Succession of microbial consortia associated with traditional Tejuino fermentations

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Introduction. Tejuino is a traditional slightly alcoholic beverage prepared through spontaneous fermentation of nixtamalized maize flour and is consumed in several states of Mexico [1]. The elaboration process is mostly performed at household level and nothing is known about the associated microbial consortia. Besides food safety issues, knowledge about the microbial successions during the fermentation and their impact on the aroma profile of the final product could lead to the standardization of the process.
The objective of this work was the characterization and assessment of associated microbial consortia of traditional Tejuino fermentations.

Methods. Two artisanal Tejuino elaboration processes from two different producers were analyzed; a solid state fermentation (P1) and a submerged fermentation (P2). Representative samples were taken from all stages of the process including maize dough preparation, several points during fermentation and the final product. Samples were immediately transferred on ice to the laboratory and standard microbiological methods for cultivation and isolation of microorganisms were applied. A broad range of culture media (MRS, M17, PCA, EMB, GYC, WL and PDA) were used at different conditions (30°C and 37°C; aerobiosis or microaereophilic; supplemented with cloranfenicol or ethanol). Microscopic characterization combined with Gram stain and catalase activity test were used for differentiation and grouping.

Results.
From the first producer (P1) a total of 301 bacteria were identified as 161 (54%) gram negative and 140 (46%) gram positive strains. In the latter group, 61 (44%) isolates were tested as catalase negative and 79 (56%) as catalase positive. From the same process 54 yeasts were isolated. From the second producer (P2) 208 isolates were recognized as 54 (26%) gram negative and 154 (74%) gram positive, where 96 (62%) isolates showed catalase activity and 58 (38%) did not. From this process 58 yeasts were isolated.
Combining the results of these methods and the range of culture media used in this study, differential counts for (total) mesophilic bacteria, lactic acid bacteria (30°C and 37°C), acetic acid bacteria, enterobacteria, yeasts and filamentous fungi were generated.

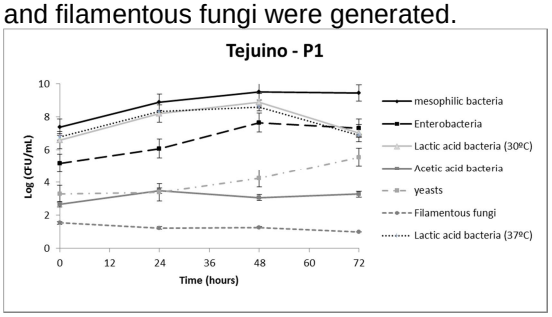

Fig.1 Microbial succession during Tejuino elaboration at producer 1.

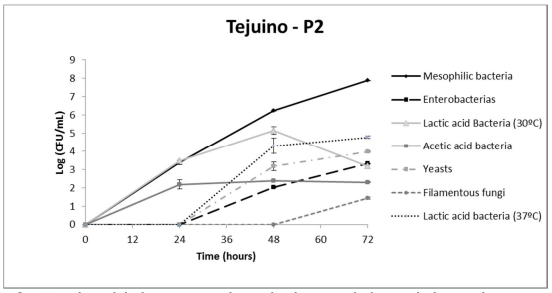

Fig.2 Microbial succession during Tejuino elaboration at producer 2.

Besides further molecular identification of the isolates, the samples will be subjected to PCR-DGGE analysis.

Conclusions. Traditional elaboration processes of Tejuino contain complex microbial consortia which vary in function of the process.

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References.
1. Wacher-Rodarte, C. (1995). "Alimentos y bebidas fermentados tradicionales". In: *Biotecnología Alimentaria*. García-Garibay, M., Quintero, R., López-Munguía, A. Limusa, México. 313-349.