

Microbial communities of home-made fermented vegetables

Anne Thierry^{1*} (anne.thierry@inrae.fr), Marie-Noelle Madec¹, Anne-Sophie Bage,
Victoria Chuat¹, Laurent Marché², Florence Valence¹

¹UMR1253 STLO, CIRM-BIA, INRAE, Institut Agro, F35000, Rennes, France

²UMR1014 SECALIM, INRAE, Oniris, Nantes, France

Fermentation is an ancestral process for food preservation, which has recently received a renewed interest. Fermented vegetables are little consumed in Western Europe, in contrast with central Europe and Asia. FLEGME is a citizen science project that gathers various actors: citizens, SMEs, agricultural schools, culinary journalists, researchers.... One of its goal is to characterize the microbial communities and the safety of home-made fermented vegetables. Fermented vegetables were collected from citizens that manufacture this type of products for their personal consumption. Several microbial groups were analysed by culture-dependent methods, including lactic acid bacteria (LAB), yeasts, as some pathogenic bacteria. pH was also measured. 1 – 3 isolates were randomly picked up on LAB plates and identified by 16S sequencing. Samples were also analysed by metabarcoding analysis. The set of 75 samples received included 23 types of legumes, mainly cabbage (27%), followed by carrots (19%) and beets (12%). Their median pH was 3.6. Only 2 samples had a pH over 4.5. LAB represented the dominant population. Their median concentration was 7.5×10^4 CFU/g, but varied from non-detectable values to 6×10^8 CFU/g. No significant relationship was found between LAB counts and the type of vegetable. However, LAB counts significant depended on the age of samples, which ranged from 2 weeks to 4 years: high LAB counts were most frequently observed in the youngest samples (< 100 days). Yeasts were detected in nearly half the samples, with counts ranging from 10^2 to 9×10^7 CFU/g. Enterococci were detected in only 5 samples at counts < 10^5 CFU/g. No pathogenic bacteria were detected. 90 LAB clones were isolated, belonging to 31 species, the most common being *Levilactobacillus brevis* and *Lactiplantibacillus plantarum/paraplantarum* (21 and 20 % of total isolates). Metagenomic results showed that *Lactobacillus* was the most represented genera, followed by *Lactococcus*, then *Weissella* and *Staphylococcus*.