Genomic selection in relation to bovine milk composition and processability

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Genomic selection is a new technology in which selection decisions are based on direct genomic values (DGVs) or genomic enhanced breeding values (GEBVs). The objective of this study was to evaluate the relations between DGVs and several milk traits important for both the nutritional value and processability of milk. This is a new approach and can be used to increase the knowledge on how genomic selection can be used in practice. Morning milk samples from Swedish Holstein cows were analyzed for milk composition and technological properties. DGVs were received for each cow for milk, protein and fat yield, milk index, udder health, Nordic total merit and a quota was calculated between fat and milk yield as well as protein and milk yield. The results show that linear correlations exist ($P<0\cdot10$) between the studied DGVs and contents and yields of parameters in the protein ($P=0\cdot002$–$0\cdot097$), fat ($P=0\cdot024$–$0\cdot055$) and mineral profiles ($P=0\cdot001$–$0\cdot099$) as well as for cheese characteristics ($P=0\cdot004$–$0\cdot065$), thus making it possible to obtain detailed information on milk traits that are not registered in the milk recording scheme. Hence, genomic selection will be an efficient tool for breeding and dairy industry to select cows early in life for targeted milk production.

Keywords: Genomic selection, direct genomic value, milk composition, milk processability.

Genomic selection (GS) is a new technology in which selection decisions are based on direct genomic values (DGVs) or genomic enhanced breeding values (GEBVs). During recent years GS has revolutionized dairy cattle breeding and has the potential to double the rate of genetic gain as well as reduce the costs for dairy breeding companies by 92% (Schaeffer, 2006). The DGVs are predicted from thousands of genetic markers in the form of single nucleotide polymorphisms (SNP) covering the whole genome (Meuwissen et al. 2001; Goddard & Hayes, 2007; Hayes et al. 2009; Calus, 2010; Mark & Sandoe, 2010; Su et al. 2010). This enables all quantitative trait loci (QTL) to be in linkage disequilibrium with at least some of the markers. To estimate DGVs, a reference population consisting of animals with known genotype and phenotypic data is required. By linking these data sets together, estimates of SNP effects for each trait are acquired. For subsequent generations, DGVs can be obtained directly through a DNA sample, thus allowing genetic evaluation and selection early in life (Goddard & Hayes, 2007; Hayes et al. 2009).

In order for GS to be successfully applied within breeding programs, the accuracy of the prediction of DGVs has to be considered. The accuracy depends on several factors, of which some are the heritability of a trait, the number of animals in the reference population and the number of SNP markers that are used to estimate the SNP effects (Hayes et al. 2009; Calus, 2010). By increasing the number in the latter factors, the accuracy of GS will be greater (Hayes et al. 2009). So far, most studies have based the accuracy of genomic predictions on simulated data. The recent rapid development of genome-wide dense SNP marker maps, that makes it possible to choose makers evenly distributed throughout the genome, has however increased the studies of accuracies based on real cattle populations (Harris et al. 2008; Hayes et al. 2009; Luan et al. 2009; VanRaden et al. 2009; Su et al. 2010). It has been shown that the reliabilities of DGVs are considerably greater than for conventional parent average (Hayes et al. 2009; Su et al. 2010).

The composition of cow's milk is of great importance for its nutritional value as well as its processability (Walstra et al. 1999). Several factors influence milk composition, of which some are genetic factors, which shows the importance of powerful genetic selection programs. Lately, the dairy industry has an increasing economic interest of providing

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milk for specific products, thus making GS an efficient tool in selecting cows early in life for targeted milk production. The aim of this paper is to study DGVs for traditional production traits in relation to several milk traits important for both the nutritional value and processability, including parameters in the protein, fat and mineral profiles, as well as actual technological properties of milk, such as cheese characteristics. The purpose is to investigate correlations between DGVs for traditional production traits included in the present breeding objective and novel production traits. To our knowledge, this is the first time that DGVs for traditional production traits have been studied in relation to bovine milk composition, nutritional value and processability.

Materials and Methods

Animals and milk samples

Morning milk samples and blood samples were collected in September 2008 from 23 Swedish Holstein (SH) cows in the second lactation, belonging to the research farm Nötcenter Viken (Falköping, Sweden). An integrated part of the Swedish breeding occurs at this research farm, which has a unique nucleus breeding herd producing a large number of bull dams. The investigated cows descended from 13 proven bulls. To exclude extremes in the beginning of the lactation, the cows were in lactation week 7–53. All cows in the study were healthy (mean somatic cell count (SCC) below 100 000 cells/ml), fed the same diet and milked three times a day. At the time of sampling, the cows had been fed in the stable for several weeks and been adjusted to the winter feeding regime. Milk yield of the whole sampling day (the total of three milkings) was recorded for each cow. The samples were cooled directly after collection and stored at 4 °C overnight. The following day, the samples were thoroughly mixed and subsampled before aliquots of whole and skim milk were either analyzed directly or stored at −20 °C until time of analysis. Skim milk was prepared by defatting the samples using centrifugation at 2000 *g* for 30 min.

Milk composition

For all the sampled cows, fresh milk samples were analyzed for contents of protein, fat, lactose and urea as well as for the freezing point by using an infrared technique and for somatic cells by using flow cytometry. This was performed at a certified dairy analysis laboratory (Eurofins Steins Laboratory, Jönköping, Sweden), all according to Glantz et al. (2009). Yields per cow per day were calculated by multiplying each percentage by the milk yield of the sampling day. Additionally, data were obtained on milk, protein and fat yield as well as contents of protein and fat for the sampled cows' 305-days lactation during the second lactation from the national cow database.

In addition, a more comprehensive study of milk composition traits was made on nine of the analyzed SH cows. The nine cows with the lowest SCC out of the 23 cows were selected for the comprehensive study. Milk samples stored at −20 °C were analyzed for contents of casein, whey proteins and non-protein nitrogen using the Kjeldahl method, contents of free fatty acids using a colorimetric technique, fatty acid composition using gas chromatography and contents of total Ca and P using inductively coupled plasma mass spectrometry, as described previously (Glantz et al. 2009). The components were analyzed at another certified dairy analysis laboratory (Eurofins Steins Laboratory, Holstebro, Denmark). In addition, pH was measured on fresh milk samples. Duplicate measurements were made on each sample. Yields per cow per day were calculated as described above.

Free Ca^{2+} concentration was measured at 25 and 32 °C in skim milk samples using an Orion 97–20 Ionplus Calcium Electrode (Thermo Electron Corporation, Beverly, MA, USA), all according to Glantz et al. (2011). Each sample was analyzed in triplicate.

Technological properties

Milk samples from the nine selected cows described above were also analyzed for technological properties, such as cheese characteristics and size determination of casein micelles and fat globules.

Rheological measurements. Using the method described by Glantz et al. (2011), rennet-induced gelation was carried out at 32 °C on fresh skim milk samples for 40 min with low-amplitude oscillation measurements (Stresstech rheometer; Reologica Instruments AB, Lund, Sweden) using chymosin (0·90 ml Chy-Max Plus/l, 200 international milk clotting U/ml; Christian Hansen A/S, Hørsholm, Denmark) to obtain gel strength and gelation time. After 40 min gel formation, stress sweeps were run to study the stress dependence of the viscosity to obtain the yield stress. The samples were subjected to an increasing shear stress in 100 intervals from 0·1 to 300 Pa. The yield stress was defined as the shear stress at the first local maximum of the viscosity. All samples were analyzed at least in duplicate.

Model cheeses. Model cheeses were produced from skim milk as described earlier (Glantz et al. 2011) using glucono-δ-lactone (3·76 g/kg Roquette, Lestrem Cedrix, France) (Lucey et al. 1997) and chymosin (1·25 ml Chy-Max Plus/l, 200 International Milk Clotting Units/ml, Christian Hansen A/S, Denmark) to determine cheese yield (expressed as g cheese/100 g milk), pH and cheese hardness, all according to (Glantz et al. 2011). One batch of cheese was made for each sample and for each batch of cheese, triplicate measurements were made to obtain cheese hardness.

Casein micelle size determination. Photon correlation spectroscopy was used to determine the z-average

Table 1. Means, SD and coefficients of variation (CV) of analyzed milk composition traits from individual Swedish Holstein cows

Milk trait	Mean	SD	CV (%)	n[†]
Milk yield (kg)	34·1	13·3	39	23
Protein content (g/100 g)	3·45	0·45	13	23
Protein yield (kg)	1·14	0·39	34	23
Casein content (g/100 g)	2·56	0·38	15	9
Casein yield (kg)	0·69	0·11	16	9
Whey protein content (g/100 g)	0·69	0·14	20	9
Whey protein yield (kg)	0·18	0·03	17	9
Non-protein nitrogen content (g/100 g)	0·030	0·003	10	9
Non-protein nitrogen yield (g)	8·31	2·17	26	9
Urea (mmol/l)	5·16	0·70	14	23
Fat content (g/100 g)	4·04	1·23	30	23
Fat yield (kg)	1·38	0·75	54	23
Free fatty acids (mEq/l)	0·24	0·04	17	9
Sum of saturated FA[‡]	63·5	4·6	7	9
Sum of monounsaturated FA[‡]	27·2	3·3	12	9
Sum of polyunsaturated FA[‡]	4·03	0·91	23	9
Sum of C20 and >C20[‡]	0·75	0·16	21	9
Sum of n-3 FA[‡]	1·27	0·40	31	9
Sum of n-6 FA[‡]	2·27	0·42	19	9
Lactose content (g/100 g)	4·38	0·25	6	23
Lactose yield (kg)	1·51	0·62	41	23
Calcium content (mg/100 g)	116	19	16	9
Calcium yield (g)	31·4	7·3	23	9
Ca^{2+} (25 °C) (mM)	2·3	0·4	17	9
Ca^{2+} (32 °C) (mM)	2·1	0·3	14	9
Phosphorus content (mg/100 g)	97	14	14	9
Phosphorus yield (g)	26·3	5·7	22	9
Somatic cell count (log/ml)	4·94	0·57	12	23
Freezing point (°C)	−0·524	0·011	2	23
Milk pH	6·59	0·06	1	9

[†] n = number of cows
[‡] Mean fatty acid (FA) as a proportion (wt/wt) of the total fat fraction of 100%

hydrodynamic diameter of casein micelles at 90° scattering angle at 25 °C on skim milks diluted in simulated milk ultrafiltrate (Jenness & Koops, 1962) as described previously (Glantz et al. 2010). Each sample was analyzed in triplicate.

Fat globule size determination. The volume-weighted droplet diameter, d(4,3), of the fat globules was determined in fresh milk samples at 20 °C by using light diffraction, all according to Glantz et al. (2009). All samples were analyzed in duplicate.

Analysis and estimation of direct genomic values

All 23 cows were genotyped with the Illumina BovineSNP50 BeadChip (Illumina, Inc., San Diego, CA, USA). Analysis and estimation of DGVs were conducted at Århus University, Denmark. The reference population consisted of approximately 16 000 progeny tested bulls from the cooperation within EuroGenomics (David et al. 2010). Most of the bulls in the reference population were typed with the above-mentioned Illumina BovineSNP50 BeadChip. In one of the

Table 2. Means, SD and coefficients of variation (CV) of analyzed technological properties of milk from individual Swedish Holstein cows (n = 9)

Property	Mean	SD	CV (%)
Gel strength (Pa)	102	59	58
Gelation time (min)	7·2	5·3	74
Yield stress (Pa)	22	8	36
Cheese pH	6·06	0·23	4
Cheese yield (%)	7·3	1·3	18
Cheese hardness (N)	11·7	3·5	30
Casein micelle size (nm)	173	16	9
Fat globule size (µm)	3·7	0·4	11

participating countries, some of the bulls had also been typed with a customized chip. Information from the customized chip was imputed, making the same information available for all the bulls. Genotype information was exchanged between the participating partners within EuroGenomics and phenotypes were available through Interbull. Standard editing procedures were applied concerning calling rate and minor allele frequencies. Used model of estimation of DGV was GBLUP and response variables were deregressed proofs weighted according to expected daughter contribution. DGVs were calculated for each cow for milk (DGV_{milk}), fat (DGV_{fat}) and protein yield ($DGV_{protein}$), milk index ($-0.25 \cdot DGV_{milk} + 0.25 \cdot DGV_{fat} + DGV_{protein} + 100$; $DGV_{milk\ index}$), Nordic total merit (NTM; DGV_{NTM}), which is a combined value of production, functional and conformation traits, and udder health (mastitis resistance; $DGV_{udder\ health}$). The estimated DGVs for udder health include information from three different sources, that is SCC, treatment of mastitis and udder conformation (udder depth and fore udder attachment). In addition, a quota was calculated between DGV_{fat} and DGV_{milk} as well as $DGV_{protein}$ and DGV_{milk} to obtain DGVs for fat ($DGV_{fat\%}$) and protein content ($DGV_{protein\%}$).

Statistical analyses

Linear correlations between DGVs and milk traits were estimated with Pearson correlation combined with the corresponding P-values. The level of significance was set at $P < 0.10$. Statistical analyses were performed using Minitab (version 14, Minitab Ltd., Coventry, UK).

Results

An extensive study of milk parameters and technological properties was performed on morning milk samples from individual SH cows, in order to study relations between DGVs and milk traits. Means, SD and coefficients of variation of the analyzed parameters and technological properties are summarized in Tables 1 & 2. The values obtained for milk components are in the range found previously in milk from individual SH cows (Wedholm et al. 2006a; Hallén et al.

Table 3. The Pearson correlation coefficient between direct genomic values (DGV) and milk composition and technological properties based on data from one morning milk sampling[‡]

Milk trait	Milk	Protein	Protein%	Fat	Fat%	Milk index[§]	Udder health[¶]	NTM[††]	n[‡‡]
Milk composition									
Milk yield	0·890**	0·617†	−0·756*		−0·632†				23
Protein content	−0·756*		0·870**		0·356†				23
Protein yield	0·628†	0·628†					−0·645†		23
Casein content	−0·782*		0·882**		0·596†			−0·591†	9
Casein yield	0·619†	0·593†					−0·606†		9
Whey protein content	−0·624†		0·738*		0·587†				9
Whey protein yield						0·602†	−0·659†		9
Non-protein nitrogen yield	0·824**	0·651†							9
Fat content							−0·454*	−0·405†	23
Free fatty acids				0·690*		0·734*			9
Lactose yield	0·906**	0·634†	−0·768*		−0·658†				23
Calcium content			0·717*		0·595†		−0·579†		9
Calcium yield	0·640†	0·688*				0·671*			9
Ca^{2+} (25 °C)							0·583†	0·807**	9
Ca^{2+} (32 °C)							0·712*	0·900**	9
Phosphorus content			0·760*				−0·580†		9
Phosphorus yield	0·657†	0·649†				0·593†			9
Milk pH							−0·705*		9
Freezing point							−0·422*	−0·351†	23
Technological properties									
Gel strength			0·683*						9
Gelation time							−0·698*		9
Yield stress			0·822**						9
Casein micelle size							−0·846**		9
Cheese pH			−0·700*	0·582†					9
Cheese yield	−0·794*		0·716*		0·706*			−0·638†	9

† $P<0·10$; * $P<0·05$; ** $P<0·01$; *** $P<0·001$

‡ Results are shown only for components correlated significantly ($P<0·10$) with at least 1 DGV

§ $-0·25 \cdot DGV_{milk} + 0·25 \cdot DGV_{fat} + DGV_{protein} + 100$

¶ Mastitis resistance

†† NTM = Nordic total merit. Combined value of production, functional and conformation traits

‡‡ n = number of cows

2008; Näslund et al. 2008) and SH bulk milk (Glantz et al. 2009). The values obtained for technological properties are in the range reported earlier in SH bulk milk (Glantz et al. 2009, 2010). Despite the high amount of milk produced by the cows, the contents of milk components are equal to or somewhat higher compared with average contents of protein and fat for the SH breed (Swedish Dairy Association, 2009). The coefficients of variation for milk components range from 6% for lactose content to 30% for fat content. Moderate coefficients of variation are observed for milk proteins and minerals (13–20%), whereas the coefficients of variation for yield parameters are higher (16–54%). For most of the technological properties, the coefficients of variation are moderate or high (>18%).

Linear correlations between DGVs and milk traits based on one morning milk sampling are presented in Table 3. Results are shown only for components or technological properties correlated significantly ($P<0·10$) with at least one of the studied DGVs. Both DGV_{milk} and $DGV_{protein}$ correlate positively with milk yield ($P=0·001$ and $0·077$, respectively) and yields in the protein ($P=0·006–0·093$) and mineral profiles ($P=0·041–0·064$), whereas $DGV_{protein\%}$ and $DGV_{fat\%}$ have positive correlations with contents of these traits ($P=0·002–0·097$). Negative correlations exist between DGV_{milk} and protein profile contents ($P=0·013–0·072$). DGV_{fat} on the other hand, shows no correlation with yields or contents of milk components, except for a positive correlation with free fatty acids ($P=0·040$). Negative correlations exist between $DGV_{udder\ health}$ and yields of the protein profile ($P=0·054–0·084$) as well as contents of fat ($P=0·030$) and minerals ($P=0·099$). However, no significant correlation exists between $DGV_{udder\ health}$ and SCC. Furthermore, DGV_{NTM} correlates negatively with casein ($P=0·094$) and fat content ($P=0·055$) as well as freezing point ($P=0·099$). Additionally, correlations also exist between the studied DGVs and technological properties of milk. DGV_{milk} and DGV_{NTM} show a negative correlation with cheese yield ($P=0·011$ and $0·065$, respectively), in

Table 4. The Pearson correlation coefficient (r) between data from one morning milk sampling and data from 305-days lactation on milk, protein and fat yield as well as protein and fat content ($n = 23$)

Milk trait	r
Milk yield	0·601**
Protein yield	0·694***
Protein content	0·572**
Fat yield	0·462*
Fat content	0·409*

*$P < 0.05$; **$P < 0.01$; ***$P < 0.001$

contrast to $DGV_{protein\%}$ and $DGV_{fat\%}$ having positive correlations ($P = 0.030$ and 0.033, respectively). $DGV_{protein\%}$ and $DGV_{udder\ health}$ both correlate with gelation properties ($P = 0.006–0.043$). One may also consider non-linear relationships, such as exponential relationships, that may exist between DGVs and milk traits, however, no such correlations were found in this data set.

The correlations presented above are based on data from one morning milk sampling. To ensure that these samples represent the entire lactation, available data for the cows' 305-days lactation were correlated with both the data from one morning milk sampling and the studied DGVs. The results from these analyses are presented in Tables 4 & 5. Significant linear correlations are found between one morning milk sampling and data from 305-days lactation regarding milk ($P = 0.002$), protein ($P = 0.000$) and fat yield ($P = 0.023$) as well as protein ($P = 0.004$) and fat content ($P = 0.047$; Table 4). Similar to the one morning milk sample, DGV_{milk} and $DGV_{protein}$ correlate positively with 305-days milk ($P = 0.032$ and 0.088, respectively) and protein yield ($P = 0.087$ and 0.044, respectively). DGV_{fat} also correlates positively with 305-days milk and protein yield ($P = 0.085$ and 0.024, respectively). However, DGV_{fat} also has a positive correlation with fat yield ($P = 0.004$). Additionally, DGV_{milk} correlates negatively and $DGV_{fat\%}$ positively with protein ($P = 0.012$ and 0.094, respectively) and fat content ($P = 0.049$ and 0.044, respectively). Thus, similar correlations for DGVs are obtained using one morning milk sample and data on 305-days lactation, thus confirming the usefulness of one milk sampling.

Discussion

With the limited number of animals in this study, estimation of DGVs for novel traits of milk composition and technological properties based on observation from the present investigation was not possible. However, the DGVs for production traits included in the traditional evaluations have a reliability that is considerably larger than corresponding pedigree index, due to the connection to a large reference population. This has made it interesting to investigate the correlations between proofs for traditional production traits and the novel traits. Ongoing research will increase the number of genotyped cows with records to enhance milk composition and technological properties to a level exceeding this study. The ultimate goal is, however, in the future to have sufficient direct or most likely indirect records of the novel traits to be able to calculate DGVs for bulls in the reference population based on large daughter groups.

The results from this investigation show that linear correlations exist between the studied DGVs and milk composition traits and technological properties. To our knowledge, this is the first time DGVs for traditional production traits have been evaluated in relation to bovine milk composition and processability data. Earlier studies on genetic correlations show a negative correlation between milk yield and protein (-0.39), casein (-0.38) (Ikonen et al. 2004) and fat content (-0.58) (Schennink et al. 2008), which is in agreement with the results obtained in our study. The positive linear correlations existing for DGV_{milk}, $DGV_{protein}$ and DGV_{fat} with milk and protein yield as well as for $DGV_{protein\%}$ and $DGV_{fat\%}$ with protein content are expected and have been shown for genetic and phenotypic correlations previously (Stoop et al. 2007; Schennink et al. 2008; Nixon et al. 2009). Both a positive genetic (0.86) and phenotypic correlation (0.91) between protein and lactose yield has been reported by Stoop et al. (2007), which is in accordance with the results found in this study. A high SCC has been shown to be associated with a high fat content and protein yield (Carlén et al. 2004; Stoop et al. 2007; Cunha et al. 2008). This is in accordance with the negative correlations found between $DGV_{udder\ health}$ and protein yield and fat content in our study. No significant correlation was found between $DGV_{udder\ health}$ and SCC in this study, which may be explained by the fact that $DGV_{udder\ health}$ includes information not only on SCC but also on treatment of mastitis and udder conformation. Thus, the linear correlations obtained between the studied DGVs and milk components are apparently reasonable and valid. The same holds for the technological properties of the milk. This study indicated a negative correlation between $DGV_{udder\ health}$ and gelation time, which is in accordance with earlier studies that report on an association between a high SCC and longer gelation time (Amenu & Deeth, 2007; Cassandro et al. 2008; Barowska et al. 2009). However, Wedholm et al. (2006b) found no effect of SCC on milk clotting properties. The negative correlation between DGV_{milk} and cheese yield seems reasonable, given that high contents of protein and fat result in a high cheese yield (Lucey & Kelly, 1994; Wedholm et al. 2006b). This also confirms the positive correlations existing between $DGV_{protein\%}$ and $DGV_{fat\%}$ and cheese yield. In this study, model cheeses were produced without protein standardisation, pH adjustment or salt addition. Therefore cheese yield as defined in this study is highly dependent on the protein concentration in the milk and the results from this study could be compared with other research studies on model cheeses, such as the study of Wedholm et al. (2006b). Hence, the results show the possibilities of obtaining valuable information on both detailed milk composition and technological properties for

Table 5. The Pearson correlation coefficient between direct genomic values (DGV) and milk composition[‡] based on data from 305-days lactation ($n = 23$)[§]

	DGV					
Milk trait	Milk	Protein	Protein%	Fat	Fat%	Milk index[¶]
Milk yield	0·449[*]	0·364†		0·367†		
Protein yield	0·365†	0·424[*]		0·469[*]		0·430[*]
Protein content	− 0·514[*]		0·587[**]		0·357†	
Fat yield				0·573[**]		
Fat content	− 0·414[*]				0·424[*]	

† $P<0.10$; * $P<0.05$; ** $P<0.01$; *** $P<0.001$
‡ Milk, protein and fat yield as well as protein and fat content
§ Results are shown only for components correlated significantly ($P<0.10$) with at least 1 DGV
¶ $-0.25 \cdot DGV_{milk} + 0.25 \cdot DGV_{fat} + DGV_{protein} + 100$

individual animals through DGVs for traditional production traits. This gives opportunities to select the most interesting heifers based on their DNA profile. By including new properties in the GS analyses, such as polyunsaturated fatty acids and gelation time, heifers can in the future be selected early in life to produce milk for specific dairy products and bulls with desired DGVs for the traits can be selected for breeding purpose.

The coefficients of variation for milk components are in the range to be expected and what has been reported earlier or somewhat higher (Schennink et al. 2007; Cassandro et al. 2008; Stoop et al. 2008). For gelation properties, however, the coefficients of variation are higher than those reported by Cassandro et al. (2008). Studies have shown high heritability for contents of fat (0·52), protein (0·60) and lactose (0·64), whereas the heritability for yields of these components are moderate (0·34–0·47) (Stoop et al. 2007, 2008). Also for Ca and P the heritabilities are high (0·57 and 0·62, respectively), which indicates that these minerals may be changed by genetic selection (van Hulzen et al. 2009). The heritability for saturated fatty acids (0·19–0·59) is higher than for mono- and polyunsaturated fatty acids (0·09–0·21) (Schennink et al. 2007; Stoop et al. 2008). The moderate coefficients of variation for the fat fraction (Table 1) thus imply that milk fat composition may be altered by genetic selection. More interestingly, however, are the opportunities arising for technological properties of milk. It has been shown that moderate heritability exists for gelation time (approximately 0·25) and gel strength (between 0·15 and 0·40) (Ikonen et al. 1999; Cassandro et al. 2008). Hence, the results indicate that these properties can be changed by genetic selection, which is an unused variation within the Nordic breeding work. This opens up for new challenges for the breeding and dairy industry.

It is often not possible for farmers to optimize every specific trait or character and usually farmers will focus on combined values. DGV_{NTM} is a total merit index that is a combination of production, functional and conformation traits, which makes it an important economic tool for farmers. The results in this study show a tendency for lower casein and fat content as well as cheese yield when breeding for a high NTM. Therefore, it is of the outmost importance to not only consider the DGVs related to production traits when studying the impact of DGVs on milk traits, but also other DGVs that are essential to the farmers, such as DGV_{NTM}. If these DGVs are not considered, there is a risk that milk traits may be adversely altered. This may result in contents and yields of milk components that are unfavourable from a processing and nutritional perspective.

We have demonstrated the potential of using DGVs of traits included in the breeding objective of today to obtain information on detailed milk composition and technological properties early in the heifers' life. However, further studies using more animals, larger reference population and more SNP markers will reveal relationships with greater accuracy. Through the use of GS, new and interesting approaches are arising when a blood sample can be used to predict composition and technological properties of milk, thus making it possible for breeding and dairy companies to select cows for targeted milk production. This, in turn, will certainly increase the economic output for the industry as well as for the farmers, given that the industry changes the payment system for additional components to the farmers. The results obtained in this study are a first evaluation of the relations between DGVs for traditional production traits and novel milk traits. Today, these results can be used for indirect selection on traits that are not registered in the milk recording scheme, such as casein and minerals or technological properties. The future challenge will be to enhance the recording of new important traits in a reference population, making direct selection available for traits and properties that improve milk quality and are of economical importance.

References

Amenu B & Deeth HC 2007 The impact of milk composition on cheedar cheese manufacture. *Australian Journal of Dairy Technology* **62** 171–184

Barowska J, Litwinczuk Z, Wolanciuk A & Brodziak A 2009 Relationship of somatic cell count to daily yield and technological usefulness of milk from different breeds of cows. *Polish Journal of Veterinary Sciences* **12** 75–79

Calus MPL 2010 Genomic breeding value prediction, methods and procedures. *Animal* **4** 157–164

Carlén E, Strandberg E & Roth A 2004 Genetic parameters of clinical mastitis, somatic cell score, and production in the first three lactations of Swedish Holstein cows. *Journal of Dairy Science* **87** 3062–3070

Cassandro M, Comin A, Ojala M, Dal Zotto R, De Marchi M, Gallo L, Carnier P & Bittante G 2008 Genetic parameters of milk coagulation properties and their relationships with milk yield and quality traits in Italian Holstein cows. *Journal of Dairy Science* **91** 371–376

Cunha RPL, Molina LR, Carvalho AU, Facury Filho EJ, Ferreira PM & Gentilini MB 2008 Subclinical mastitis and the relationship between somatic cell count with number of lactations, production and chemical composition of milk. *Arquivo Brasileiro de Medicina Veterinária e Zootecnia* **60** 19–24

David X, de Vries A, Feddersen E & Borchersen S 2010 International genomic cooperation – European perspective. In *Interbull Workshop on the Use of Genomic Information in Genetic evaluations*, Interbull bulletin 41, Paris, France

Glantz M, Devold TG, Vegarud GE, Lindmark Månsson H, Stålhammar H & Paulsson M 2010 Importance of casein micelle size and milk composition for milk gelation. *Journal of Dairy Science* **93** 1444–1451

Glantz M, Lindmark Månsson H, Stålhammar H, Bårström L-O, Fröjelin M, Knutsson A, Teluk C & Paulsson M 2009 Effects of animal selection on milk composition and processability. *Journal of Dairy Science* **92** 4589–4603

Glantz M, Lindmark Månsson H, Stålhammar H & Paulsson M 2011 Effect of polymorphisms in the leptin, leptin receptor, and acyl-coenzyme A: diacylglycerol acyltransferase 1 (*DGAT1*) genes and genetic polymorphism of milk proteins on cheese characteristics. *Journal of Dairy Science* **94** 3295–3304

Goddard ME & Hayes BJ 2007 Genomic selection. *Journal of Animal Breeding and Genetics* **124** 323–330

Hallén E, Wedholm A, Andrén A & Lundén A 2008 Effect of beta-casein, kappa-casein and beta-lactoglobulin genotypes on concentration of milk protein variants. *Journal of Animal Breeding and Genetics* **125** 119–129

Harris BL, Johnson DL & Spelman RJ 2008 Genomic selection in New Zealand and the implications for national genetic evaluation. In *The Interbull Meeting Niagara Falls*, NY, US

Hayes BJ, Bowman PJ, Chamberlain AJ & Goddard ME 2009 Genomic selection in dairy cattle: progress and challenges. *Journal of Dairy Science* **92** 433–443

Ikonen T, Ahlfors K, Kempe R, Ojala M & Ruottinen O 1999 Genetic parameters for the milk coagulation properties and prevalence of noncoagulating milk in Finnish dairy cows. *Journal of Dairy Science* **82** 205–214

Ikonen T, Morri S, Tyrisevä A-M, Ruottinen O & Ojala M 2004 Genetic and phenotypic correlations between milk coagulation properties, milk production traits, somatic cell count, casein content, and pH of milk. *Journal of Dairy Science* **87** 458–467

Jenness R & Koops J 1962 Preparation and properties of a salt solution which simulates milk ultrafiltrate. *Netherlands Milk and Dairy Journal* **16** 153–164

Luan T, Woolliams JA, Lien S, Kent M, Svendsen M & Meuwissen THE 2009 The accuracy of genomic selection in Norwegian Red cattle assessed by cross-validation. *Genetics* **183** 1119–1126

Lucey J & Kelly J 1994 Cheese yield. *Journal of the Society of Dairy Technology* **47** 1–14

Lucey JA, van Vliet T, Grolle K, Geurts T & Walstra P 1997 Properties of acid casein gels made by acidification with glucono-δ-lactone. 1. Rheological properties. *International Dairy Journal* **7** 381–388

Mark T & Sandoe P 2010 Genomic dairy cattle breeding: risks and opportunities for cow welfare. *Animal Welfare* **19** 113–121

Meuwissen THE, Hayes BJ & Goddard ME 2001 Prediction of total genetic value using genome-wide dense marker maps. *Genetics* **157** 1819–1829

Näslund J, Fikse WF, Pielberg GR & Lundén A 2008 Frequency and effect of the bovine acyl-CoA:diacylglycerol acyltransferase 1 (DGAT1) K232A polymorphism in Swedish dairy cattle. *Journal of Dairy Science* **91** 2127–2134

Nixon M, Bohmanova J, Jamrozik J, Schaeffer LR, Hand KJ & Miglior F 2009 Genetic parameters of milking frequency and milk production traits in Canadian Holsteins milked by an automated milking system. *Journal of Dairy Science* **92** 3422–3430

Schaeffer LR 2006 Strategy for applying genome-wide selection in dairy cattle. *Journal of Animal Breeding and Genetics* **123** 218–223

Schennink A, Heck JML, Bovenhuis H, Visker MHPW, van Valenberg HJF & van Arendonk JAM 2008 Milk fatty acid unsaturation: genetic parameters and effects of stearoyl-CoA desaturase (SCD1) and acyl CoA: diacylglycerol acyltransferase 1 (DGAT1). *Journal of Dairy Science* **91** 2135–2143

Schennink A, Stoop WM, Visker MHPW, Heck JML, Bovenhuis H, van der Poel JJ, van Valenberg HJF & van Arendonk JAM 2007 DGAT1 underlies large genetic variation in milk-fat composition of dairy cows. *Animal Genetics* **38** 467–473

Stoop WM, Bovenhuis H & van Arendonk JAM 2007 Genetic parameters for milk urea nitrogen in relation to milk production traits. *Journal of Dairy Science* **90** 1981–1986

Stoop WM, van Arendonk JAM, Heck JML, van Valenberg HJF & Bovenhuis H 2008 Genetic parameters for major milk fatty acids and milk production traits of Dutch Holstein-Friesians. *Journal of Dairy Science* **91** 385–394

Su G, Guldbrandtsen B, Gregersen VR & Lund MS 2010 Preliminary investigation on reliability of genomic estimated breeding values in the Danish Holstein population. *Journal of Dairy Science* **93** 1175–1183

Swedish Dairy Association 2009 *Cattle Statistics*. Stockholm, Sweden: Swedish Dairy Association

Walstra P, Geurts TJ, Noomen A, Jellema A & van Boekel MAJS 1999 *Dairy Technology: Principles of Milk Properties and Processes*. New York, NY: US Marcel Dekker Inc.

van Hulzen KJE, Sprong RC, van der Meer R & van Arendonk JAM 2009 Genetic and nongenetic variation in concentration of selenium, calcium, potassium, zinc, magnesium, and phosphorus in milk of Dutch Holstein-Friesian cows. *Journal of Dairy Science* **92** 5754–5759

VanRaden PM, Van Tassell CP, Wiggans GR, Sonstegard TS, Schnabel RD, Taylor JF & Schenkel FS 2009 Reliability of genomic predictions for North American Holstein bulls. *Journal of Dairy Science* **92** 16–24

Wedholm A, Hallén E, Larsen LB, Lindmark Månsson H, Karlsson AH & Allmere T 2006a Comparison of milk protein composition in a Swedish and a Danish dairy herd using reversed phase HPLC. *Acta Agriculturae Scandinavica Section A* **56** 8–15

Wedholm A, Larsen LB, Lindmark Månsson H, Karlsson AH & Andrén A 2006b Effect of protein composition and the cheese-making properties of milk from individual dairy cows. *Journal of Dairy Science* **89** 3296–3305