Survival of lactic acid bacteria from Traditional Mountain Malga (TMM) cheese

after in vitro human gastrointestinal digestion

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Objectives of this study were to investigate the ability of TMM-cheese resident LAB to survive to the digestion process and the influence of chemical-physical characteristics of the cheese, in particular the fat content, on this ability. The human gastrointestinal digestion of 18 TMM-cheese samples after 7 months of ripening was simulated in vitro. Microbial counts before and after the digestion showed a significant reduction of total bacteria, enterococci, mesophilic and thermophilic cocci counts. Mesophilic and heterofermentative rod-shaped bacteria showed a not significant count reduction. Coliforms were always less than 10 Log CFU/g before and after in vitro digestion. Thirty-six putative LAB (18 cocci-shaped and 18 rod-shaped) were isolated after the digestion and identified as belonging to Lactococcus lactis and Lactobacillus paracasei through partial sequencing of 16S rRNA gene. Three strains of Lactococcus lactis, three of Lactobacillus paracasei and a mix of them were inoculated in triplicate in whole pasteurized milk and digested after fermentation: a microbial reduction ranging between 3.3 and 3.8 Log CFU/g was observed, suggesting that TMM-cheese isolates are not naturally able to survive to the gastrointestinal digestion. The same strains were used to ferment milk with different fat content (about 0.5, 1.5 and 3.5%) and highest counts were registered in fermented whole milk (3.5 % fat), suggesting that a slight increase of fat percentage may determine a higher resistance to in vitro gastrointestinal digestion. Finally, samples of milk cream (fat content of 27%) were subjected to simulated digestion. Comparing the microbial counts of TMM-cheese, milk cream and fermented whole milk samples, a reduction of 0.8, 1.9 and 3.3 orders of magnitude was observed, respectively. In conclusion, both the fat content and the texture of TMM-cheese showed a effect of protection on lactic acid bacteria during transit in the gastrointestinal tract.