

Food Micro 2016

Systems-based Approaches to Food Microbiology

FOODMICRO2016-487

FUNCTIONAL METAGENOMIC AND VOLATILOME PROFILE OF THE MICROBIOTA OF FERMENTED SAUSAGES

Ilario Ferrucino*¹, Alberto Bellio², Manuela Giordano¹, Guerrino Macori², Clara Ippolito², Kalliopi Rantsiou¹, Lucia Decastelli², Luca Coccolin¹

¹DISAFA - Microbiology and food technology sector, University of Turin, Grugliasco (TO), ²SC Controllo Alimenti e Igiene delle Produzioni, Istituto Zooprofilattico Sperimentale PVL, Torino, Italy

Developing Scientist Competition: Yes

Presentation Preference: Oral

Abstract Content: Fermented sausages host complex microbial consortia that play an important role in shaping the typical sensorial properties of the final product. In this study two batches of sausages were followed from 0 to 40 days of fermentation: control and inoculated with starter cultures of *Lactobacillus sakei* and *Staphylococcus xylosum*. Analyses were performed to determine loads of the microbial community and microbial metabolites by gas chromatography-mass spectrometry. A shotgun metagenomic approach was used to monitor changes in bacterial populations and metabolic potential during the fermentation. DNA was extracted from samples and sequenced with a MiSeq instrument. About 5M paired-end reads/samples were generated. The reads were mapped against the draft genomes of *Sus scrofa*. For functional characterization, the remaining reads were aligned to a custom reference database including the protein coding portions of selected genomes chosen as the common taxa found on meat products. In addition, the taxonomic composition was also assessed. During the ripening time a significant reduction on the count of Enterobacteriaceae was observed on inoculated samples. The volatilome of sausages evolves during the ripening and the metabolites produced in the highest quantities were: acetoin, isopentyl alcohol, butanoic and acetic acid in inoculated samples while ethyl alcohol and 1-hydroxy-2-propanone characterized the control samples. When plotting the correlation between the taxa and Volatile Organic Compounds (VOCs) it appeared that the indigenous microbiota found in the control samples was mainly linked to unpleasant molecules, while *L. sakei* was mainly correlated with the acids contributing with fatty/gamy/cheesy/dairy notes and *S. xylosum* related with the esters with their ethereal/fruity/sweet nuances. The pathway enrichment analysis of the metagenomes showed an increase in the abundance of pathways related to aminoacid and lipid metabolism in control samples compared to the inoculated due to the metabolic activity of the natural microbiota that impacted the characteristics of the sausages.

Disclosure of Interest: None Declared

Keywords: Fermented meat , Metabolic pathways, Shotgun metagenomic, VOCs