

Milk Genomics from a Technological Perspective

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Within the Danish-Swedish Milk Genomics Initiative one of the important technological properties profiled and studied in detail was the rennet-induced coagulation properties, and how these are influenced by milk composition, genes, storage, calcium addition etc. Milk and tissue samples were obtained from approximately 400 cows of each of Danish Friesian (DH), Danish Jersey (DJ) and Swedish Red (SR) and constituted the basis of overall as well as in-depth profiling of the variances in the composition of Scandinavian dairy milk at the cow level. The analyses included important features of both milk fat, proteins and metabolites, as well as important technological properties, in addition to free oligosaccharides, calcium distribution and vitamins. Furthermore, all cows were genotyped using 777 K Illumina BovineHD BeadChip.

The distinct milk coagulation properties among breeds were related to some extent, but not exclusively, to casein gene polymorphisms. The studies revealed new genetic variants present in Danish dairy milk, including the C variant of α_{S1} -CN, the I variant of β -CN and the E variant of κ -CN. The great variation in coagulation properties among individual cows and breeds were examined more closely using proteomic techniques to identify genetic variants and isoforms in milk proteins, and the importance of post translational modifications (PTMs) for both first and second phase of milk coagulation was shown.

The results showed that the coagulation descriptors rennet coagulation time (RCT) and curd firming rate (CFR) were differentially related to milk compositional parameters, and reacted differently to cold storage of raw milk. In addition, a range of milk metabolites were found to be significantly different between good and non-coagulating milk. Heritability estimation confirmed that milk coagulation is under genetic influence and GWAS identified new genomic regions both in relation to milk coagulation as well as non-coagulation. Besides a major QTL around the casein genes identified in both the SR and DH, additional regions affecting milk coagulation were identified in close proximity to genes influencing glycosylation and phosphorylation, as well as proteolysis. The project has revealed the presence of large biological variation in milk composition and linked this to genetic information, which could potentially be exploited in breeding schemes, either in order to obtain differentiated products, or to achieve an overall improved milk composition in relation to technological properties and exploitation of milk components as ingredients.