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Molecular identification and characterization of yeast strains isolated from Mawè, Gowè, Ogi and Tchoukoutou, traditional fermented products from Benin

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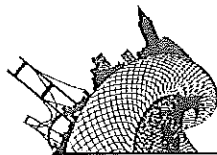
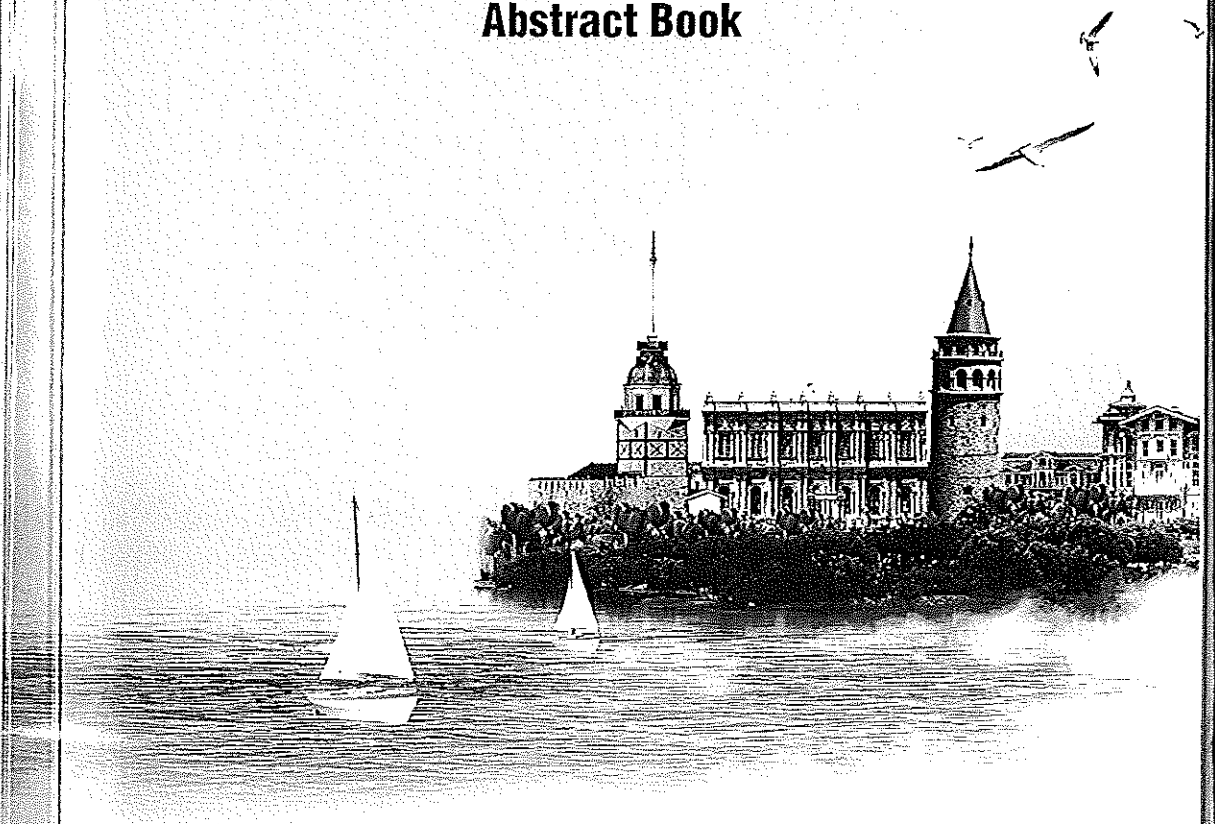


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Abstract Book



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Immunity during ripening

SON¹, Hans BLOM¹

¹ Aquaculture, Food safety and

Biotechnology and Food Science, Ås,

is made by salting and ripening of
ween 3.5 to 8.0 °C. The main purpose
ia present at several stages of the
es most commonly used in production
d from rakfisk brine throughout a
using different salt concentrations,
rigin. Bacterial plate counting was
dependent characterization of mixed
rRNA genes, and pure spectra was
Bacterial plate counting for day 0 and
day 7, a higher ripening temperature
bers from 10² CFU/ml at the lowest
10⁶⁻⁷ CFU/ml by week 4, which was
first 7 days the bacterial community
that became predominant throughout
weeks, and consisted of different
ter. The lactic acid bacteria detected
rine collected at one producer had
ctic acid bacteria. Fluctuations of
ethods were in accordance with the
displayed consistency within each
s. We presume that succession of
ure and the salt concentration, rather

p-493

Molecular identification and characterization of yeast strains isolated from Mawè, Gowè, Ogi and Tchoukoutou, traditional fermented products from Benin

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Mawè, Gowè, Ogi and Tchoukoutou are sorghum and maize-based traditional fermented products largely consumed by the local population of Benin, West Africa. Their preparation remains as a house art and they are the result of natural and spontaneous fermentation processes. Few studies investigated the indigenous biota involved in the fermentation, especially using molecular tools. Here we focused on the yeast ecology. We investigated the yeast diversity occurring in the four final products, as sold at local markets, and the yeast dynamics during the fermentation processes of Mawè and Tchoukoutou. A total of 420 isolates were collected. All of them were identified by PCR-Denaturing Gradient Gel Electrophoresis (DGGE) followed by sequencing of the D1/D2 domain of the 26S rRNA gene. The predominant yeast species identified were characterized by rep-PCR and the fingerprints obtained were clustered. *Issatchenkia orientalis* was the yeast most frequently isolated in all the final products. Only in Gowè samples, *Candida tropicalis* and *Kluyveromyces marxianus* were also largely present. During Mawè fermentation process, the yeast population increased from 2.9 to 5.5 log CFU/g while for Tchoukoutou production it varied from 4.9 to 6.4 log CFU/g. *Candida glabrata* and *Issatchenkia orientalis* were the yeast species mostly involved in the Mawè production process. At the end of its fermentation, *Issatchenkia orientalis* and *Saccharomyces cerevisiae* dominated. Other species were also detected at less extent during the process. The yeast that almost exclusively dominated the fermentation of Tchoukoutou was *Saccharomyces cerevisiae*, with the exception of the very early stages. The cluster analysis of the rep-PCR fingerprints underlined a low biodiversity at strain level of the dominant species. In general, the results showed how few autochthonous species dominate the fermentation. Among them, some strains should be considered for starter selection. Moreover, as food-borne yeasts have been associated with probiotic effects on human health, the selection should also consider this aspect in order to increase the nutritional value of traditional fermented foods in West Africa.