

JOINT EVENT

4th World Congress and Expo on **APPLIED MICROBIOLOGY**
&
2nd International Conference on **FOOD MICROBIOLOGY**
November 29-December 01, 2017 Madrid, Spain

Evolution of the lactic acid bacterial biofilms on different wood typologies applied for the production of vats intended for cheese making

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The present work was carried out to evaluate the lactic acid bacterial biofilms formation on wooden vat produced with seven different woods, derived from trees species grown in Sicily. The biofilm formation on the wooden surfaces was performed as reported by Gaglio et al. Microbiological and scanning electron microscopy analyses did not show differences in terms of microbial levels and composition within the neoformed biofilms (Fig.1). The specific investigation of *Salmonella* spp., *Listeria monocytogenes*, *Escherichia coli* and positive-coagulase staphylococci did not generate any colony for all vats before and after microbial activation. Lactic acid bacteria (LAB) populations dominated the surfaces of all vats and the highest concentration of approximately 7.63 Log CFU/cm² was registered for thermophilic cocci. All colonies of different morphologies were isolated and characterized for their physiological and biochemical characteristics before being investigated genetically at strain level by RAPD-PCR and species level by a polyphasic approach consisting of 16S rRNA gene sequencing. As reported in a preview investigation conducted on wooden vat surfaces, we found species within the genera *Enterococcus*, *Lactobacillus*, *Lactococcus*, and *Streptococcus*. The species most frequently present were *Lactobacillus fermentum* and *Lactococcus lactis*. The technological characterization of the LAB found at high numbers on to the surfaces of the wooden vats showed interesting dairy properties. In order to deeply investigate on the safety of the wooden vat, a test of artificial contamination on new Calabrian chestnut vats was carried out showing that the acidity and the bacteriocin generated by LAB represent efficient barriers to their adhesion. This study highlights the importance to use the wooden vats for traditional cheese production and provides evidences for their safety in terms of bacterial community evolution.

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