Effects of Breed, Feeding System, and Parity on Udder Health and Milking Characteristics

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ABSTRACT

The objective of this study was to quantify differences in udder health and milking characteristics among the Holstein-Friesian (HF), Montbéliarde (MB), Normande (NM), Norwegian Red (NRF), Montbéliarde × Holstein-Friesian (MBX), and Normande × Holstein-Friesian (NMX) genotypes, while considering the effect of feeding system and parity. A total of 749 lactations were available for inclusion in the analysis from 309 cows in 1 research herd over 5 yr. Somatic cell score (SCS; i.e., natural logarithm of somatic cell count) was used as an indicator of udder health. Milking duration (seconds/d) was defined as the sum of the milking duration in the a.m. and milking duration in the p.m. Average daily milk flow (AMF; kg/min) was defined as total daily milk yield divided by total daily milking duration. Peak milk flow (kg/min) was defined as the maximum rate of milk flow achieved in the daily milking process. The SCS of the NRF (10.31 units) and MB (10.47 units) breeds was less than that of the HF (10.96 SCS units), whereas that of the NM (10.88 SCS units), MBX (10.93 SCS units), and NMX (10.84 SCS units) breeds was similar to that of the HF. The MBX and NMX had the greatest AMF (1.56 and 1.54 kg/min, respectively) and the NM had the lowest (1.33 kg/min). Animals offered a high concentrate diet had greater AMF, peak milk flow, and milking duration. The differences expressed by the divergent breeds may reflect differences in the past breeding goals among the breeds, namely the inclusion of traits aimed at maintaining or improving udder health. **Key words:** dairy, udder health, milking characteristic, breed

INTRODUCTION

Inferior udder health can be a source of economic loss for both dairy farmers and milk processors. It can result

in reduced milk yield and milk quality (Bartlett et al., 1991), changes in milk composition (Auldist et al., 1995), increased involuntary culling (Berry et al., 2005), and veterinary and treatment costs (Berry and Amer, 2005). Furthermore, in Ireland, milk pricing is tiered based on monthly arithmetic mean bulk SCC with penalties imposed on milk with high SCC.

Previous studies (Mrode and Swanson, 1996) reported heritability estimates of 0.11 to 0.15 for SCC in the Holstein-Friesian breed, suggesting that SCC is under modest genetic control. Milking speed is an important functional trait in dairy cattle because of its impact on labor cost (Boettcher et al., 1998), involuntary culling (Berry et al., 2005), and udder health (Grindal and Hillerton, 1991; Rupp and Boichard, 1999). Boettcher et al. (1998) and Rupp and Boichard (1999) reported heritability estimates of 0.15 to 0.17 for subjectively scored milking speed and moderate genetic correlations (0.41 to 0.44) between subjectively scored milking speed and SCS in primiparous animals. Furthermore, a strong positive correlation between peak milk flow and mastitis incidence has previously been reported (Grindal and Hillerton, 1991).

Genetic differences exist between breeds because of their etiology. In their country of origin, dairy cow breeds have evolved based on traits considered to be of economic importance such as milk production, health, and fertility. Cows are also exposed to different management practices (McCarthy et al., 2007), feeding systems (Dillon et al., 2003), and environmental conditions (Wicks and Leaver, 2006). Selection within the Holstein-Friesian breed has, until recently, been predominantly for milk production (Miglior et al., 2005) with little or no direct selection for functional traits other than those correlated with superior type. In 1994, the United States introduced genetic evaluations for lactation SCS (Schutz, 1994) that were subsequently incorporated into a net merit index (Van Raden, 2004). In Ireland, SCC was incorporated into an economic breeding index in 2006 (Berry and Amer, 2005). Breeds such as the French Montbéliarde and the French Normande have been simultaneously selected for both milk and beef production in the past. In France, SCC has been

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included in the total merit index since 2001 (Ducrocq et al., 2001) for both the Montbéliarde and Normande breeds. In Scandinavian countries, a more balanced total merit index, incorporating production and cow functionality, has been in place since the early 1970s. Norway has incorporated clinical mastitis in its total merit index since 1978. Heringstad et al. (2001) reported a gradual increase in the relative emphasis on clinical mastitis in this index from less than 3% in 1978 to 21% in 1998 and subsequently noted an average decrease of 0.08% in the number of clinical mastitis cases per year from 1976 to 1996 (Heringstad et al., 2003).

Milk production systems in the United States are largely based on total confinement, whereas Denmark, France, and Ireland have approximately 35, 55, and 70% of grazed grass included in the diet (Dillon et al., 2005). Considerable incongruity exists in the literature concerning the effect of feeding system on udder health. Previous research carried out with pastured cows provided varying concentrate inputs showed no difference in SCS (Turner et al., 2003; McCarthy et al., 2007). Deterioration in udder health as measured by increased SCC and mastitis incidence has also been associated with increased parity (McCarthy et al., 2007).

Given the previously reported genetic variation in udder health and milking characteristics and different breeding strategies, it is likely that significant differences exist among breeds for udder health and milking characteristics. Therefore, the objective of this paper was to quantify differences in udder health and milking characteristics among Holstein-Friesian, Montbéliarde, Normande, Norwegian Red, Montbéliarde $\times$ Holstein-Friesian, and Normande $\times$ Holstein-Friesian cows and to determine if these differences are consistent across feeding systems and parities.

MATERIALS AND METHODS

A 5-yr study to compare Holstein-Friesian (**HF**), Montbéliarde (**MB**), Normande (**NM**), Norwegian Red (**NRF**), Holstein-Friesian $\times$ Montbéliarde (**MBX**), and Holstein-Friesian $\times$ Normande (**NMX**) took place on the Ballydague Dairy Research Farm at Moorepark Dairy Research Centre, Ireland, from January 2001 through December 2005. This study was a continuation of a breed comparison trial described by Dillon et al. (2003), but included crossbreds of MB and NM with HF, as well as pure NRF cows chosen based on their past selection for fertility and general health. In year one, 92% of the animals were primiparous and 8% were of second parity. In year two, 37, 58, and 5% were of first, second, and third parity, respectively. In year three, 28, 23, 45, and 4% were of first, second, third, and fourth parity,

respectively. In year four, 26, 22, 15, 34, and 3% were of first, second, third, fourth, and fifth parity, respectively. In the final year, 27, 19, 18, 12, and 24% were of first, second, third, fourth, and fifth parity respectively. Breed groups were not balanced for parity (1, 2, 3, 4, or 5) or calving date.

Purebred MB and NM cows were available upon completion of a 5-yr comparison of Dutch HF, MB, NM, and Irish HF, as described by Dillon et al. (2003). In 1999, NRF calves were imported and reared with the other breeds. Crossbreds and HF were generated by randomly mating HF, MB, and NM sires to HF cows from herds within Moorepark Dairy Research Centre. Replacement animals were generated within the herd during the 5 yr. A total of 23, 19, 11, 17, 17, and 19 sires were represented in the HF, MB, NM, NRF, MBX, and NMX breeds, respectively. Sires used were common across pure and crossbreds and were also representative of sires commonly used in Ireland. The HF sires used were of North American HF ancestry.

Lactation records of 96 and 73 MBX and NMX F₁ crossbreds, 42 and 23 MBX and NMX backcrosses, produced by mating F₁ crossbreds with HF sires, and 2 and 1 MBX and NMX backcrosses, produced by mating F₁ crossbreds with MB and NM sires respectively, were available. Table 1 has the herd profile for the 5-yr analysis.

Feeding System and Cow Management

Throughout the 5 yr, the trial was carried out on the same permanent grassland site consisting of almost 100% perennial ryegrass. The soil type on the farm was free-draining acid brown earth of sandy loam to loam texture. Cows were out on grass from mid February until late November each year and housed during the winter months, while they were dry for the most part (Dillon et al., 2003). During winter, they were offered grass silage *ad libitum* and dry cow minerals at a rate of 100 g/cow per day. Calcined magnesite (Calmag, NutriBio Ltd., Cork, Ireland) in powder form was used for pasture dusting on the paddocks at a rate of 60 g/cow per day to prevent Mg deficiency during the risk period. A 10-wk dry period was given to first-lactation animals, whereas an 8-wk dry period was deemed adequate for multiparous animals. Grass silage *ad libitum* and 6 kg of concentrate were offered daily postcalving and before turnout to pasture. In mid to late April every year, calving date and milk yield were used as criteria to group cows into blocks of 2 within breed groups. The breed groups were then randomized across 2 spring-calving, grass-based feeding systems: low concentrate feeding system (**LC**) and high concentrate feeding system (**HC**). Those on the LC feeding system were offered

Table 1. Number of dairy cows included in the 5-yr analysis

Group	Breed ¹						Feeding system ²	
	HF	MB	MBX	NM	NMX	NRF	HC	LC
Animals, n								
Yr 1	22	20	14	13	13	26	54	54
Yr 2	32	22	25	9	20	22	65	65
Yr 3	38	30	28	16	22	30	82	82
Yr 4	33	31	36	14	22	31	97	70
Yr 5	35	39	37	16	20	37	86	88
Lactation records, n								
Parity 1	69	50	53	24	33	54	147	136
Parity 2	43	35	38	15	25	36	99	93
Parity 3	31	24	24	15	16	27	69	68
Parity 4	13	15	17	8	14	17	49	35
Parity 5	4	8	8	6	9	12	20	27

¹HF = Holstein Friesian; MB = Montbéliarde; MBX = Montbéliarde × Holstein-Friesian; NM = Normande; NMX = Normande × Holstein-Friesian; NRF = Norwegian Red.

²HC = high concentrate feeding system; LC = low concentrate feeding system.

approximately 530 kg/cow over the total lactation, whereas those on the HC feeding system had a greater concentrate input (approximately 1,030 kg/cow). Concentrates were offered on a flat-rate basis within feeding system in individual stalls twice daily in a 20-unit side-by-side herringbone milking parlor. The ingredient composition of the concentrate (pelleted) offered (kg/t as fed) was as follows: barley 250 kg, corn gluten 260 kg, beet pulp 350 kg, soybean meal 110 kg, and minerals plus vitamins 30 kg. The chemical composition of the concentrate offered (g/kg of DM) was 180 and 800 CP and cellulase/gamane digestibility, respectively.

Data Collection

Throughout the trial, the cows grazed as a single herd and were milked at 0700 and 1600 h daily. Milk yield was recorded daily using electronic milk meters. Somatic cell count was determined from a.m. milk samples using a Bentley Somacount 300 (Bentley Instruments Inc., Chaska, MN). The mean number of SCC records per cow per year was 14. However, in the first 4 yr of the study, SCC sampling was infrequent compared with yr 5, which had an average of 22 SCC records per cow (every 2 wk).

Milking duration (s) and milk flow (kg/min) were automatically recorded 7 d/wk at both a.m. and p.m. milking for yr 3, 4, and 5 of the study using the same electronic milk meters. The time from cluster attachment to cluster removal determined milking duration. When milk flow decreased below 0.2 kg/min and a minimum milking time of 4 min had elapsed, clusters automatically detached, thus eliminating any possible effects of overmilking on the milking characteristics variables measured. The milk meter computed the rate of milk flow continuously by calculating the change in weight

every 20 s. The maximum flow was the peak of this value. Milking was performed at a 48-kPa vacuum, with a pulsation ratio of 65:35 at a rate of 60 cycles/min.

Data Editing and Analysis

A total of 11,040 test-day records from 749 lactations of 309 cows were available for inclusion in the SCC analysis. Data were restricted to between 5 and 305 DIM and a minimum lactation length of 100 d; 10,982 test-day records from 743 lactations remained. The natural logarithm of SCC was used to ensure normally distributed residuals; this variable will henceforth be referred to as SCS.

A total of 122,316 daily records from 505 lactations (258 cows) were included in the analysis for milk yield and milking characteristics. Data records were only retained if observations were available for both a.m. and p.m. milking. The data were further restricted to between 5 and 305 DIM. Peak milk flow (PMF; kg/min), milking duration, and milk yield were recorded at each milking. Outliers were defined as values that were 2 interquartile ranges above or below the 75% and 25% percentile, respectively, for individual part-day measurements; 3.7% of records were removed. Milking duration (MD; s/d) was defined as the sum of the milking duration in the a.m. and milking duration in the p.m. Average daily milk flow (AMF; kg/min) was defined as total daily milk yield divided by total daily milking duration. Milking duration was positively skewed. The natural logarithm of MD was used to normalize the distribution.

Analysis on a Per-Lactation Basis. Lactation-average SCS was defined as the mean of all SCS test-day records within cow-lactation. Average AMF, PMF, and MD were first calculated for each week and then aver-

aged within lactation. Data were analyzed using mixed model methodology in PROC MIXED (SAS Institute, 2006) assuming a first-order autoregressive covariance structure among parity records within cow with heterogeneous variances. This covariance structure gave the best Akaike's information criterion. Class variables included in the model were breed, feeding system, parity, and year. Cow was included as a random effect. Parity was included as a repeated effect. Continuous covariates included in the analysis were calving day of year and lactation length. Interactions between independent variables were also tested. The initial model was developed using a backward stepwise procedure with $P < 0.05$ as the inclusion criterion. Residual diagnostics were undertaken on the final model.

Analysis on a Per-Stage Basis. Each lactation was divided into 10 stages: wk 1 to 4, wk 5 to 8, wk 9 to 12, wk 13 to 16, wk 17 to 20, wk 21 to 24, wk 25 to 28, wk 29 to 32, wk 33 to 36, and wk 37 to 44. Average weekly SCS, AMF, PMF, and MD were calculated within these 10 stages. Similar to lactation-average analysis, stage SCS, AMF, PMF, and MD were analyzed using mixed model methodology in PROC MIXED (SAS Institute, 2006). Stage was included as a repeated effect with a first-order autoregressive covariance structure with heterogeneous variances assumed among stages within cow-lactation, and cow was included as a random effect. Class variables included in the model were breed, feeding system, parity, stage of lactation, and year. The initial model was developed using a backward stepwise procedure with $P < 0.05$ as the inclusion criterion. Interaction between breed and lactation stage was also investigated.

Association Between Milk Yield and SCS, AMF, PMF, and MD. The effect of a 1-unit increase in average daily milk yield on lactation SCS, AMF, PMF, and MD was determined by including average daily milk yield as a continuous variable in the final multiple regression model of the average lactation data. Similarly, the interaction between breed and milk yield was determined by subsequently including the interaction in the final multiple regression model of the average lactation data. The associations of SCS with AMF, PMF, and MD were derived by including AMF, PMF, and MD separately in the lactation-average SCS multiple regression model.

RESULTS

Lactation-average SCS over all breeds was 10.55 SCS (back transformed SCS; 38,177 somatic cells/mL) over the 5 yr. Lactation-average ($\pm$ standard deviation) AMF and PMF were 1.48 (± 0.29) kg/min and 3.64 (± 0.89) kg/min, respectively, whereas the median of the MD was

834 s/d, and the first and third quartiles were 990 and 696 s/d, respectively.

Effect of Breed and Feeding System on Lactation Averages

The interaction between breed and feeding system was not significant for daily average milk yield, SCS, and all milking characteristics and was, therefore, omitted from the analysis. Thus, Table 2 presents only the main effects. The HF had greater ($P < 0.01$) lactation-average daily milk yield compared with all other breeds with the exception of the MBX. The NM and MB had lower ($P < 0.01$) daily average milk yield compared with all breeds, whereas both the crossbreds and the NRF were similar. Compared with the NRF (30,031 somatic cells/mL), SCS was greater ($P < 0.05$) for the HF (57,526 somatic cells/mL), NM (53,104 somatic cells/mL), MBX (55,826 somatic cells/mL), and NMX (51,021 somatic cells/mL) breed groups, whereas SCS of the MB (35,242 somatic cells/mL) was not different.

The NM and MB had lower AMF ($P < 0.01$) compared with all breeds. The crossbreds achieved the greater AMF. The effect of breed of dairy cow on PMF tended toward significance ($P = 0.079$). The NM had the lowest PMF, whereas that of the crossbreds was greater compared with all breeds. Milking duration was not affected by breed. Differences between breeds for AMF, PMF, and MD were not apparent after adjustment for milk yield.

Animals offered a HC diet achieved greater daily average milk yield, AMF, PMF, and MD ($P < 0.001$) compared with those on the LC feeding system. Somatic cell score did not differ between the feeding systems. The effect of feeding system on AMF and MD remained significant ($P < 0.01$) following adjustment for milk yield.

Effect of Breed and Feed System on Lactation Stage Averages

There was no significant interaction between breed and feeding system on stage of lactation effects; hence, only the main effects are reported in Figures 1 to 4. Daily average milk yield, SCS, and all milking characteristics varied across stages of lactation ($P < 0.01$). Daily average milk production peaked at 28.4 kg/d in wk 7 of lactation, followed by a gradual decline until the end of lactation. The lactation profile for SCS was essentially the inverse of the milk yield lactation profile. Postcalving, SCS decreased to a minimum in wk 5 to 8 after which it increased to the end of lactation. Somatic cell score ranged from 10.27 SCS (wk 5 to 8) to 11.20 SCS (wk 37 to 44).

Table 2. Effect of breed¹ and feeding system² on milk yield (kg/d), SCS, average milk flow (AMF; kg/min), peak milk flow (PMF; kg/min), and average milking duration (MD; log s/d)

Variable	Breed					Feeding system			
	HF	MB	NM	NRF	MBX	NMX	SEM ³	P-value	LC
Milk (kg/d)	22.6 ^a	20.1 ^b	19.1 ^b	21.5 ^c	22.0 ^{ac}	21.4 ^c	0.30	<0.001	19.9
SCS	10.96 ^a	10.47 ^b	10.88 ^a	10.31 ^b	10.93 ^a	10.84 ^a	0.127	<0.001	10.79
AMF (kg/min)	1.52 ^{acd}	1.41 ^b	1.33 ^b	1.48 ^{ad}	1.56 ^c	1.54 ^{cd}	0.030	<0.001	1.40
PMF (kg/min)	3.67	3.58	3.22	3.68	3.81	3.76	0.119	0.079	3.55
MD (log s/d) ⁴	6.78 (880)	6.74 (846)	6.75 (854)	6.75 (854)	6.74 (846)	6.72 (829)	0.019	0.359	6.74 (846)
									0.010

^{a-d}Means within a row with different superscripts differ ($P < 0.05$).

¹HF = Holstein Friesian; MB = Montbéliarde; MBX = Montbéliarde × Holstein-Friesian; NM = Normande; NMX = Normande × Holstein-Friesian; NRF = Norwegian Red.

²HC = high concentrate feeding system; LC = low concentrate feeding system.

³SEM = pooled standard error of the mean.

⁴Mean MD in s; antilog of MD least squares means are presented in parentheses.

The interaction between stage of lactation and breed was significant for daily average milk yield ($P < 0.05$), AMF ($P < 0.01$), PMF ($P < 0.001$), and MD ($P < 0.001$) and is detailed in Figures 1 and 2. Breed significantly affected SCS in each stage of lactation ($P < 0.001$) but the effect of breed did not differ significantly by stage (Figure 1). Similar to the lactation-average findings, when all breeds were compared with the NRF, the HF ($P = 0.065$) and MBX ($P = 0.012$) had greater SCS, and the MB, NMX, and NM breeds were not different.

All breeds reached peak AMF in wk 5 to 8 of lactation, followed by a gradual decline until nadir AMF at the end of lactation. The crossbreds displayed a greater AMF ($P < 0.05$) in wk 5 to 8 compared with the MB and NM. In contrast, the NM displayed a lower ($P < 0.01$) AMF at peak compared with all breeds, except the MB. The lactation profile for PMF was relatively static compared with the lactation profile of milk yield and AMF for all breeds. The greatest PMF was observed for the MB, NM, MBX, and NMX in wk 1 to 4, whereas the HF and NRF had greater PMF in wk 9 to 12 and wk 13 to 16, respectively. Following wk 21 to 24, PMF declined to a minimum at the end of lactation for all breeds. Maximum MD was reached in wk 5 to 8 of lactation after which it declined until the end of lactation across all breeds. The HF had the greatest MD in wk 5 to 8 compared with all breeds ($P < 0.05$) apart from the NRF, with which it was similar.

An interaction between stage of lactation and feed was observed for daily average milk yield ($P < 0.05$), AMF ($P < 0.01$), PMF ($P < 0.001$), and MD ($P < 0.001$) and is detailed in Figures 3 and 4. Somatic cell score was similar for the first 2 stages of lactation (feeding systems not applied during this period). Feeding system influenced SCS ($P < 0.05$) from wk 21 to 36 inclusive. Similarly, animals in the LC feeding system exhibited lower AMF ($P < 0.001$) and PMF ($P < 0.001$) from wk 9 to 36, and from wk 13 to 44, respectively. From wk 13 (stage 4), MD of the animals on the LC feeding system was lower through to the end of lactation ($P < 0.001$).

Effect of Parity on SCS and Milking Characteristics

Parity had a significant effect ($P < 0.001$) on all traits analyzed (Table 3). Milk yield and SCS increased with parity. First-parity animals had the lowest AMF ($P < 0.001$), PMF ($P < 0.001$), and MD ($P < 0.001$) compared with all parities. Third-parity animals had the greatest AMF, whereas fifth-parity animals had greater PMF and MD.

Figure 1. Effect of Holstein-Friesian (▲), Montbéliarde (◆), Normande (○), Norwegian Red (●), Montbéliarde × Holstein-Friesian (□), and Normande × Holstein-Friesian (△) on average milk yield (kg/d) and SCS across different stages of lactation. Vertical bars indicate one pooled standard error.

Associations Among Milk Yield, SCS, and Milking Characteristics

The interaction between breed and milk yield influenced ($P < 0.001$) SCS, AMF, PMF, and MD (Table 4), implying that for each unit increase of milk yield by breed, the response in SCS, AMF, PMF, and MD were different for some breeds. The response in SCS was similar for NRF, MBX, and NMX, whereas MD was similar for the MB and MBX breeds. On analysis of the entire data set, effects on SCS as a result of an increase in average daily milk yield (Table 5) were observed (P

< 0.001), and the effect of an increase in AMF on SCS tended toward significance ($P < 0.074$). A 1-unit increase in daily average milk yield caused a favorable decrease in SCS; however, a 1-unit increase in PMF and MD did not influence SCS. No interactions were observed for breed with any milking characteristic on SCS.

DISCUSSION

The objective of this study was to determine if differences in udder health and milking characteristics existed among HF, MB, NM, NRF, MBX, and NMX dairy

Figure 2. Effect of Holstein-Friesian (▲), Montbéliarde (◆), Normande (○), Norwegian Red (●), Montbéliarde × Holstein-Friesian (◻), and Normande × Holstein-Friesian (△) on average milk flow (kg/min), peak milk flow (kg/min), and milking duration (back-transformed MD presented in minutes) across different stages of lactation. Vertical bars indicate one pooled standard error.

Figure 3. Effect of high concentrate feeding system (Δ) and low concentrate feeding system ($\square$) on average milk yield (kg/d) and SCS across different stages of lactation. Vertical bars indicate one pooled standard error.

cows on a grass-based system of milk production and to investigate if these differences were affected by concentrate feed level and parity. In this study, breed influenced daily average milk yield, SCS, and AMF; feeding system influenced daily average milk yield and all milking characteristics; and average milk yield, SCS, and all milking characteristics were influenced by parity.

Lactation-average SCS and all milking characteristics ranked similarly for all breeds between the HC and LC feeding system. No genotype by environment ($G \times E$) interaction was apparent for lactation-average SCS, which is in agreement with the reports of Castillo-Juarez et al. (2000), McCarthy et al. (2007), and Kear-

ney et al. (2004). However, results from Calus et al. (2006) based on herd test-day bulk milk SCC showed that a $G \times E$ interaction was present for SCS across DIM and herd environment. Previous research revealed little or no importance of breed or strain $\times$ feeding systems in temperate dairy production systems using Jerseys and HF (Holmes, 1995). However, the importance of $G \times E$ interactions for udder health is still relatively unknown.

Breed Effects

Observed phenotypes are a function of genotypic (breed) and environmental effects. Previous literature

Figure 4. Effect of high concentrate feeding system (△) and low concentrate feeding system (□) on average milk flow (kg/min), peak milk flow (kg/min), and milking duration (back-transformed MD presented in minutes) across different stages of lactation. Vertical bars indicate one pooled standard error.

Table 3. Effect of parity on milk yield (kg/d), SCS, average milk flow (AMF; kg/min), peak milk flow (PMF; log s/d), and milking duration (log s/d)

Variable	Parity 1	Parity 2	Parity 3	Parity 4	Parity 5	P-value	SEM ¹
Milk (kg/d)	17.2 ^a	20.5 ^b	22.1 ^c	22.7 ^d	23.2 ^d	<0.001	0.21
SCS	10.44 ^a	10.52 ^a	10.57 ^a	11.04 ^b	11.09 ^b	<0.001	0.096
AMF (kg/min)	1.29 ^a	1.48 ^b	1.57 ^c	1.52 ^d	1.52 ^d	<0.001	0.020
PMF (kg/min)	3.13 ^a	3.57 ^b	3.75 ^c	3.81 ^c	3.84 ^c	<0.001	0.069
MD log s/d	6.68 ^a	6.71 ^b	6.73 ^c	6.80 ^d	6.82 ^e	<0.001	0.012

^{a-e}Means within a row with different superscripts differ ($P < 0.05$).

¹SEM = pooled standard error of the mean.

suggests significant genetic variation in SCC and milking characteristics (Mrode and Swanson, 1996; McCarthy et al., 2007); hence, differences in expressed phenotype between breeds may be expected if the breeding programs responsible for the development of the different breeds are diverse. The United States breeding program has exerted considerable influence on dairy cow populations internationally, due to the replacement of native genotypes with US Holsteins (Hansen, 2000). Evans et al. (2006) reported a significant introgression of North American Holstein-Friesian genes into the Irish dairy cow population, increasing from 8% in 1990 to 63% in 2001, with a corresponding increase in milk yield from approximately 5,033 kg in 1990 to 5,775 kg in 2001. Because milk yield is positively genetically correlated with SCC (Mrode and Swanson, 1996), the greater SCS of the HF, compared with some of the other breeds reported in this study, is perhaps not surprising, considering the progress achieved by the HF in milk production. Similar trends for the HF were reported in previous research that included different breeds (Washburn et al., 2002).

In contrast to the US breeding program, Norway's criteria for the "ideal cow" were formulated with a broad breeding goal that encompassed dairy, beef, health, and reproduction traits (Heringstad et al., 2001). Consistent with the breeding goals of the Norwegian index, the NRF maintained a lower SCS throughout lactation.

The MB and NM breeds, with origins in France, had intermediate SCS compared with the HF and NRF. A genetic evaluation for SCC was introduced in France in 2001 by Institut National de la Recherche Agronomique (Ducrocq et al., 2001). Although the MB and NM do not stem from a breeding program with long-term selection for udder health traits, the differences in SCS among all 6 breeds suggest that the breeds differ genetically to disease susceptibility.

Grindal and Hillerton (1991) reported that cows with greater PMF are more susceptible to mastitis. A similar trend was observed by McCarthy et al. (2007) of greater SCS in addition to greater PMF with a New Zealand strain of HF. In this study, despite the crossbreds having the greater PMF and relatively greater SCS compared with all other breeds, a positive relationship between SCS and PMF was not observed. This may relate to the relatively low milk production levels and, therefore, closer range among breeds than in studies in which cows were provided more concentrate feed.

The positive genetic correlation between milk production and milk flow rates have previously been documented (Petersen et al., 1986); hence, the greater AMF of the crossbreds may be a consequence of the greater daily average milk yield attained over their purebred counterparts (MB and NM). Analogous studies (Gandini et al., 2007) of the effect of breed on MD reported a difference between breeds; however, these were not

Table 4. Change in SCS and milking characteristics (standard error in parenthesis) as a result of the interaction between breed and milk yield

Variable	Breed ¹						P-value ²
	HF	MB	NM	NRF	MBX	NMX	
SCS $\times 10^2$	-10.25 (0.036) ^a	-19.63 (0.047) ^b	-6.97 (0.066) ^c	-11.04 (0.043) ^d	-10.83 (0.038) ^d	-11.36 (0.047) ^d	<0.001
AMF (kg/min) $\times 10^2$	3.94 (0.005) ^a	3.66 (0.006) ^b	2.76 (0.009) ^c	4.45 (0.006) ^d	4.01 (0.005) ^e	5.12 (0.006) ^f	<0.001
PMF (kg/min) $\times 10^2$	6.52 (0.009) ^a	3.60 (0.013) ^b	5.76 (0.018) ^c	8.30 (0.011) ^d	4.09 (0.011) ^e	9.97 (0.010) ^f	<0.001
MD (log s/d) $\times 10^2$	1.91 (0.003) ^a	2.14 (0.004) ^b	2.60 (0.006) ^c	1.68 (0.004) ^d	2.15 (0.003) ^b	1.46 (0.004) ^e	<0.001

^{a-f}Means within a row with different superscripts differ ($P < 0.05$).

¹HF = Holstein Friesian; MB = Montbéliarde; MBX = Montbéliarde $\times$ Holstein-Friesian; NM = Normande; NMX = Normande $\times$ Holstein-Friesian; NRF = Norwegian Red.

²P-value = significance of the interaction between breed and milk yield.

Table 5. Effect of one unit increase in milk yield (kg/d), average milk flow (AMF; kg/min), peak milk flow (PMF; log s/d), and milking duration (log s/d) on SCS

Variable	SCS	P-value	SEM ¹
Milk (kg/d) $\times 10^2$	-11.51	<0.001	0.026
AMF (kg/min) $\times 10^2$	-48.58	0.074	0.270
PMF (kg/min) $\times 10^2$	7.93	0.290	0.075
MD log s/d $\times 10^2$	-51.02	0.235	0.429

¹SEM = standard error of the mean.

significant, which is consistent with the findings in this study. The AMF reported in this study was lower than has been previously documented (Gandini et al., 2007; McCarthy et al., 2007); however, this may be attributable to differences in milk yield produced by the animals in the respective studies. Oldenbroek (1984) reported that HF heifers milked faster than Dutch-Friesian and Dutch Red and Whites, but because of their greater milk yield, they had similar milking times. In contrast, this study did not observe differences in MD between breeds before or after accounting for milk yield. The nadir of the SCC curve coincided with peak milk production; hence, a dilution effect has been suggested as a possible contributor (Wicks and Leaver, 2006). This theory is further supported by the current study, in which a decrease in SCS per 1-kg increase in daily average milk yield was observed.

Currently, crossbreeding is not common on Irish dairy farms; however, interest is growing because of the potential to improve profitability and efficiency through favored selection traits and heterosis. The F₁ and back-cross cows were grouped together to represent the early stages of a crossbreeding strategy. Exclusion of back-cross cows from the analysis did not significantly affect the results for udder health and milking characteristics. Heterosis for SCS was not significant, similar to previous findings of VanRaden and Sanders (2003). The authors are unaware of previous research on the effect of heterosis on milking characteristics. In this study, heterosis for PMF and MD was not significant. However, heterosis for AMF was evident in both crossbred groups at 6.5 and 8% for the MBX and NMX, respectively. Heterosis for milk yield was estimated to be 3 and 2.6% for the MBX and NMX, respectively.

The opportunity for milkability characteristics to be incorporated into a breeding program as an indicator of clinical mastitis will be determined by the genetic correlation between milking speed and clinical mastitis and the ease (cost) with which it can be measured. Presently, the majority of measurements on milking speed are subjective; that is, they are measured by the farmer on a scale from slow to fast. Electronic milk meters have the ability to accurately compare milk-flow

rates and milking duration, so that data facilitating improved estimation of these traits should be possible. An udder health index that incorporates SCS, udder traits, and milking speed has been proposed by Boettcher et al. (1998).

Feeding System Effects

Few studies have investigated the effect of feeding system on udder health (Ouweltjes et al., 2007). Similarly, there is a paucity of information on interactions between breed or genotype and feeding systems in dairy cattle on udder health and milking characteristics. Consistent with previous studies carried out on a grass-based system of production, varying levels of concentrate offered (Turner et al., 2003; McCarthy et al., 2007) did not influence lactation-average SCS. However, feeding system had an effect on SCS in late lactation (from wk 21 to 36 inclusive). In the current study, animals on the HC diet had lower SCS, which was probably a dilution effect because greater milk yield was achieved by animals on the HC diet.

In corroborating research in which all production originated from within a grazing environment (McCarthy et al., 2007), animals offered a high concentrate diet had greater AMF and MD. As tabulated (Table 2), animals offered the HC diet produced more milk. Therefore, the greater milk production coupled with the greater AMF attained by those animals in the HC feeding system support the positive correlation between milk yield and AMF (Petersen et al., 1986). McCarthy et al. (2007) and Weiss et al. (2004) observed a positive correlation between milk yield and AMF of 0.64 and 0.29, respectively. In addition, positive correlations have been reported between milk yield and MD (Petersen et al., 1986; Weiss et al., 2004). Similarly, results from this study indicate positive correlations for milk yield with AMF, PMF, and MD and suggest that these correlations differ depending on breed.

Feeding system differences in AMF and MD persisted after adjustment for milk yield; we are unsure why this was the case. It may be that milk yield is not the sole driving force behind the effect of feeding system on AMF and MD. The effect of feeding system on all traits was mediated through, not only milk yield, but also the effect of stage of lactation. Stage of lactation has been previously identified as a determining factor of SCS and milk flow characteristics (Olde Riekerink et al., 2007).

Parity Effects

Analogous studies on the effect of parity on SCS reported an increase in lactation-average SCS as parity increased (McCarthy et al., 2007). This effect may be

attributable to an increased incidence rate of clinical mastitis with increasing parity as reported by Olde Riekerink et al. (2007). In agreement with other international literature (Schepers et al., 1997), the shape of the lactation curve for lnSCC differed among parities.

Changes in udder anatomy with advancing age have been previously documented (McDonald, 1968) to have an association with milking characteristics and indirectly with SCC. Compared with primiparous cows (McDonald, 1968), multiparous cows have longer and more dilated streak canals, which have been shown (Grindal and Hillerton, 1991) to leave cows more susceptible to mastitis and a greater milk flow rate. Petersen et al. (1986) reported that the effect of parity differed for pedigree groups for milk flow rates. This is further supported by the results of this study, in which a significant interaction between breed and parity for PMF was observed.

CONCLUSIONS

The results from this study highlight differences among dairy cattle breeds for milk yield, SCS, and milking characteristics. These likely relate to differences in the breeding goals from which these breeds were established, namely the intensity of selection for milk yield and the inclusion of traits aimed at maintaining or improving udder health. The current study found no $G \times E$ interaction for udder health. Similarly, a lack of $G \times E$ interaction was found for milking characteristics. In general, SCS and all milking characteristics increased concurrently with parity. The moderate heritability of milking speed, the positive correlations of milk yield with milking characteristics, and the previously reported correlations between milking speed and SCS indicate that potentially greater improvement in udder health could be achieved by the inclusion of milking characteristics in an udder health index.

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