

Summary

Bovine milk is a major source of nutrients in the human diet and contains between 3% and 6% fat. 'Milk fat' is the collective term used for a large number of individual fatty acids (FA), which can roughly be divided into saturated FA (SFA) and unsaturated FA (UFA). The composition of FA in milk varies considerably between cows and herds, mainly due to differences in the genetics and nutrition of cows. Since FA composition in milk is related to the processability of milk and also estimated to be related to human health, there is an increasing interest in the possibilities for modifying FA composition. As FA composition in milk is influenced by genetic factors, possible breed differences might be employed for modifying FA composition in the desired direction. In worldwide dairy cattle breeding, since the 1980s, a change has been observed from the use of native breeds toward the use of large and internationally-used mainstream breeds. In the Netherlands, this change has become clearly visible as native dual purpose breeds like Meuse-Rhine-Yssel (MRY), Dutch Friesian (DF) and Groningen White Headed (GWH) are to a large extent being replaced by the globally mainstream breed Holstein Friesian (HF). As a result, these native breeds are now numerically small. Therefore, in this thesis, two fields of interest were combined: the production of milk with a specific milk fat composition and the conservation of native cattle breeds. The overall objective of the thesis was to investigate whether native dual purpose breeds comprise different genetic variations for milk fat composition among one another and compared to the mainstream HF breed.

Chapter 2 describes the detailed FA composition in milk produced on farms using the native dual purpose breeds MRV, DF, GWH and the globally mainstream Jersey (JER) breed. In total, milk samples were collected on 12 farms and for each breed, around 50 cows were sampled on three farms. All milk samples were analysed by gas chromatography (GC). For all studied individual FA (13), groups of FA (9) and unsaturation indices (5), differences in FA composition were found among the groups of farms using different cattle breeds. The proportion of the UFA group relative to the total FA was largest for GWH (26.7%) compared with MRV (24.3%) and DF (23.2%), and smallest for JER (22.7%). This suggests that selecting specific FA composition differences in farms using different breeds in the Netherlands can attribute to modifying the FA composition in bovine milk production.

Because GC is an expensive and time-consuming method for analysing FA composition in milk, the use of mid-infrared spectrometry (MIR) for analysing FA composition in milk of different breeds was validated (Chapter 3). Calibration equations used to predict FA composition using MIR were based on a dataset containing 1236 milk samples from multiple cattle breeds from Ireland, Scotland and the Walloon region of Belgium. These calibration equations were used to predict 11 individual (mainly short- and medium-chain) FA and three groups of FA of milk from 190 cows in the Netherlands across the breeds MRV, DF, GWH and JER. The FA composition of these 190 milk samples from Dutch cows were also analysed by GC and used as the gold standard. For the majority of FA composition, the predictions were highly accurate (validation $R^2 > 0.80$). This implies that MIR can be a suitable method for predicting FA composition among different breeds and countries.

In Chapter 4, FA composition in milk was predicted using MIR for a large number of cows, including different breeds in the Netherlands. The data contained MIR spectra of in total 1769 purebred cows belonging to the breeds MRY, DF, GWH and JER, 15 050 purebred HF cows and 7626 crossbred cows belonging to the breeds HF, MRY, DF, GWH and JER. Using MIR, FA content in milk was predicted. Analyses were conducted either by adjusting or not adjusting for fat percentage in order to be able to compare different breeds, independent of the level of fat percentage in milk. After adjusting for differences in fat percentage, differences among breeds in detailed fat composition disappeared or became smaller for several short- and medium-chain FAs, whereas for several long-chain unsaturated FAs, more significant breed differences were found. This indicated that short- and medium-chain FA content were for all breeds stronger related to total fat percentage than it was for long-chain FA content. In conclusion, the observed differences in fat composition in milk between HF, MRY and DF were insignificant. JER cows tended to produce a relatively higher SFA content, whereas GWH tended to produce a relatively higher UFA content and especially less short-chain SFA and more long-chain FA when adjusting for differences in fat percentage per breed.

Besides the variation in FA composition between breeds, the within-breed variation for 14 individual FAs and 14 groups of FAs in milk of the breeds HF and MRY was also investigated (Chapter 5). Additive genetic variances and heritabilities were estimated using records of 96 315 HF cows, as well as a MRY population containing 2049 cows. Heritabilities of the groups of FAs for HF ranged from 0.19 to 0.53 and for MRY from 0.11 to 0.28. For the majority of the individual FAs, the additive genetic variances for HF were on average 1.9 times higher compared to the MRY population, except for most of the polyunsaturated FAs. This implied that there was less potential for selection according to detailed FA content in the MRY breed compared to HF cows.

To gain a better insight into the background of genetic variations in FA composition between and within breeds, in Chapter 6, similarities in genomic variation associated with detailed milk fat composition between the Holstein Friesian (HF) breed and native dual purpose breeds MRY, DF and GWH were investigated. The genotypic and phenotypic information of 1867 cows were used in this investigation. Genomic breeding values (GEBV) were estimated for the milk composition of MRY, DF and GWH breeds, using single nucleotide polymorphism (SNP) effects estimated in HF. Comparing the native Dutch dual purpose breeds, the GEBV calculated for the MRY breed were clearly least reliable, indicating that the genetic variation associated with milk fat composition of MRY differed most from HF. For both DF and GWH, the estimated SNP effects for FA composition based on HF data showed a substantial predictive ability for several traits and were highest in GWH. In addition, correlations between the allele frequencies of the breeds MRY, GWH, DF and HF were calculated. These correlations proved similar between any pair of the native Dutch dual purpose breeds and HF when considering all SNPs (on average 0.68). Focussing on SNPs that had a large effect on milk FA composition in HF (at regions on BTA 5, 14 and 26), however, showed strong differences in allele frequencies when comparing the native Dutch dual

purpose breeds with HF (average correlation 0.50-0.53). Nevertheless, there was no consistent relationship between differences in GEBV reliability and allele frequencies when using target subsets of SNPs with increasingly larger effects in HF. In conclusion, differences were detected between the native breeds MRY, DF and GWH in genomic variations of regions that are associated with FA composition in HF, while most variation in these main regions was clearly observed in HF. The similarity between the native dual purpose breeds and HF in variances in FA associated with genomic variation was visibly lowest for the native MRY breed.

In the general discussion (Chapter 7), the genetic variability in cattle associated with milk FA composition was first discussed. Overall, it was concluded that no large differences existed in milk FA composition among the native Dutch dual purpose breeds and the mainstream HF breed. The main observed difference was that the GWH breed seemed to produce relatively less SFA and more UFA, especially long-chain UFA. Concerning the *DGAT1* gene, which is highly related to FA composition in HF, the native Dutch dual purpose breeds had less genetic variation compared to HF and appeared to mainly carry the genotype AA. However, limited differences in levels of FA composition in milk were found among breeds when comparing different breeds on different farms; however, this did not indicate any obvious variations. It is suggested that this was partly the result of the substantial diversity of farmers using different native dual purpose cattle breeds.

In the second part of the discussion, attention was paid to the diversity of farmers using different cattle breeds and the use of numerically small cattle breeds in the Dutch dairy sector. Opportunities for native dual purpose breeds lie in the use of these breeds in specific farming systems (e.g., organic and social-care farming) and at a cultural level (e.g., the cultural heritage of local use and craft animal products), rather than in competing with the HF breed. Finally, in the long-term, it is important to conserve breeds, as they may possibly be needed for adaptation to unknown future production environments.