

TITLE: BACTERIAL COMMUNITY IN MANUFACTURED MINAS FRESCAL CHEESE AND SCREENING OF ANTIMICROBIAL-RESISTANCE GENETIC MARKERS, AS PREDICTIVE OF MICROBIOLOGICAL SAFETY.

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Microbial contamination in the food industry is worrisome and results in major economic losses. Although sanitary legislations consider pathogens as quality indicators, neglected drug-resistant putative bacteria (DRB) may occur and poses a health issue. Antimicrobials are widely used in livestock and DRB may spread throughout production chain up to consumers and surrounding environment. With regards to Minas Frescal Cheese (MFC) and its economic and cultural values, although discussions on sanitary safety arise, there are almost no data on its role as reservoir of DRB and antimicrobial-resistance genetic markers (AR genes) available to be spread. In this regards, our objectives were to evaluate the structure of bacterial community and acid lactic bacteria in manufactured MFC from retail market in Minas Gerais; and the occurrence of medically relevant AR genes as predictive of microbiological safety. Metagenomic DNA from 5 samples (same batch) of 7 different cheese brands were used as template in REP-PCR (evaluation of bacterial community) and PCR-DGGE (evaluation of acid lactic bacteria populations). Similarity matrices were obtained using UPGMA grouping method. AR genes representative of drugs commonly used in the human medicine were screened by PCR, including genetic markers related to Mex-type efflux pumps. The MFC were brand-clustered (> 70% of similarity) suggesting reproducibility along production chain. Between brands, the similarity observed (30%) may be related to the lactic acid bacteria core, although several OTUs were observed in the PCR-DGGE fingerprint. Of 24 resistance markers, 7 were detected mainly related to beta-lactams, aminoglycosides and efflux pumps: *bla_z⁺* (100%), *bla_{TEM}⁺* (91.4%), *aacA-aphD⁺* (60%), *mexF⁺* (48.6%), *mexD⁺* and *Y⁺* (28.6%), and *mecA⁺* (25.7%). The emergence of AR genes in the food chain is considered a cross-sectoral issue. The observed differences in microbial community structure among different brands may raise questions about standardization and origin of supplies which results in both qualitative and quantitative contamination. The observation of AR genes is of special interest due to their clinical relevance. With the need for further prospective and complementary studies, our data confirm issues on the occurrence of DRB along the productive chain of QMF, which can therefore act as reservoir of drug resistant putative bacteria with great impact on human health.

Keywords: Cheese, DNA fingerprint, bacterial community, antimicrobial resistance

Development Agency: CNPq, CAPES, FAPEMIG, PPGCBIO/UFJF