Proportion Saturated And Unsaturated Fatty Acids In Milk Of Four Cattle Breeds In The Netherlands

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Introduction

A large shift in breed composition of the Dutch dairy cattle population has taken place over the last decades. This shift was mainly driven by a change in breeding goal towards high milk production and resulted in a population dominated by the Holstein Friesian (HF) breed. Recently, in dairy cattle breeding, more attention is paid to other traits like robustness and also milk quality related to human health. Selecting cows, which are able to produce a more desirable milk composition, would be an important instrument to change milk quality in favor of human health. From that perspective, differences in milk composition and heritabilities of milk quality traits are estimated within several studies.

The fatty acid (FA) composition is one of the main elements in milk which has an effect on human health. For example, the intake of saturated FA (SFA) is found to be positive associated to the occurrence of heart diseases and obesity in several studies (e.g. Mensink *et al.* (2003)). Estimated heritabilities of the proportions SFA, unsaturated FA (UFA) and the ratio SFA/UFA in milk of Dutch Holstein Friesian (HF) cows, are reported in the range from 0.20 to 0.30 (Schennink *et al.* (2009); Stoop *et al.* (2008)). Breed differences in FA composition are also reported in several other studies (Carroll *et al.* (2006); Lawless *et al.* (1999); Soyeurt *et al.* (2006)). The major breeds, mainly HF and Jersey (JER), are included in the majority of these studies, while only a few studies included local or regional breeds.

To what extent the Dutch dairy breeds add to the total genetic variance in individual milk fat composition is an important question as the Dutch dairy industry is interested in possibilities to modify the milk composition. The aim of this paper, therefore, is to analyze the differences in SFA and UFA proportions among cattle breeds in the Netherlands. For the local Dutch breeds Dutch Friesian (DF), Meuse-Rhine-Yssel (MRY), and Groningen White Headed (GWH), and one international breed (JER), SFA and UFA proportions in the milk were determined.

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Material and methods

Data collection, analysis of milk samples and traits. To study the proportion SFA and UFA in milk of different cattle breeds in the Netherlands, in total 192 milk samples were collected. The milk samples were single measurements taken during morning milking from December 2008 until March 2009 of the breeds DF (47 samples from 3 farms of which one organic), MRY (54 samples from 3 farms of which one organic), GWH (45 samples from 3 farms of which one organic), and JER (46 samples from 3 farms of which two organic). The milk samples were treated directly after collection with 0.03% (*w/w*) sodium azide to avoid microbiological growth. On each farm the selected animals were of the same breed and varied as much as possible in age, stage of lactation and sire.

The milk samples were analyzed using Gas Chromatography (GC) at the laboratory of Qlip N.V. (Leusden, The Netherlands) to obtain the detailed FA composition. The percentage of total fat was obtained from standard mid-infrared spectrometry using a Fourier-transformed interferogram (MilkoScan FT 6000, Foss Electric, Denmark).

The groups of SFA and UFA were defined as follow SFA: C4:0, C5:0, C6:0, C7:0, C8:0, C9:0, C10:0, C11:0, C12:0, C14:0, C14:0 *iso*, C15:0, C15:0 *iso*, C15:0 *ante iso*, C16:0, C16:0 *iso*, C17:0, C17:0 *iso*, C17:0 *ante iso*, C18:0, C19:0, C20:0 and UFA: C10:1, C12:1, C14:1, C16:1, C17:1, C18:1 *trans*-6, C18:1 *trans*-9, C18:1 *trans*-10, C18:1 *trans*-12, C18:1 *cis*-9, C18:1 *cis*-11, C18:1 *cis*-12, C18:2 *cis*-9-12, C18:3 *cis*-9-12-15, C18:2 *cis*-9-*trans*-11, C20:3 *cis*-8-11-14.

Statistical analyses. To investigate breed differences in total fat percentage, proportions of SFA, and proportions of UFA Least Square Means (LSM) were calculated using the General Linear Model procedure with the Bonferroni adjustment for multiple comparisons in the Statistical Analysis System version 9.1 (SAS-Institute, 2003).

The model included:

$$y_{ijklmno} = \mu + dim_i + parity_j + b_j * age_{jk} + breed_l + system_m + farm_n(breed_l * system_m) + e_{ijklmno}$$

where $y_{ijklmno}$ was the dependent variable for cow *o* in the class *i* for stage of lactation, during parity *j*, with calving age *k*, from breed *l*, from farm *n* being an organic or conventional farm system *m*. The μ was the overall intercept of the model; dim_i was the class variable stage of lactation containing 12 classes, were class 1 was days 1-30, class 2 days 31-60, etc, and class 12 days > 330; $parity_j$ was a class variable containing 9 lactation numbers (were 9 was lactation 9 and higher); age_k was calving age in days which interacted with $parity_j$; $breed_l$ was a class variable; $system_m$ was a class variable indicating a conventional or organic farm; $farm_n(breed_l*system_m)$ was a nested class variable with farm nested within breed and system; and $e_{ijklmno}$ is the residual.

Results and discussion

For the model factors calving age, parity, and stage of lactation, ordinary means and standard deviations were calculated for each breed (Table 1). The means and standard deviations of these factors show that for each breed cows were selected with different calving ages, parities, and lactation stages. On average the MRY cows were somewhat younger, while the JER cows were somewhat older and the FH cows were on average shortest in lactation, while the JER were on average longest in lactation.

Table 1: The means and standard deviations of the factors in the model

Breed	DF		MRY		GWH		JER	
N	47		54		45		46	
	mean	stddev	mean	stddev	mean	stddev	mean	stddev
Calving Age (d)	1566	919	1497	731	1717	958	1805	927
Parity	2.9	2.5	2.8	1.9	3.2	2.5	3.6	2.4
Stage of Lactation (d)	143.51	112.26	174.35	130.46	159.67	93.21	211.13	131.68

The LSM results showed the same trend as the ordinary means of all traits (results not shown). The JER milk contained on average the highest percentage of total fat, while the GWH milk contained on average the lowest percentage of total fat (Table 2). The differences between the breeds in milk production traits, like total fat percentage, within the dataset used are comparable to the national milk production statistics (CRV (2009)), which supports that the selected farms are representative for the different breeds (results not shown).

The local Dutch breed GWH produced relatively less SFA and most UFA, while the mainstream JER produced relatively most SFA and, consequently, less UFA (Table 2). For the Dutch HF breed proportions of 70.76% SFA and 25.69% UFA were reported by Schennink *et al.* (2009). For the US HF breed SFA proportions in milk were reported ranging from 67.11 to 67.25 and SFA proportions ranging from 32.54 to 32.68 (Bobe *et al.* (2008); Bobe *et al.* (2007)). For a Belgian cattle population including several breeds an average SFA proportion of 66.26 was reported (Soyeurt *et al.* (2006)). Differences in trait definition of SFA and UFA between studies in the comparison above are very minor and therefore ignored. Differences in management factors between studies however are important. A major management factor is access to pasture. Grazing based feeding has an increasing effect on the proportion of UFA and a decreasing effect on the proportion of SFA (Heck *et al.* (2009)). The sampled cows in the current study were all kept indoors (no grazing). This indoor housing system was also the case in the study of Schennink *et al.* (2009).

Breed effects were estimated to be significant ($P < 0.05$) in the model for all three traits. Per trait, at least two breeds were estimated to be significant different from each other (Table 2).

Table 2: For each trait the LSM of all breeds, standard error and model R^2.

	LSM				SE	Model R^2
Breed	DF	MRY	GWH	JER		
Trait						
Total fat (%)	4.58^{b}	4.54^{b}	4.47^{b}	5.93^{a}	0.38-0.41	0.69
SFA (g/100g fat)	$73.62^{a,b}$	72.08^{b}	68.60^{c}	74.35^{a}	1.71-1.85	0.60
UFA (g/100g fat)	$23.81^{b,c}$	24.70^{b}	27.18^{a}	22.80^{c}	1.60-1.74	0.57

^{a,b,c} different superscripts within a row indicate significance differences at $P<0.05$.

The breed differences in current study were quantified using only phenotypic information. Differences among breeds can also be quantified with genotypic information. The unsaturated fractions of some short chain FA and most long chain FA, for example, are affected by the *DGAT1* and *SCD1* genes (Schennink *et al.* (2008); Schennink *et al.* (2009); Stoop *et al.* (2009)). Breed differences found in the current study can also possibly partly be explained by differences in frequencies of the allele variants of the *DGAT1* and *SCD1* genes. The effects of such genes in these breeds, however, have not been investigated so far.

Conclusion

These results clearly show breed differences in the proportions of SFA and UFA in milk. This indicates that Dutch cattle breeds add to the genetic variability in milk fat composition. Based on these results the GWH breed produces the most favorable milk composition. To be able to determine which breed produces the most favorable milk FA composition and to what extent the breeds add to the genetic variability, detailed information on individual FA composition and more records per breed are needed.

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