

**TITLE:** MICROBIAL DIVERSITY OF ARTISANAL MINAS CHEESE VARIETIES  
ACCESSED BY HIGH-THROUGHPUT SEQUENCING

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**ABSTRACT:**

Artisanal Minas cheese is one of the most valued and commercialized cheeses in Brazil, corresponding a relevant economic activity for each region where they are produced. The manufacturing and commercialization of Minas cheese are regulated by a specific state legislation that defined seven main varieties according to the region in which they are produced. Although the artisanal Minas cheeses have very similar production procedures, each variety has typical sensorial attributes that are determined in part by the metabolism of the natural microbiota present in all processing steps. Here, we used high-throughput 16S rRNA (V4 region) and ITS-1 amplicon sequencing to characterize both the bacterial and fungal community composition (core and rind communities) of each of the seven Minas cheese varieties, aiming to determine if there is microbial profiles for each of them. By this approach, we identified 217 bacterial and 417 fungal amplicon sequence variants – ASVs – (considered here as phylotypes) which Serro cheese presented the most diverse microbiota (both bacterial and fungal) and Campos das Vertentes cheese the less diverse microbiota among the varieties. Major differences on microbial composition were observed between rind and core microbiota for three of the seven varieties depicting the differences between these two microenvironments regarding to ecological and metabolic processes. We also detected the presence of some widespread phylotypes among the varieties, belonging to well-known genera related to cheese microbiota, as Lactic Acid Bacterial – LAB – genera *Lactococcus* and *Streptococcus* as well as the fungal *Candida* and *Thichosporon*, which must perform key metabolic pathways during the artisanal Minas cheese manufacturing. On the other hand, we observed specific ASVs to one or several artisanal Minas cheese varieties, highlighting the importance of representative indigenous microbial communities for the determination of typical sensorial attributes for each artisanal Minas cheese variety.

**Keywords:** cheese, 16S rRNA, food, microbiome, high-throughput sequencing

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