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## Next Generation Challenges in Food Microbiology

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# Food Microbial Ecology

## O1.6 Fermentation of plant-based ingredients using lactic acid bacteria as an emerging alternative to dairy-based fermented products

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The market for plant-based alternatives for meat and dairy products has grown rapidly. However, the publicly available knowledge about microbial characteristics of such products is still quite limited. This also relates to the application of lactic acid bacteria (LAB), traditionally used in dairy fermentations, in the production of plant-derived fermented foods.

The aim of this study was to assess the performance of 44 LAB strains in 6 different plant-based substrates and to evaluate key properties of the strains as relevant to fermented dairy alternatives. This included growth, acidification capacity, utilisation of carbohydrate sources, production of aromatic compounds and removal or reduction of undesirable (off-flavour) compounds. In total, 22 Lactiplantibacillus plantarum and 22 Lactococcus lactis and Lactococcus cremoris strains of dairy and non-dairy origin were cultured in oat, yellow pea and fava bean protein concentrate emulsions and additionally in rice, amaranth and quinoa flour emulsions for 24-48 hours. In addition, the ability of the strains to grow on different carbon sources was investigated for 4 sugars (glucose, sucrose, raffinose and galactose) that were added to plant-based emulsions at the concentration of 1%. All analyses were conducted in a high throughput screening system.

Most of the representatives of Lactiplantibacillus plantarum, Lactococcus lactis and L. cremoris demonstrated good capacity to grow in selected plant-based substrates with higher acidification rates when sugars were added. The further aroma formation analysis (performed by GC-MS) allowed for the identification of strains with the ability to increase desirable aroma compounds such as diacetyl, acetoin and 2,3-pentanedione, and strains that are able to decrease off-flavours levels, for instance, hexanal, pentanal, and nonanal. The next stage of our work will involve matching these phenotypes with genotypes (based on the whole genome sequences of the strains).

Our findings on the many variables (e.g. strains, plant substrates, carbohydrates) in relation to measured key outcomes of the plant-based fermentations will be used to develop new algorithms and predictive tools that can support the rational selection of LAB strains and fermentation conditions to obtain fermented plant-based products with desired properties.