

TITLE: CAN CHEESE PRODUCTION MODE SHAPE THE COMPOSITION OF ENVIRONMENTAL MICROBIOTA FROM CANASTRA CHEESEMAKING FACILITIES?

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Artisanal Minas Canastra cheese or Canastra Cheese is the most famous artisanal cheese in Brazil whose traditional mode of production has been recognized as immaterial heritage of Minas Gerais state. In recent years, variations of the traditional “washed” Canastra cheese, such as “Royal Canastra” and “Bloomy Canastra” have gained attention of the consumer market, leading some producers to enclose these new modes of cheese production in the same facility of “washed” Canastra or even directing all the production to these new products. Recent studies in fermented food production have revealed that the environmental microbiota present in food production plants can influence the fermentation process, causing from refined sensorial signatures to serious spoilage problems. Here we used the culture-independent method of high-throughput sequencing of bacterial 16S rRNA and fungal ITS-1 genes to access the composition environmental microbiota from two distinct Canastra Cheese cheesemaking facilities: “washed Canastra” and “bloomy Canstra”. Our main goal was to verify if there are differences in the composition of the environmental microbiota between cheesemaking facilities that adopt two distinct modes of cheese production. Additionally, we also investigated the seasonal climate effect on the environmental microbiota composition by sampling the facilities in both wet and dry seasons as well as the effect of daily sanitization of the production environment, sampling the facilities before and after the sanitization. We found a contrasting structuring pattern of the composition between bacterial and fungal communities: while for bacterial communities we could observe focal points of similarity and strong differences in overall composition between cheesemaking plants (washed x bloomy), seasons (wet x dry) and rooms (production x maturation), to fungal communities we found similarities in overall composition of cheesemaking plants, seasons and rooms with focal points of differences. Our investigation of daily sanitization effect revealed that the daily sanitization of the environments removes meaningfully bacterial groups introduced in cheesemaking environment during production, in which we verified the reduction of 17 focal points of similarity between bacterial communities to only four of them. Moreover, these remaining focal points of similarity correspond to places whose sanitization is performed with less accuracy or regularity such doors, windows and pipes.

Keywords: source tracking, microbiome, high-throughput sequencing, cheese

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