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Impact of farm management on microflora of raw bovine milk: a Swedish farm based study

Manufacturers of long-ripened hard cheese worldwide share the problem with a costly variation in ripening time required to achieve the characteristic flavor of a specific cheese. The variation is partly considered to originate from the composition and properties of the raw milk, which in turn is influenced by on-farm management. Non-starter lactic acid bacteria stemming from the raw milk, especially *Lactobacillus*, have been identified as crucial for flavor development in cheese. Thus, the aim of this study was to explore the impact of farm management on raw milk microflora.

Bulk milk samples from 45 farms located in northern Sweden were collected monthly during one year and samples from 6 of these months were used in the current study. Farm visits were conducted on two occasions to collect data on management factors, e.g. feeding and forage production, milking system, hygiene and udder health. The microbial community of the raw milk was investigated with DNA based amplicon sequencing approach targeting 16S rRNA with illumina Miseq platform. Canonical correspondence analysis (CCA) was used to elucidate correlations between microbial data and farm management factors.

Amplicon sequencing indicated that the overall microbial diversity richness was at similar level, no variation was observed between farms or between months of sampling. However, taxa evenness as measured by Simpson index was lower in December. The two psychrotrophic genera *Pseudomonas* and *Acinetobacter* were the most commonly dominant bacteria observed. Lactic acid bacteria – order Lactobacillales – had an average relative abundance of 11.8%, varying from 0.1 – 77%. CCA analysis showed a strong correlation between milking system and microflora present in raw milk. For instance, all OTUs from *Streptococcus* had higher relative abundance in robot milking systems; the only OTU from *Lactobacillus* was higher in conventional milking systems. Results are currently being validated with additional sequencing data from extra months.

In conclusion; several on-farm management factors correlating with milk microflora were identified. Results from our research will be used in the development of best practice protocols for production of raw milk that will benefit manufacture of long-ripened cheese.

Keywords: farm management, microflora, bovine milk