

Composition and enzymatic activity in bulk milk from dairy farms with conventional or robotic milking systems

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Short title: Milking systems and milk quality in commercial dairy herds

Summary (max 300 words)

The objective of this research communication was to evaluate effects of milking system on composition and enzymatic activities of bulk milk from Swedish dairy farms under commercial conditions. Bulk milk samples from 104 dairy farms, 51 with automatic milking (AMS) and 53 with conventional milking systems (CMS), were collected and analysed for contents of total fat and protein, free fatty acids (FFA), caseins and whey proteins, somatic cell counts (SCC), pH, plasmin and plasminogen derived activities, and total proteolysis. Our results showed a lower protein content and higher SCC in milk from AMS herds compared to milk from CMS herds. Moreover, plasmin, plasminogen and plasmin/plasminogen derived activities were lower in AMS milk, but despite this, total casein and the β -casein fraction (% of total protein) were lower in AMS than in CMS milk. Average total proteolysis was higher in milk from AMS herds, suggesting that other proteases than plasmin, e.g. cellular and bacterial proteases, contributed to the degradation of casein. This is supported by a positive correlation between SCC and total proteolysis ($p < 0.001$), as well as negative correlations between SCC and β -casein fraction ($p < 0.05$), and between total proteolysis and β -casein fraction ($p < 0.05$). In conclusion, comparing the quality of bulk milk from commercial dairy herds using AMS or CMS, respectively, we found a significant influence from milking system.