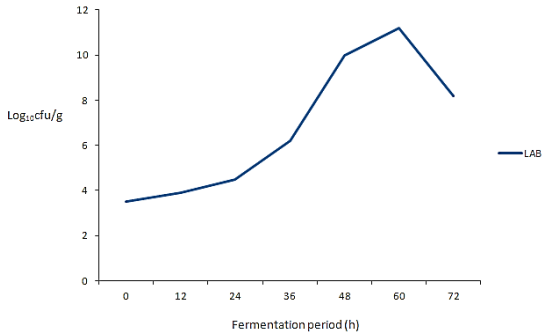

Figure 2; lactic acid bacterial (LAB) count following days of fermentation of millet for ogi production.

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