Genotypic and technological characterization of Lactic acid bacteria from African fermented foods

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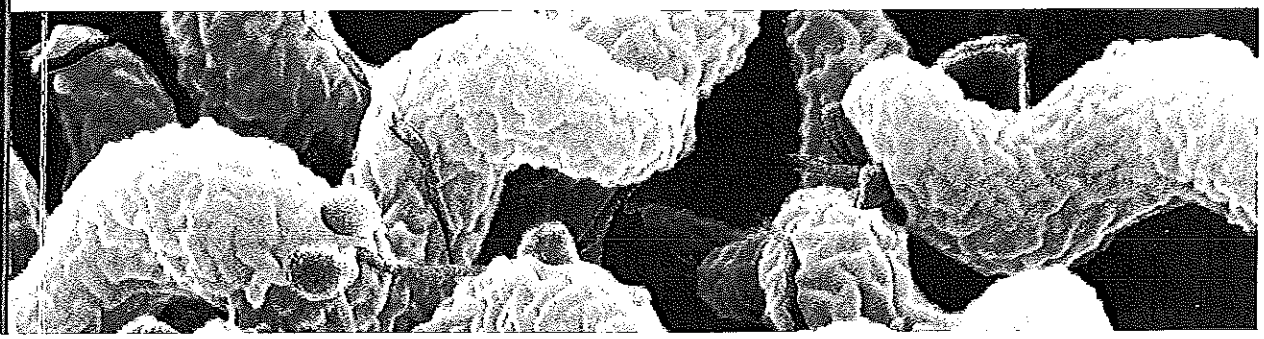

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Nielsen (3), L Jespersen (3)

another depending on the
used, the processing condi-
st certain tribes of the West
and so little or no scientific
e the microorganisms pres-
ut. The survey revealed that
d calabashes or plastic con-
the environment, processing
fermentation was followed
the end of the fermentation
e from 4.00 to 9.00 log CFU/
liversity was evaluated using
ene. The predominant lactic
helveticus, Lactobacillus del-
us italicus, Weissella cibaria
anisms are involved in *nunu*
d controlled fermentations.

roduction by starter cul-

(4)

ation of *lanhouin* were tested
le cells pattern was enumer-
tion and the role of individual
aphy/Mass Spectrometry (GC-
amples. For all fermentations,
d 3.7×10^6 cfu/g after 48 h of
licheniformis respectively. The
ntation progressed. The hista-
of 41 aroma compounds were
inant ones. These compounds
lcohols, 8 amines, 3 aldehydes
phenol, thiazoles and pyrroles

PEA1.39 **Bacterial community present in a fermented beverage produced from cotton seed with rice by Brazilian Amerindians**

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Cauim is a fermented beverages prepared by Tapirapé Amerindians in Brazil from substrates such as cassava, rice, peanuts, pumpkin, banana, cotton seed and maize. The process is traditional and rudimentary. Here we study the microorganisms associated with seed cotton and rice fermentation using a combination of culture-dependent and independent methods. Samples of cotton seed cauim were collected every 8 h of fermentation for analysis of the microbiota present during 48 h of fermentation. The bacterial population reached values around 8.0 log CFU / mL. A total of 162 strains of bacteria consisting of 33 morphotypes were isolated and identified by polyphasic taxonomy. The bacteria were grouped into Gram-negative (12.96%), Gram-positive catalase positive (58.15%) and Gram-positive catalase negative (41.84). Among the Gram-positive species *Lactobacillus* sp (13.47%), *Bacillus* sp (12.76%), *Lactobacillus plantarum* (11.34%), *Corynebacterium amycolatum* (10.63%), and *Lactobacillus agilis* (9.92%) were the most frequent microorganisms. The genus *Lactobacillus*, comprised the largest number of isolates and 15 different species. It was observed a decrease in pH value from 6.92 (T0) to 4.76 (T48 h) and the presence of lactic acid were only detected from the sample T40 h, reaching higher values in sample T48 (23.96 g / L). DGGE analysis were performed in order to observe the dynamics of communities of bacteria, revealing that there was a predominance of *Lactobacillus* throughout the fermentation. It was possible to observe that after 32 hours, the population did not modified significantly. The results showed by DGGE technique were in agreement with the identification by the culture dependent method.

PEA1.40 **Genotypic and technological characterization of *Lactic acid bacteria* from African fermented foods**

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Fermented indigenous African foods consist of those groups of foods that are prepared in homes, villages and small scale cottage industries. The fermentation is done to improve flavour, texture and prolong shelf-life among others. The predominant genera in fermented indigenous African foods are mainly *Lactobacillus* (both homo- and hetero-fermentative), *Leuconostoc* and to a lesser extent *Pediococcus, Lactococcus* and *Weissella*. The aim of this study was to characterize LAB from fermented indigenous African foods by molecular techniques and explore their technological properties which could result in the selection of appropriate multifunctional starter cultures. 33 isolates from 3 different fermented indigenous African foods; namely fermenting cocoa beans, dolo/pito wort, and a cereal based dough, were grouped using rep-PCR amplification technique and then followed by sequencing of the 16S rRNA gene. Species-specific oligonucleotides based on the *rec*A gene was used to identify strains belonging to *Lactobacillus plantarum* and *Lactobacillus paraplantarum* which shows over 98% percentage identity of the 16S rRNA sequence for both species. Similarly, *Pediococcus acidilactici* and *Peddiococcus pentosaceus* strains were identified with species-specific oligonuleotides based on the 16S rRNA and *ldhD* genes Technological characterization included growth speed, milk acidification, inhibition of pathogenic and spoilage microorganisms, carbohydrates fermentation patterns, minimum inhibitory concentration of bile salt, selection of bile salt mutant strains and enzymatic potentials using the API ZYM kit (bioMérieux, Inc). The isolates were able to ferment a wide range of complex carbohydrates. 50% of the isolates were able to inhibit growth of *Listeria monocytogenes* 4140, *Escherichia coli* and *Salmonella typhimurium*. 15 strains belonging to *Lb. plantarum, Lb. paraplantarum, Ped. pentosaceus*, and *Ped. acidilactici* were able to grow on MRS agar with bile salt concentration of 2%. 16 of the 19 substrates used to assay the enzymatic potentials were hydrolysed with concentrations ranging from 5nmoles to over 40nmoles. None of the strains was able to produce the following enzymes; β-glucuronidase, α-mannosidase and α-fucosidase. Some of the strains are selected for further technological characterization with the intention to develop new starter cultures and probiotic strains for both the European and African food and feed industry