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## Dynamic follow-up of a Kombucha fermentation

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Kombucha is an increasingly popular traditional beverage obtained by fermenting sweetened tea in the presence of a microbially rich floating biofilm. The final product contains many organic acids and CO<sub>2</sub> and may also contain low levels of ethanol along with other metabolites. During fermentation, a symbiotic relationship between yeasts and acetic acid bacteria and, in some cases, lactic acid bacteria has been described. Our previous work on industrial scale fermentations highlighted that *Acetobacter*, *Gluconobacter*, *Gluconacetobacter*, *Komagataeibacter* and *Oenococcus* bacterial genera and *Dekkera*, *Zygosaccharomyces* and *Hanseniaspora* yeast genera could be of technological importance for Kombucha fermentations.

The goal of this study was to dynamically follow a lab scale Kombucha fermentation using a selected microbial consortium. Metagenetics (bacteria and yeast), microbiological, physico-chemical and biochemical (organic acids by LC-QTOF, volatiles by GC-MS) parameters were followed as well as biofilm formation using FISH-confocal microscopy and scanning electron microscopy over 27 days.

Results showed sugar consumption by the microbial consortium and the successive production of multiple organic acids (especially acetic, lactic, gluconic and glucuronic acids) and volatile compounds, particularly volatile fatty acids, alcohols and their corresponding esters as well as a decrease in aldehydes over time. Active biofilm formation by acetic acid bacteria could also be monitored by microscopy and highlighted the distinct presence and positioning of the different microbial groups.

These results provide novel information on the microbial dynamics of species within a defined consortium and their functional roles during fermentation and should lead to better fermentation control and product quality in the future.