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BOOK OF ABSTRACTS

Exploring biodiversity in microbial ecosystems along the food chain

P1.20

Dynamics and biodiversity of bacterial and yeast communities during fermentation of cocoa beans

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Forastero hybrid cocoa bean fermentations were carried out in Box (B) and in Heap (H) with or without the inoculation of *Saccharomyces cerevisiae* and *Torulaspora delbrueckii* as starter cultures. Bacteria, yeasts and microbial metabolites (volatile and non-volatile organic compounds) were monitored during fermentation in order to assess the link between microbiota and the release of metabolites during this process. The presence of starter cultures was detected during the first two days of fermentations by means of culture-dependent analysis. However, it did not show statistical difference in any physico-chemical or microbiological analysis. Plate counts revealed the dominance of yeasts at the beginning of the fermentation followed by acetic acid bacteria (AAB) and lactic acid bacteria (LAB). *Hanseniaspora opuntiae, S. cerevisiae, Pichia, Acetobacter pasteurianus* and *Lactobacillus fermentum* were the most abundant OTUs during both fermentation processes (B and H), reporting different relative abundances. Only the diversity of fungal species indicated a higher level of complexity in B compared to H fermentations ($P < 0.05$) and also revealed a statistically significant difference between starter cultures initially inoculated ($P < 0.01$). However, the analysis of microbial metabolites indicated different distribution of volatile and non-volatile compounds between the two procedures B and H ($P < 0.05$), rather than between the inoculated and non-inoculated fermentations. Box fermentations showed a faster carbohydrate metabolism and higher production of organic acid compounds than in heap fermentations, which boosted the formation of alcohols and esters. Overall, the microbial dynamics and associations between bacteria, yeast and metabolites were found to depend on the type of fermentation. In spite of the limited effectiveness of the starter strains inoculated, this study provides new information on the microbial development of Box and Heap cocoa fermentations, by coupling for the first time yeast/bacteria amplicon-based sequencing data with microbial metabolites detection. The information so far available suggests that microbial communities have been an important factor in the evolution of aroma compounds. Understanding the pathways taken place during the formation of aroma by micro-organisms could be used to improve fermentation processes and to enhance chocolate quality.

Keywords: Cocoa beans; fermentation; yeast; bacteria; volatile and non-volatile organic compounds