

Farm Level Economic Implications of Genetic Selection for Improving Milk Fat Composition

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ABSTRACT

The objective of the study was to assess the farm level economic implications of value-adding genetic selection strategies to improve milk fat composition. Selection based on a quantitative trait (ratio of total saturated to total unsaturated fatty acids in milk) or a known genotype (for the *DGATI* gene) was considered. Technical and economic performance of hypothetical herds were computed by a herd optimization and simulation model. It was assumed that the herds are already bred for the specific milk composition, and the transition period was not considered. Correlated effects of the selection scenarios on milk production, female fertility, and functional longevity traits were accounted for. Results showed that increasing the total unsaturated fatty acids in milk by traditional selection leads to lower net revenue, whereas selection based on *DGATI* genotype results in slightly higher net revenue. Our results, therefore, suggest that genetic selection based on *DGATI* genotype is a more profitable strategy for dairy farmers than selection based on phenotypes for SFA/UFA ratio. Key words: dairy cattle, genetic selection, milk composition, farm economics.

INTRODUCTION

In the past decades, there has been a steady move in global dairying from producing bulk commodities towards producing specialized, value-added dairy products aimed at niche markets (Boland et al., 2001, Creamer et al., 2002). Although methods to increase the value added have been developed at different stages within the dairy supply chain, recently attention has been directed to creating value-added on-farm. Consequently, dairy farmers consider shifting from producing commodity milk to producing milk with specialized composition to meet consumer or industrial demands (e.g., Dooley et al., 2005a, Demeter et al., 2009a). Raw milk with special characteristics can be produced by applying new knowledge in herd management, animal nutrition, and genetic selection. The present paper focuses on the last aspect, i.e. producing raw milk with specialized composition by means of genetic selection.

Genetic aspects of milk composition have been extensively investigated over the past decades. Genetic research has traditionally focused on improving milk composition by altering fat and protein content. This was stimulated by payment schemes to farmers that, in most countries, are based on fat and protein content. In recent years, however, the rapid progress in the fields of genomics and bioinformatics has developed an unprecedented biological information base and tool set (German et al., 2006). Consequently, there is a growing industry interest in more detailed alteration of milk composition to better utilize milk's biological potential (Dooley et al., 2005a, Demeter et al., 2009a). An important research direction has been the use of genetic selection to change fat composition in milk. Milk fat composition is important due to its effect on human health (e.g., German and Dillard, 2006, Steijns, 2008). Therefore, changing milk fat profile can improve the nutritional quality of milk as raw material and hence can lead to improved dairy products for human health.

Recent genetic research has shown opportunities to improve milk fat (Soyeurt et al., 2007, Bobe et al., 2008, Stoop et al., 2008) composition. However, little is known about the economic implications of these selection strategies for dairy farmers. Until now, little progress has been made in modeling the implications of value-adding selection scenarios. The objective of the study was to assess the economic implications of value-adding genetic selection strategies aiming at improving milk fat composition. Selection based on a quantitative trait or a known genotype was considered. Four selection scenarios were considered, and selection only for a single trait or genotype was assumed in each scenario. Technical and economic outputs of a herd were obtained by a herd optimization and simulation model (Demeter et al., 2011). This research tool ensured that the selection's potential correlated response on other economically important traits are properly taken into

account. Results were computed for base scenario (herd without selection) and compared with results of hypothetical herds that are bred for specialized milk composition. In this study, selection in Dutch Holstein-Friesian cattle was simulated as a case.

MATERIALS AND METHODS

Model Description

To study the expected production of hypothetical herds that produce milk with valuable composition, we used the herd optimization and simulation model of Demeter et al. (2011). This model was chosen because of its twofold ability. First, it can determine economically optimal insemination and replacement decisions for individual dairy cows under the specified production conditions. Second, the model can be used to simulate whole-herd technical and economic outputs that would follow from the optimal breeding and culling policies for the individual cows. The first step is vital because it ensures that the selection's possible effects on other economically important traits are properly accounted for. Therefore, the production system can be optimized both at the base situation (i.e. without selection) and after selecting for a valuable trait. Subsequently, technical and economic values are always derived from optimized production systems (Dekkers, 1991). The overall model consists of two main parts: a bioeconomic and a mathematical model. In the following, these model parts are briefly introduced, however, for detailed description we refer the reader to Demeter et al. (2011).

Bioeconomic Model. The function of the bioeconomic model was to compute the revenues and costs of individual dairy cows during their productive life. The model considered only the activity of milk production, with milk revenues, calf revenues, culled cow revenues, feed costs, replacement costs, insemination costs, sundry costs (opportunity cost, regular veterinary cost, and cost of fixed production assets), and losses due to involuntary culling. The farmer's labor was not included in the calculation of costs, and thus the net revenues represent the financial compensation to the farmer for labor and management. The bioeconomic model calculated revenues and costs in monthly intervals for all individual cow states. A cow state was the combination of the main properties that characterize a cow. A cow could be in a state described by one of the 12 parities (1 to 12), 8 present open periods (2 to 9 mo), 8 previous open periods (2 to 9 mo), 18 lactation stages (1 to 18 mo), 13 classes for estimated milk yield potential when entering the herd as heifer (1 to 13), 13 classes for updated milk yield potential when starting a new lactation (1 to 13), and 169 classes for actual milk yield level (1 to 169). The input values and model parameters were selected to simulate the performance of DHF cows. Prices represented the 2008-2009 Dutch farming conditions.

Mathematical Model. The function of the mathematical model was twofold. First, it optimized insemination and replacement decisions for all individual cow states. Second, the mathematical model performed Markov chain simulations to obtain whole-herd results that followed from the optimal policies for the individual animals within the herd. The optimization problem for inseminations and replacements was modeled as a multi-level hierarchic Markov process (**MLHMP**) (Kristensen and Jørgensen, 2000). This technique combines the advantageous properties of two different optimization methods (policy iteration and value iteration) in a multi-level hierarchic manner. With this technique detailed real-world applications with large state space can be solved with fast convergence and exact solution. Optimal insemination and replacement decisions were found by maximizing the total expected discounted net revenues (annual discount rate of 5%). The necessary revenues, costs, physical quantities, and transition probabilities were computed by the bioeconomic model. The mathematical model (together with the bioeconomic model) was programmed entirely in Java and used as a plug-in to the MLHMP software system developed by Kristensen (2003).

Selection Traits, Genotypes, and Scenarios

Background. This study is part of the Dutch Milk Genomics Initiative (**DMGI**), which focuses on the genetic background of detailed milk composition (see e.g., Heck, 2009, Schennink, 2009, Stoop, 2009, Schopen, 2010). In the project, approximately 2,000 first parity cows from 400 herds (distributed throughout the Netherlands) were selected. Selection was based on pedigree information of the cooperative cattle improvement organization CRV (Arnhem, the Netherlands). Cows descended from one of either 5 proven sires, 50 test sires, or 15 additional proven sires. Each cow was at least 87.5% Holstein-Friesian. Three morning milk samples per cow were collected between February and July 2005. Blood samples of cows and semen samples of bulls were used to extract DNA. Additional management information on herd size, feeding practice, and health were available from 88% of the farms.

The selection scenarios were modeled on Dutch Holstein-Friesian (**DHF**) cattle. This choice was due to the large amount of recent information available in this breed on the genetic background of detailed milk composition. We considered scenarios to improve milk fat composition. Two selection scenarios based on a quantitative trait selection and two scenarios based on genotype selection were assessed. Each quantitative trait was a fat composition trait, which is affected by many loci and is measured on a continuous scale. Each genotype was considered at a single locus, which is known to affect milk fat composition. Furthermore, single-trait selection was assumed in each scenario (i.e. selection on single trait or genotype).

Trait Related to Fat Composition. The quantitative trait concerning milk fat was the ratio of saturated fatty acids (**SFA**) to unsaturated fatty acids (**UFA**) in milk. Increasing UFA content in milk appears to be a realistic selection objective in dairy cattle. More UFA seems to be positively associated with human health, as it might decrease cardiovascular disease risk, cholesterol levels, obesity, and diabetes (Maijala, 2000, Williams, 2000). Also, milk with higher UFA content can be processed into butter with improved spreadability (Stegeman et al., 1992). Furthermore, cows producing milk with more UFA seem to be less prone to severe negative energy balance (Van Knegsel et al., 2007). A recent study by Stoop et al. (2008) has shown genetic variation in the ratio SFA/UFA with moderate heritability (0.28) in DHF cows. They found a mean SFA/UFA of 2.80 in winter samples, indicating that approximately 74% of the total milk fat was saturated and 26% was unsaturated. Stoop et al. (2008) reported the ratio SFA/UFA of 2.17 and 3.38 for the lowest and highest 5% of the cows in their sample.

We considered two strategies for decreasing the SFA/UFA ratio. The first involves using bulls with superior EBV for decreasing SFA/UFA ratio to breed a subset of cows to produce the next generation. This strategy can be implemented in the current breeding scheme, without affecting the breeding scheme. Consequently, there will be no genetic improvement in the population average of the bulls over generations. By using superior bulls, the genetic improvement in the offspring will reach a plateau with an asymptotic improvement equal to the selection differential of the selected bulls. We considered using the best 25 out of 200 annually tested sires, i.e. using the 12.5% best bulls with respect to decreasing SFA/UFA ratio. The selection differential of the bulls is the product of selection intensity, accuracy, and additive genetic standard deviation. The selection intensity equals 1.65; assuming 100 progeny with information and a heritability of SFA/UFA of 0.28 (Stoop et al., 2008), the accuracy equals 0.82; and the additive genetic standard deviation of SFA/UFA equals 0.16 (Stoop et al., 2008). The obtained selection differential equals -0.22 . Therefore, the continuous use of top bulls would result in a new SFA/UFA ratio of 2.58 (**scenario FTB**).

The second strategy implements a new breeding scheme with the sole objective to decrease SFA/UFA ratio. In this strategy, the cows and bulls with the best EBV for the trait of interest are chosen as parents to produce the next generation. This breeding program will lead to a continuous genetic improvement of the whole population over generations. Following Stoop (2009), we quantified the amount of genetic gain that can be achieved with this strategy

by using the SelAction software (Rutten et al., 2002). The results showed that the single-trait genetic selection on SFA/UFA ratio in DHF cattle would result in a yearly genetic gain of -0.027 . In this study, we modeled the effects of a breeding program after 25 years. The time frame was chosen to be in line with scenario 1, where the maximum improvement can be achieved in approximately the same time. A 25 years breeding program would lead to a total genetic gain in SFA/UFA ratio of -0.67 , leading to a ratio of 2.13 (**scenario FBS**).

Genotype Related to Fat Composition. Another way to improve milk fat composition may be to select cows based on *DGAT1* genotype. The *DGAT1* gene, which codes for acyl-coenzyme A:diacylglycerol acyltransferase 1, is located on chromosome 14 in cattle (Grisart et al., 2002, Winter et al., 2002) and plays a key role in triacylglycerol synthesis. The *DGAT1* gene was chosen because Schennink et al. (2007) has recently found that a lysine-to-alanine polymorphism in *DGAT1* (**K232A**) affects milk fatty acid (FA) composition in DHF cows. The *DGAT1* K232A polymorphism explained a large part of the genetic variation in milk fat composition, e.g. 40% of the genetic variation in palmitic acid (C16:0), 53% of the genetic variation in unsaturated C18 FA, and 36% of the genetic variation in the ratio SFA/UFA. Later, Schennink et al. (2008) showed that the same polymorphism also explains some of the genetic variation in the milk fat unsaturation indices. The latter two studies by Schennink and colleagues (2007, 2008) concluded that breeding cows with the AA genotype is desirable due to its association with more UFA, less palmitic acid (C16:0), and more unsaturated C18 FA. We modeled two herds: one with cows that are homozygous for the A allele (**scenario DGAT1A**) and one with cows that are homozygous for the K allele (**scenario DGAT1K**).

Correlated Effects of Selection Scenarios

The mathematical model optimizes the dairy production system by finding the economically optimal insemination and replacement policies. Therefore, it is imperative to know the correlated effects of the selection traits on biological traits that influence insemination and replacement decisions. These traits are production, reproduction, and functional longevity (Van Arendonk, 1985, Van Arendonk and Dijkhuizen, 1985, Rogers et al., 1988a, 1988b). Therefore, when selection influences either of these traits, the production system needs to be re-optimized to draw unbiased conclusions on the economic implications.

Effects on Milk Production. Milk production traits have large effect on optimal culling decisions. When the production level in the herd increases, insemination decisions are not affected but replacement becomes more intense due to higher voluntary replacement (Van Arendonk, 1985, Rogers et al., 1988a). When production level decreases, the opposite effect occurs. Herd production level, therefore, influences optimal herd composition and thus farm profitability. In the herd optimization model, production traits are captured by three key biological inputs: mature mean 305-d milk yield (kg), mature mean 305-d fat content (%), and mature mean 305-d protein content (%). Correlated effects on these traits were quantified by different approaches for scenario FTB, scenario FBS, and scenario DGAT1A and DGAT1K.

In scenario FTB, the correlated effects of using bulls with superior EBV are inferred by using standard breeding formulas. More specifically, the correlated responses of lowering SFA/UFA ratio are calculated from the following components: selection intensity, accuracy for the selection trait, genetic correlation between selection criteria and production traits, and additive genetic standard deviation of production trait. The necessary genetic parameters were taken from the studies of Stoop et al. (2008). Genetic parameters in the latter study were based on first parity morning milk yield, morning milk fat content, and morning milk protein content. Therefore, correlated responses were calculated for these production traits. Then the obtained results were used as proxies for the mature 305-d production traits in our model.

In FBS, correlated effects on production traits were inferred by using the SelAction software (Rutten et al., 2002). Correlated responses were calculated on morning production traits, and then these effects were used as proxies for the mature 305-d production traits. We

illustrate the calculations through the correlated effect of FBS on milk yield. The annual correlated response of a new breeding scheme to decrease SFA/UFA ratio on morning milk yield was 0.053 kg. Therefore, the total effect of a breeding scheme after 25 years is 1.325 kg. In the study of Stoop et al. (2008), from which genetic parameters were taken, the mean morning milk yield was 13.50 kg. An increase of 1.325 kg, therefore, represents a proportional change of 9.81% in morning milk yield. We assumed that 305-d milk yield changes to the same extent as morning milk yield. Consequently, the base mature mean 305-d milk yield of 9,000 kg was increased by 9.81% when modeling FBS (Table 1). Correlated effects of FBS and PBS on the base mean 305-d production traits are presented in Table 1.

For scenarios related to genotypes, the correlated effects of selecting on *DGATI* genotype are inferred from an unpublished association study in the DMGI project (**STUDY 1**). Associations between a large set of biological traits and *DGATI* genotypes were tested by fitting linear mixed models. The dataset was provided by CRV and included EBV of approximately 4,000 test bulls for 48 traits. These traits included milk yield, milk composition, body conformation, reproduction, longevity, and health. Each bull in the dataset was born between 1985 and 2005 and was at least 80% Dutch Holstein-Friesian. The statistical model included the effects of breed, birth year, animal, and *DGATI* genotype. Family relationships between animals were accounted for. Production traits included 305-d milk yield, 305-d fat content, and 305-d protein content. EBV for each production trait was combined for parity 1, 2, and 3, by weighting the parity specific EBV with 0.41, 0.33, and 0.26, respectively (CRV, 2010). Correlated effects on these combined production traits were calculated and used as proxies for mature 305-d production traits. Calculations are explained in the following.

Table 1. Proportional (%) changes in key biological inputs due to correlated response in the examined scenarios¹.

Biological inputs	Scenarios			
	FTB	FBS	DGAT1A	DGAT1K
Production				
Mean 305-d milk yield	+3.27	+9.81	+3.82	-5.68
Mean 305-d fat content	-8.46	-25.23	-6.82	+10.65
Mean 305-d protein content	-1.73	-4.99	-1.88	+2.99
Marginal conception probabilities	NS	NS	+3.44	+4.71
Marginal involuntary culling probabilities	+2.93	+9.27	NS	NS

¹NS indicates that the correlated response was statistically nonsignificant ($P > 0.05$). In this case, the default biological input value was not changed when modeling the scenario.

Consider the correlated effect of selecting for AA *DGATI* genotype on milk yield as an example. The parameter estimates from STUDY 1 showed that relative to the AK genotype, AA genotype was associated with 356 kg higher 305-d yield, whereas the KK genotype was associated with 351 kg lower 305-d yield ($P < 0.0001$). Assuming a frequency of 0.6 for the *DGATI* A allele, the genetic mean for 305-d milk yield of the base scenario becomes 72.07 kg. By selecting for AA genotype, the frequency of A allele becomes 1, resulting in a new genetic mean of 356.2 kg, which corresponds to an improvement of 284.13 kg. Assuming a mature mean 305-d yield of 9,000 kg, the mean 305-d yields for parity 1, 2, and 3 were computed by using age correction factors from Demeter et al. (2011). Next, the parity specific 305-d yields were weighted with 0.41, 0.33, and 0.26, resulting in weighted 305-d milk yield of 7,448 kg. Consequently, the increase of 284.13 kg represent an 3.82% increase in weighted 305-d yield. When modeling scenario DGAT1A, therefore, we increased the mature mean 305-d milk yield of 9,000 kg by 3.82% (Table 1). The correlated effects of the genotype-related scenarios on the three base 305-d production traits are shown in Table 1.

Effects on Reproduction. The reproductive performance of the cows determines optimal insemination decisions, which in turn influence culling decisions. Therefore, reproductive performance largely influences optimal herd composition and hence farm profitability. In the biological model, reproduction is modeled in monthly intervals in a twofold manner (for details see Demeter et al., 2011). In the first step, it is assumed that the first oestrus occurs in the second month after calving, with equal distribution within the month. In the second step, probabilities of conception after service are calculated using heat detection and conception rates, assuming a fixed cycle length of 21 d. Thus, effects of the selection scenarios on two aspects of cow reproduction needed to be considered: (a) effects on the period until the first oestrus and (b) effects on the conception rates following an insemination during lactation.

The quantified effects of the scenarios on reproduction were inferred from the studies of Demeter et al. (2009b). Those studies examined the phenotypic association in DHF cattle between fertility traits and major milk FA, and candidate genes that influence milk fat composition. From the fertility traits, we considered two particular: (a) interval (d) between calving and the first insemination (**DFS**) and (b) nonreturn rate (0/1) for insemination 28 d after the first insemination (**NR28**). The first trait was used as a proxy to measure the impact on the occurrence of the first oestrus. The second trait, although related to the first insemination in the first lactation, was used as a proxy to measure the impact on monthly conception rates following any insemination in any lactation. The regression coefficients from Demeter et al. (2009b) do not reflect the genetic relationship between the selection traits and the fertility traits. However, in this study we assumed that the effects were genetic effects.

Only the statistically significant ($P < 0.05$) relationships were taken into account when modeling the scenarios. Regarding DFS, Demeter et al. (2009b) found no significant relationship with the traits involved in our scenarios. Regarding NR28, no association was found for SFA/UFA ratio. However, the *DGAT1* polymorphism had significant relationship with NR28. Relative to the AA genotype, the AK genotype had 0.06 lower and the KK genotype had 0.01 higher NR28 (Demeter et al., 2009b). These estimates were converted into inputs for modeling scenario DGAT1A and DGAT1K as follows. Assuming a frequency of 0.6 for the *DGAT1* A allele, the genetic mean for NR28 of the base scenario becomes -0.03 . When selecting for AA genotype, the frequency of A allele becomes 1, resulting in a genetic mean of 0, which corresponds to an improvement of 0.03. Because the sample mean of NR28 was 0.79 in the study of Demeter et al. (2009b), the increase by 0.03 translates to 3.44% increase. Therefore, we proportionally increased the marginal conception probabilities by 3.44% in DGAT1A (Table 1). When selecting for KK genotype, NR28 increases by 0.04, which is a 4.71% improvement. Therefore, the marginal conception probabilities were proportionally increased by 4.71% in DGAT1K (Table 1).

Effects on Functional Longevity. Functional longevity (or functional stayability) can be defined as the cow's ability to delay involuntary replacement (Essl, 1998). Involuntary replacement refers to disposal that is not subject to decision making (i.e. due to low production). In the herd optimization model, the probability of involuntary replacement was calculated in monthly intervals from the probability of involuntary culling during the given parity and the monthly proportions of involuntary disposal within the parity (see Demeter et al., 2011). Although involuntary replacement has no effect on insemination decisions, it impacts herd composition and hence herd outcome. More intense involuntary culling, for example, leads to considerable economic losses (e.g., Van Arendonk, 1985, Rogers et al., 1988b, Demeter et al., 2011). Therefore, correlated effects of the scenarios on functional longevity were tested and accounted for in our analyses. Correlated effects were inferred by different approaches for scenarios based on phenotypes and scenarios based on genotypes.

For scenarios based on phenotypes, correlated effects were computed from an unpublished association study in the DMGI project (**STUDY 2**). Associations between functional longevity and SFA/UFA ratio were tested by fitting linear mixed models. Data

included observations on 1,917 cows, and lifetime information was available until 26 February 2010 (censoring date). The longevity trait was the length of productive life (**LPL**), i.e. the interval (d) between the date of first calving and date of culling. Mean LPL was 1308 d. Cows that did not have LPL information (i.e. were still in production) were also included in the analysis, with LPL at censoring date. Phenotypes on SFA/UFA ratio were pre-adjusted for age, season, lactation stage, and herd effects. The final model included the effects of month of culling, age at first calving, 305-d fat and protein corrected milk yield in first parity, and SFA/UFA ratio or CN-index. Significant ($P < 0.05$) association was found for SFA/UFA ratio. The parameter estimate was 96.55 ($P < 0.03$), indicating that increasing SFA/UFA ratio by one unit would result in 96.55 d longer LPL. This finding was further confirmed by the parameter estimates of additional analyses on binary stayability traits.

Because statistically significant effects were found only for SFA/UFA ratio, correlated effects were computed for scenario FTB and FBS. First, scenario FTB envisions decreasing SFA/UFA ratio by 0.22. Given the parameter estimate from STUDY 2, such decrease would result in 21.24 d shorter LPL. Given the sample mean of 1308 d, such decrease corresponds to 1.62% decline in LPL. Sensitivity analyses on the herd optimization model have shown that increasing the monthly marginal probabilities of involuntary culling by 2.93% (without re-optimizing decisions) results in approximately 1.62% decline in the simulated LPL. Therefore, marginal involuntary culling probabilities were increased by 2.93% when modeling scenario FTB (Table 1). Second, scenario FBS envisions decreasing SFA/UFA ratio by 0.67. This change in SFA/UFA ratio would lead to 64.69 d shorter LPL, which corresponds to 4.95% decline. Sensitivity analyses have shown that 9.27% increase in the monthly marginal probabilities of involuntary culling leads to approximately 4.95% decline in the simulated LPL. Consequently, marginal involuntary culling probabilities were increased by 9.27% when modeling scenario FBS (Table 1). Similarly to the effects on reproduction, we assumed that the correlated effects on functional longevity were genetic effects of the selection traits.

Correlated effects on functional longevity for scenarios based on genotypes were inferred from STUDY 1. Associations between the EBV of approximately 4,000 test bulls for functional longevity and *DGATI* genotypes were tested. Results showed no statistically significant ($P > 0.05$) associations. Consequently, the involuntary culling probabilities were unchanged when modeling genotype-related scenarios (see also Table 1).

Scope of the Study

Before reporting and discussing the results, it is important to highlight the underlying assumptions and outline what results were generated. Two key assumptions were included in the present study. First, the correlated effects of the selection scenarios were assumed to be known without error, although variation exists around the parameter estimates that were used for computing the correlated effects. Second, in the examined scenarios we attempted to model the performance of hypothetical dairy herds that are bred to produce milk with specialized composition. In other words, the actual transition period was not considered.

The generated results described the technical and economic performance of a herd that follows from optimal insemination and culling decisions for the individual cows. Results reflected averages and included productive herd life (mo/cow), calving interval (d/cow), annual total culling rate (%), proportion of voluntary cullings (%), milk yield (kg/cow/mo), fat yield (kg/cow/mo), protein yield (kg/cow/mo), roughage intake (kg DM/cow/mo), concentrate intake (kg DM/cow/mo), milk revenue (€/cow/mo), feed cost (€/cow/mo), insemination cost (€/cow/year), and net revenue (€/cow/mo). Results of the scenarios were compared with results of the base scenario, i.e. herd without genetic selection. Base results were generated by using default management, biological, and price input values from Demeter et al. (2011). When modeling the scenarios, the correlated effects on the selected biological traits were accounted for, but management and price input values were assumed to remain constant.

RESULTS

Results of the base and the modeled scenarios are presented in Table 2. Under the base scenario, the average productive herd life was 42.2 mo, indicating an annual culling rate of 28.4%. Voluntary culling accounted for 42.5% of all replacements. Average monthly milk yield was 734.6 kg per cow, with fat and protein yields of 31.4 and 25.6 kg. Milk revenue was €257.6 per month per cow, while monthly feed cost was €66.0 per cow. Average monthly net revenue, which was the financial compensation to the farmer's labor, was €39.9 per cow. Translating this figure to herd income, assuming a herd of 75 cows, which is the average herd size in the Netherlands, the resulting annual herd net revenue was approximately €35,900.

Under scenario FTB and FBS, which aimed to lower the mean SFA/UFA ratio to 2.58 and 2.13 (from 2.80), optimal replacement rate increased relative to the base scenario. Proportion of involuntary culling increased to 58.7% in FTB and 61.3% in FBS, due to negative effects on functional longevity. In FTB, monthly milk and protein yields per cow increased by 22.3 and 0.3 kg, whereas fat yield decreased by 1.7 kg. In FBS, milk and protein yields increased by 66.3 and 0.9 kg, while fat yield decreased by 5.7 kg. That is, the positive correlated effect on milk yield could offset the negative impact on protein content but could not prevent the loss in fat yield. Thus, monthly milk revenues per cow dropped by €3.3 and €11.6 in FTB and FBS, due to higher yield of carrier and lower yield of milk solids. Due to less milk solids, monthly concentrate intake decreased (by 5.8 kg DM in FTB and by 20.0 kg DM in FBS), leading to lower feed costs in both scenarios. Net revenue per 100 kg milk dropped by €0.5 and €1.6 in FTB and FBS relative to base scenario. Annual net revenue from an average herd of 75 cows decreased by around €2,400 under FTB and €8,200 under FBS.

Table 2. Parameters describing optimal insemination and replacement policy and resulting technical and economic results for different scenarios.

Parameters	Scenarios				
	Base	FTB	FBS	DGAT1A	DGAT1K
Productive herd life (mo/cow)	42.2	42.0	41.6	42.4	42.5
Calving interval ¹ (d/cow)	396.5	396.5	396.6	395.2	394.5
Annual total culling rate (%)	28.4	28.6	28.8	28.3	28.3
Proportion of voluntary cullings ² (%)	42.5	41.3	38.7	42.0	42.0
Milk production (kg/cow/mo)	734.6	756.9	800.9	763.5	694.1
Fat production (kg/cow/mo)	31.4	29.7	25.7	30.5	32.9
Protein production (kg/cow/mo)	25.6	25.9	26.5	26.1	24.9
Roughage intake (kg DM/cow/mo)	401.1	401.8	403.2	401.5	401.3
Concentrate intake (kg DM/cow/mo)	156.6	150.8	136.6	156.9	155.8
Milk revenue (€/cow/mo)	257.6	254.3	246.0	257.6	257.7
Feed cost (€/cow/mo)	66.0	65.2	63.0	66.1	65.9
Insemination cost (€/cow/year)	48.2	48.2	48.4	47.0	46.6
Total net revenue (€/cow/mo)	39.9	37.3	30.8	40.0	40.3
Total net revenue (€/100 kg milk)	5.4	4.9	3.8	5.2	5.8
Annual herd net revenue ³ (€1,000)	35.9	33.5	27.7	36.0	36.3

¹Based on completed lactations.

²Includes cows that did not get pregnant during the insemination period.

³Assuming average Dutch farm size of 75 cows.

Regarding scenario DGAT1A and DGAT1K, which envisioned selection based on *DGAT1* genotypes, neither of the two scenarios influenced optimal replacement strategies, as the productive herd lives were virtually unchanged. Optimal insemination policy was slightly

affected, and calving interval decreased in both scenarios. This was due to the positive effects of both *DGATI* genotypes on conception rates. Changes in monthly milk yield per cow were profound: increased by 28.8 kg in DGAT1A and decreased by 40.0 kg in DGAT1K, relative to the base scenario. Therefore, there was a 68.8 kg difference in monthly milk yield per cow between the two scenarios. Fat and protein yields and hence feed costs did not change between the scenarios. Although insemination cost decreased due to better reproductive performance, genetic selection based on *DGATI* genotypes had virtually no effect on economic outcomes. Monthly net revenues per cow increased by €0.1 and €0.3 and hence annual herd profit increased by approximately €100 and €300 in DGAT1A and DGAT1K.

DISCUSSION

The presented results can be used to evaluate the economic consequences of genetic selection strategies aiming to alter milk composition. Regarding strategies to change milk fat composition, it is important to note that the scenarios change SFA/UFA ratio to a different extent. FTB envisions a decrease of 0.22 by using superior bulls within the current breeding scheme, while FBS lays out a more extreme scenario of decreasing SFA/UFA ratio by 0.67 by a new breeding scheme. Because FBS puts all selection pressure solely on decreasing SFA/UFA ratio, it is a less likely scenario to happen. However, FBS provides useful insights to the economic effects of a hypothetical maximum change in SFA/UFA ratio that can be achieved by traditional selection. Scenario DGAT1A and DGAT1K envision selection for the AA and the KK genotypes of the *DGATI* gene. DGAT1A would decrease SFA/UFA ratio in milk by 0.12, whereas DGAT1K would increase it by 0.15. Because the AA genotype is associated with lower SFA/UFA ratio in milk (Schennink et al., 2007), scenario DGAT1A represents an alternative to the traditional selection. The aim of including DGAT1K was to unravel the difference in the economic consequences between the two extreme genotypes.

Our results showed that FTB and FBS would decrease the annual net revenue of an average Dutch dairy herd by €2,400 and €8,200. On average, the farmer would realize €0.5 and €1.6 less net revenue on every 100 kg milk in FTB and FBS. On the contrary, scenario DGAT1A and DGAT1K resulted in €100 and €400 higher annual herd revenues. These findings show that the difference between the two extreme *DGATI* genotypes is not remarkable. This implies that changing herd composition with respect to the *DGATI* genotype would not lead to significant economic changes, independent what the current distribution of the genotypes is in the herd. Should dairy processors decide to take advantage of the natural variation with regard to milk fat composition, their payment schemes to farmers would need to be adjusted. In scenario FTB, the monthly net loss per cow was €2.6, which would need to be recovered over an average monthly yield of 749.7 kg milk. Thus, the minimum break-even premium to cover the farmer's loss amounts to €0.36 per 100 kg milk in FTB. In practice, it is likely that the premium would need to be higher to compensate the farmer the risks associated with the novel production strategy. Therefore, some premium would also be required in DGAT1A, even though our results indicate no decrease in the farmer's total net revenue.

CONCLUSIONS

The objective of the study was to assess the farm level economic implications of value-adding genetic selection strategies to improve milk fat composition. Selection based on a quantitative trait or a known genotype was considered. Results showed that increasing the total unsaturated fatty acids in milk by traditional selection leads to lower net revenue, whereas selection based on *DGATI* genotype results in slightly higher net revenue. Our results, therefore, suggest that genetic selection based on *DGATI* genotype is a more profitable strategy for dairy farmers than selection based on phenotypes for SFA/UFA ratio.

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REFERENCES

- Bobe, G., J. A. Minick Bormann, G. L. Lindberg, A. E. Freeman, and D. C. Beitz. 2008. Short Communication: Estimates of genetic variation of milk fatty acids in US Holstein cows. *J. Dairy Sci.* 91:1209-1213.
- Boland, M., A. MacGibbon, and J. Hill. 2001. Designer milks for the new millennium. *Livest. Prod. Sci.* 72:99-109.
- Creamer, L. K., L. E. Pearce, J. P. Hill, and M. J. Boland. 2002. Milk and Dairy Products in the 21st Century Prepared for the 50th Anniversary of the Journal of Agricultural and Food Chemistry. *J. Agric. Food Chem.* 50:7187-7193.
- CRV. 2010. Statistical Indicators (Chapter 7): Breeding value estimation of milk production traits with test-day model. Pages 1-23.
- Dekkers, J. C. M. 1991. Estimation of economic values for dairy cattle breeding goals: Bias due to sub-optimal management policies. *Livest. Prod. Sci.* 29:131-149.
- Demeter, R. M., A. R. Kristensen, J. Dijkstra, A. G. J. M. Oude Lansink, M. P. M. Meuwissen, and J. A. M. Van Arendonk. 2011. A multi-level hierarchic Markov process with Bayesian updating for herd optimization and simulation in dairy cattle. *J. Dairy Sci.* (submitted).
- Demeter, R. M., M. P. M. Meuwissen, A. G. J. M. Oude Lansink, and J. A. M. van Arendonk. 2009a. Scenarios for a future dairy chain in the Netherlands. *NJAS - Wagen. J. Life Sci.* 56:301-323.
- Demeter, R. M., G. C. B. Schopen, A. G. J. M. O. Lansink, M. P. M. Meuwissen, and J. A. M. van Arendonk. 2009b. Effects of milk fat composition, DGAT1, and SCD1 on fertility traits in Dutch Holstein cattle. *J. Dairy Sci.* 92:5720-5729.
- Dooley, A. E., W. J. Parker, H. T. Blair, and E. M. Hurley. 2005a. Implications of on-farm segregation for valuable milk characteristics. *Agricultural Systems* 85:82-97.
- Essl, A. 1998. Longevity in dairy cattle breeding: a review. *Livestock Production Science* 57:79-89.
- German, J. and C. Dillard. 2006. Composition, structure and absorption of milk lipids: A source of energy, fat-soluble nutrients and bioactive molecules. *Crit. Rev. Food Sci. Nutr.* 46:57-92.
- German, J. B., F. L. Schanbacher, B. Lönnerdal, J. F. Medrano, M. A. McGuire, J. L. McManaman, D. M. Rocke, T. P. Smith, M. C. Neville, P. Donnelly, M. Lange, and R. Ward. 2006. International milk genomics consortium. *Trends Food Sci. Tech.* 17:656-661.
- Grisart, B., W. Coppieters, F. Farnir, L. Karim, C. Ford, P. Berzi, N. Cambisano, M. Mni, S. Reid, P. Simon, R. Spelman, M. Georges, and R. Snell. 2002. Positional candidate cloning of a QTL in dairy cattle: Identification of a missense mutation in the bovine DGAT1 gene with major effect on milk yield and composition. *Genome Res.* 12:222-231.
- Heck, J. M. L. 2009. Milk Genomics - Opportunities to Improve the Protein and Fatty Acid Composition in Raw Milk. PhD Thesis. Wageningen University. Wageningen, The Netherlands.
- Kristensen, A. R. 2003. A general software system for Markov decision processes in herd management applications. *Comput. Electron. Agr.* 38:199-215.
- Kristensen, A. R. and E. Jørgensen. 2000. Multi-level hierarchic Markov processes as a framework for herd management support. *Ann. Oper. Res.* 94:69-89.
- Maijala, K. 2000. Cow milk and human development and well-being. *Livest. Prod. Sci.* 65:1-18.
- Rogers, G. W., J. A. M. Van Arendonk, and B. T. McDaniel. 1988a. Influence of production and prices on optimum culling rates and annualized net revenue. *J. Dairy Sci.* 71:3453-3462.

- Rogers, G. W., J. A. M. Van Arendonk, and B. T. McDaniel. 1988b. Influence of involuntary culling on optimum culling rates and annualized net revenue. *J. Dairy Sci.* 71:3463-3469.
- Rutten, M. J. M., P. Bijma, J. A. Woolliams, and J. A. M. Van Arendonk. 2002. SelAction: Software to Predict Selection Response and Rate of Inbreeding in Livestock Breeding Programs. *Journal of Heredity* 93:456-458.
- Schennink, A. 2009. Genes Involved in Bovine Milk-Fat Composition. PhD Thesis. Wageningen University. Wageningen, The Netherlands.
- Schennink, A., J. M. L. Heck, H. Bovenhuis, M. H. P. W. Visker, H. J. F. Van Valenberg, and J. A. M. Van Arendonk. 2008. Milk fatty acid unsaturation: Genetic parameters and effects of Stearoyl-CoA desaturase (SCD1) and Acyl CoA: diacylglycerol acyltransferase 1 (DGAT1). *J. Dairy Sci.* 91:2135-2143.
- Schennink, A., W. M. Stoop, M. H. P. W. Visker, J. M. L. Heck, H. Bovenhuis, J. J. Van der Poel, H. J. F. Van Valenberg, and J. A. M. Van Arendonk. 2007. DGAT1 underlies large genetic variation in milk-fat composition of dairy cows. *Anim. Genet.* 38:467-473.
- Schopen, G. C. B. 2010. Genetic Analysis of Protein Composition of Bovine Milk. PhD Thesis. Wageningen University. Wageningen, The Netherlands.
- Soyeurt, H., A. Gillon, S. Vanderick, P. Mayeres, C. Bertozzi, and N. Gengler. 2007. Estimation of heritability and genetic correlations for the major fatty acids in bovine milk. *J. Dairy Sci.* 90:4435-4442.
- Stegeman, G. A., R. J. Baer, D. J. Schingoethe, and D. P. Casper. 1992. Composition and Flavor of Milk and Butter from Cows Fed Unsaturated Dietary Fat and Receiving Bovine Somatotropin. *J. Dairy Sci.* 75:962-970.
- Steijns, J. M. 2008. Dairy products and health: Focus on their constituents or on the matrix? *International Dairy Journal* 18:425-435.
- Stoop, W. M. 2009. Genetic Variation in Bovine Milk Fat Composition. PhD Thesis. Wageningen University. Wageningen, The Netherlands.
- Stoop, W. M., J. A. M. Van Arendonk, J. M. L. Heck, H. J. F. Van Valenberg, and H. Bovenhuis. 2008. Genetic parameters for major milk fatty acids and milk production traits of Dutch Holstein-Friesians. *J. Dairy Sci.* 91:385-394.
- Van Arendonk, J. A. M. 1985. Studies on the replacement policies in dairy cattle. II. Optimum policy and influence of changes in production and prices. *Livest. Prod. Sci.* 13:101-121.
- Van Arendonk, J. A. M. and A. A. Dijkhuizen. 1985. Studies on the replacement policies in dairy cattle. III. Influence of variation in reproduction and production. *Livest. Prod. Sci.* 13:333-349.
- Van Knegsel, A. T. M., H. Van den Brand, E. A. M. Graat, J. Dijkstra, R. Jorritsma, E. Decuypere, S. Tamminga, and B. Kemp. 2007. Dietary Energy Source in Dairy Cows in Early Lactation: Metabolites and Metabolic Hormones. *J. Dairy Sci.* 90:1477-1485.
- Williams, C. M. 2000. Dietary fatty acids and human health. *Ann. Zootech.* 49:165-180.
- Winter, A., W. Krämer, F. A. O. Werner, S. Kollers, S. Kata, G. Durstewitz, J. Buitkamp, J. E. Womack, G. Thaller, and R. Fries. 2002. Association of a Lysine-232/Alanine Polymorphism in a Bovine Gene Encoding Acyl-CoA:Diacylglycerol Acyltransferase (DGAT1) with Variation at a Quantitative Trait Locus for Milk Fat Content. *Proceedings of the National Academy of Sciences of the United States of America* 99:9300-9305.