Breeding and Genetics: Dairy Cattle Breeding for Production and Non-Production Traits

644 Productive life including all lactations, longer lactations, and calf value.

P. M. VanRaden* and M. E. Tooker, *Animal Improvement Programs Laboratory, Agricultural Research Service, USDA*, *Beltsville, MD*.

Longer lactations are more profitable than in the past, and daughter pregnancy rate evaluations now allow separate selection for cow fertility and longevity. Measures of productive life were compared, and updated life expectancy factors were derived to replace those estimated in 1993. Extra credits for lactations longer than 10 mo and beyond 84 mo of age are proposed, and also for each calf produced so that an extremely long lactation will not receive more credit than multiple shorter lactations with dry periods between. Maximum credits per lactation of 10 mo, 12 mo, and unlimited were compared; the latter either included or excluded a calf value equal to 2 mo of production. Days in milk beyond 305 had not been stored in early data but were estimated from the subsequent calving date assuming a 60-d dry period. Heritabilities and genetic correlations were estimated by multi-trait REML for longevity censored at various ages and for yield traits and somatic cell score in first parity. Data included records from 1,098,329 Holsteins born from 1994 through 1997 from 5109 sires, and a relationship matrix among sires was included in the model. Cows that were still alive in 2005 received credit for predicted remaining months of productive life. Lactations beyond 84 mo added little information. Heritability of productive life was 0.073 with 10-mo, 0.069 with 12-mo, and 0.067 with unlimited lactation credits. The latter increased slightly to 0.068 with calf credit included. Corresponding genetic correlations of productive life with protein yield were 0.00, 0.03, 0.12, and 0.11, all much lower than the 0.46 estimated in 1993. Phenotypic correlations and life expectancy factors were similar to 1993 estimates. Productive life censored at 36 mo is genetically correlated by only 0.87 with final productive life and is influenced more by yield traits (those correlations ranged from 0.14 to 0.27). Adjustments for yield could make correlations more consistent across time and across censoring ages. Stable properties and high economic value are desired while retaining simple interpretation.

Key Words: Longevity, Productive Life, Lactation Length

645 Effect of inbreeding on functional longevity in Canadian dairy breeds.

A. Sewalem*[1,2], G. Kistemaker[2], F. Miglior[1,2], and B. Van Doormaal[2], [1]*Agriculture and Agri-Food Canada*, *Guelph, ON, Canada,*, [2]*Canadian Dairy Network*, *Guelph, ON, Canada*.

The aim of this study was to assess the level of inbreeding and its relationship to the functional survival of Canadian dairy breeds using a Weibull proportional hazard model. Data consisted of 72,385 cows in 1,505 herds from 2,499 sires for Jersey, 112,723 cows in 1,482 herds from 2,926 sires for Ayrshire and 1,977,311 cows in 17,182 herds from 8261 sires for Holstein. Functional longevity was defined as the number of days from the first calving to culling or death or censoring. Inbreeding coefficients (F) were grouped in to seven classes. The statistical model included the effects of stage of lactation, season of production, the annual change in herd size, type of milk recording supervision, age at first calving, effects of milk, fat and protein yields calculated as within herd-year-parity deviations, herd-year-season of calving, inbreeding and sire. The relative culling rate was calculated for animals in each class after accounting for the above-mentioned effects. The result showed that in all breeds there is a slight trend toward higher risk of culling among more inbred animals. The relative risk ratio for cows with inbreeding coefficients up to 12.5% were from 1.19, 1.16 and 1.14 times the risk ratios for non-inbred cows (F=0) for Jersey, Ayrshire and Holstein cows, respectively. There was minimal difference on the relative risk ratios among the three lowest classes of inbreeding relative to the non-inbred cows. The difference, however, was greater when the inbreeding coefficient increased beyond 12.5%.

Key Words: Functional Longevity, Inbreeding, Canadian Dairy Breeds

646 Relationship between somatic cell count and functional longevity in Canadian dairy breeds.

A. Sewalem*[1,2], G. Kistemaker[2], and B. Van Doormaal[2], [1]*Agriculture and Agri-Food Canada*, *Guelph, ON, Canada.*, [2]*Canadian Dairy Network*, *Guelph, ON, Canada*.

The aim of this study was to examine the impact of somatic cell count (SCC) on the functional survival of Canadian dairy cattle using a Weibull proportional hazard model. Data consisted of 72,385 cows in 1,505 herds from 2,499 sires for Jersey, 112,723 cows in 1,482 herds from 2,926 sires for Ayrshire and 1,977,311 cows in 17,182 herds from 8,261 sires for Holstein. Functional longevity was defined as the number of days from the first calving to culling or death or censoring. Test day SCC were averaged within each lactation. Average SCCs were grouped into 11 classes with equal number of records in each class. The statistical model included the effects of stage of lactation, season of production, the annual change in herd size, type of milk recording supervision, age at first calving, effects of milk, fat and protein yields calculated as within herd-year-parity deviations, herd-year-season of calving, SCC class and sire. The relative culling rate was calculated for animals in each class after accounting for the above-mentioned effects. The overall average SCC for Jersey breed was 185,250 with standard deviation of 59,700. The corresponding figures for Ayrshire were 213,880 and 71,200 and for Holstein 280,150 and 86,290. In all breeds there are no appreciable differences in the relative risk of culling among classes of mean SCC up to nearly breed average. However, as the mean SCC increased beyond breed average, the relative risk of cows being culled increased. For instance, cows with the highest mean classes of SCC had a risk of being culled that was 2.73, 3.27 and 2.58 times that for cows extremely low SCC for Jersey, Ayrshire and Holstein, respectively.

Key Words: Functional Longevity, Somatic Cell Count, Risk of Culling

647 Detection and confirmation of quantitative trait loci affecting traits of lifetime profit index on 23 chromosomes in Canadian Holstein cattle.

Y. Pan*[1,2], J. P. Chesnais[1,2], N. Bissonnette[3], N. Caron[1], G. B. Jansen[4], Y. Plante[5], and E. B. Burnside[1,2], [1]*The Semex Alliance*, *Saint-Hyacinthe, Quebec, Canada*, [2]*L'Alliance Boviteq*, *Saint-Hyacinthe, Quebec, Canada*, [3]*Dairy and Swine Research and Development Centre, AAFC*, *Lennoxville, Quebec, Canada*, [4]*CGIL, Animal and Poultry Science, University of Guelph*, *Guelph, Ontario, Canada*, [5]*Saskatchewan Research Council*, *Saskatoon, Saskatchewan, Canada*.

Marker assisted selection (**MAS**) can be used to increase the accuracy of young bull selection prior to progeny testing, leading to increased rates of annual genetic gain or decreased costs for young bull selection or both. The dairy cattle population structure, whereby elite bulls have many sons, themselves proven through a large number of daughters, lends itself to the application of a granddaughter design (**GDD**) to detect quantitative trait loci (**QTL**) prior to MAS. In this study, a total of 617 young bulls with Canadian genetic evaluations, originating from six sire families, were genotyped for 143 microsatellite markers distributed on 23 chromosomes, at an average interval of 11.6 cM. The traits under scrutiny were these in the Lifetime Profit Index (**LPI**), i.e. protein yield, fat yield, somatic cell score, capacity, feet and legs, milking speed, mammary system and herd life. A weighted least squares method in the program QTL EXPRESS and the FORTRAN program (Knott et al. 1996) was used to detect QTL affecting these traits. Chromosome-wise thresholds for reporting statistically significant QTL were determined by permutation tests. False discovery rates (**FDR**) were used to determine thresholds for genome-wide significance. Approximately 50 QTL detected in this study ($P < 0.10$ and $FDR < 0.20$ for the across family analysis or $P < 0.05$ and $FDR < 0.20$ for the within family analysis) had already been found in other studies. In addition, 12 new QTL were discovered affecting LPI traits at significance levels of $P < 0.05$ and $FDR < 0.20$.

Key Words: Quantitative Trait Loci (QTL), Lifetime Profit Traits (LPI), Holstein Cattle

648 Identification of a missense mutation in the gene responsible for the QTL on BTA6 affecting milk yield and composition in dairy cattle.

M. Cohen-Zinder[1], E. Seroussi[1], D. Larkin[2], J. Loor[2], A. Everts-van der Wind[2], J. Lee[2], J. Drackley[2], M. Band[2], M. Shani[1], H. Lewin[2], J. Weller*[1], and M. Ron[1], [1]*Agricultural Research Organization, The Volcani Center*, *Bet Dagan, Israel*, [2]*University of Illinois*, *Urbana*.

We previously localized a quantitative trait locus (QTL) on chromosome 6 affecting milk fat and protein concentration to a 4 cM confidence centered on the microsatellite BM143. We characterized the genes and sequence variation in this region, and identified common haplotypes spanning five polymorphic sites in the genes IBSP, SPP1, PKD2, and ABCG2 for two sires segregating for this QTL. Expression of SPP1 and ABCG2 in the bovine mammary gland increased during lactation. SPP1 was fully sequenced, and all the coding exons of ABCG2 and PKD2 were sequenced for these two sires. Only the single nucleotide change capable of encoding a substitution of tyrosine to serine (Y→S) corresponded to the segregation status of all three heterozygous and 15 homozygous sires for the QTL in the Israeli and US Holstein populations (P = 0.00008). The allele substitution fixed effects on the genetic evaluations of 335 Israeli sires were -340 kg milk, +0.15% fat, and +0.13% protein (F-value = 200). None of the other polymorphisms gave significant effects for fat and protein concentration in models that also included Y→S. The allele substitution effects on the genetic evaluations of 670 cows, daughters of the two heterozygous sires, were -226 kg milk, 0.09% fat, and 0.08% protein (F-value = 394), with partial dominance towards the S homozygotes. We therefore propose that this Y→S polymorphism is the causative site for this QTL.

Acknowledgements: This research was supported by a grant from the Israel Milk Marketing Board and the US-Israel Binational Agricultural Research and Development fund (BARD). The authors thank B. Kinghorn and I. Misztal for use of their programs and Mr. Efraim Ezra for his help in data retrieval from the Israeli herd-book.

Key Words: Quantitative Trait Locus, BTA6, Milk Protein Concentration

649 Genetic gains in milk, fat and protein yields of the Holstein breed in Brazil.

C. N. Costa*[1], N. M. Teixeira[1], A. F. Freitas[1], J. A. Cobuci[1], and K. Haguihara[2], [1]*Embrapa Gado de Leite*, *Juiz de Fora-MG, Brazil*, [2]*Brazilian Holstein Association-ABCBRH*, *São Paulo-SP, Brazil.*

Traditionally Brazilian Holstein breeders are users of semen imported from North America and Europe. Choice of semen is generally based on sire proofs from the exporting countries. Estimates of genetic gain indicate effectiveness of imports to promote genetic progress locally. First lactation 305-day records of up to 88,449 Holstein cows calving between 1984 and 2003 in a total of 1808 herds in different States of Brazil were used to estimate breeding values and genetic gains for milk, fat and protein yields. Univariate analyses were used with a model including herd-year, season, age at calving, genetic composition of the cow and genetic group of sires as fixed effects and sire by herd interaction, animal and residual as random effects. Genetic variances for milk, fat and protein yields were respectively 333,869.2; 372.3 and 258.3 kg ^{2}. Genetic trends were estimated for sires and cows by regression of the Predicted Transmitting Ability (PTA) on birth year. Estimated weighted and unweighted average annual genetic gains (kg/year) were 13,8 and 10,1 for milk, 0.32 and 0.33 for fat, respectively, for sires born from 1968 to 1996 and 0.39 and 0.29 for protein for sires born from 1976 to 1995. Genetic gains were 8.3 for milk and 0.26 for fat for cows born from 1981 to 2000 and 0.29 for protein for cows born from 1989 to 2000. Annual weighted genetic gains for sires were 0.23, 0.16 and 0.18 % of the average population for milk, fat and protein, respectively. Except for fat yield, trends from weighted PTAs were slightly larger than those from unweighted PTAs indicating breeders have used more intensively sires with larger than average genetic potential for milk and fat production. Genetic gains in the last ten-year periods were lower than those from earlier periods suggesting the population has progressed at a decreasing pace. These rates of genetic progress suggest genotype by environment interaction and that breeders have been considering traits other than production when selecting sires for breeding.

Acknowledgements: ABCBRH for providing the data and Prodetab for financial support.

Key Words: Selection, Breeding Values, Genetic Progress

650 A phenotypic study of test-day yields recorded on Holstein-Friesian cows under Tunisian conditions.

A. Ben Gara*, B. Rekik, M. Mrad, and B. Khouildi, *Ecole Supérieure d'Agriculture de Mateur*, *Mateur, Bizerte, Tunisia*.

Milk, fat, and protein yields and fat and protein percentages recoded in test-days and milk, fat, and protein yields in 305 days were studied on Holstein-Friesian cows under Tunisian conditions to determine important sources of variation and fit lactation curves.

Data included 330480 test-day records. These were of 23021 lactation records of which 6398 were first lactations. Data were collected in 136 herds from 1992 to 2002. The effects of environmental (year and season of calving), management (herd), and physiological (rank of lactation, calving age, and days in milk) factors on milk production were tested by a general linear model. Residuals were used to compute linear correlation coefficients among milk traits. Curves of test-day records and least square solutions of days in milk (DIM) from a test-day model were fitted by the incomplete gamma function.

Mean yields in 305 days were 6083 kg, 211 kg, and 190 kg for milk, fat, and protein yields, respectively, and contents were 3.42% and 3.04% for fat and protein. Milk productions varied with calving age ($p<0.01$), herd (0.01), rank of lactation (0.01), and DIM ($p<0.01$). Coefficients of determination of fitted curves ranged from 86 to 98%. The highest coefficients were obtained for protein percentage using non linear regression. DIM least square solutions improved fitting curves of only milk yield. First lactation cows started production averaging 16.7 kg, 0.64 kg, and 0.52 kg for the yields of milk, fat, and protein, respectively. They had lower peak yields but greater persistencies than multiparous cows. Correlation coefficients ranged from 0.58 to 0.88 among yield traits and from -0.31 to -0.28 between milk yield and fat and protein percentages, respectively.

Acknowledgements: Authors are thankful to CNAG, Sidi Thabet, Tunis, for providing the data.

Key Words: Test-Day Records, Lactation Curves, Dairy Cows

651 Genetic evaluation and best prediction of lactation persistency.

J. Cole* and P. VanRaden, *Animal Improvement Programs Laboratory, Agricultural Research Service, USDA*, *Beltsville, MD*.

Cows with high persistency tend to milk less than expected at the beginning of lactation and more than expected at the end. Persistency was calculated as a function of a trait-specific standard lactation curve and the linear regression of a cow's test day deviations on days in milk. The objectives of this study were to calculate (co)variance components and breeding values for best predictions of persistency of milk (M), fat (F), protein (P), and SCS in Jerseys (Table 1). Heritabilities represent the additive genetic variance of persistency that is independent of yield and defined to have variance of 1. Data included 574,929 records for 252,669 Jersey cows calving since 1997. 3,193 AI sires received evaluations for persistency. Sire EBV for M, F, and P were similar and ranged from -0.70 to 0.75 for M; EBV for SCS ranged from -0.37 to 0.28. Regressions of sire EBV on birth year were near zero (< 0.003) but in favorable directions for all traits. Genetic correlations of M, F, and P with SCS were moderate and favorable, indicating that increasing SCS decreases yield traits, as expected. Genetic correlations among yield and persistency were low to moderate and ranged from -0.09 (SCS) to 0.18 (F). This definition of persistency is more desirable than those used in test-day models, which are often correlated with yield. A measure that is not confounded with yield may provide for simpler understanding of persistency. Routine genetic evaluations for persistency are feasible and may allow for improved predictions of yield traits.

Persistency (co)variance components

Trait	M[1]	F	P	SCS
M	0.17	0.76	0.89	-0.19
F	0.79	0.13	0.81	-0.14
P	0.90	0.80	0.13	-0.16
SCS	-0.44	-0.50	-0.43	0.05

[1]Heritabilities on diagonal, phenotypic correlations above diagonal, and genetic correlations below the diagonal.

Key Words: Best Prediction, Persistency, Test Day Model

652 Genetic evaluation of calving traits across Dairy and Beef breeds of cattle in Ireland.

V. Olori*[1], A. Cromie[1], P. Donnellan[1], P. Amer[2], and R. Veerkamp[3], [1]*Irish Cattle Breeding Federation, Bandon, Co. Cork, Ireland*, [2]*Abacus Biotech Ltd., Dunedin, New Zealand*, [3]*Animal Sciences Group, Lelystad, The Netherlands*.

Dairy and beef production systems are inter-twined in Ireland. Beef bulls are used extensively in dairy herds to produce crossbred calves for fattening and as beef suckler dams. With seasonal breeding and extensive grazing, farm profits are reduced by difficult calving and prolonged gestation. These traits should thus be in the dairy and beef breeding objectives. The aim of this study was to investigate the suitability of available data and estimate genetic parameters to facilitate genetic evaluation of these traits across breeds. Records were available from AI centres (AI), pedigree herd books (HB) and an Animal Events recording system (AE). Calving difficulty (CD) was transformed to a linear scale from scores on a 4 or 5 point categorical scale depending on source. GL was derived from the latest insemination date and restricted to ±10 days of the expected GL which was computed as the direct breed effect from sire and dam plus the maternal breed effect from dam. Genetic parameters were estimated with a sire-maternal grandsire model for the direct effect and simultaneously maternal grandsire for the maternal effect. Incidence of CD and genetic parameters varied significantly between data sources. Genetic correlation between AI and AE data was 0.45 for CD and 0.67 for GL but these were not correlated with corresponding traits in the HB data. The HB data was thus excluded from further analysis. Direct and maternal h^2 for CD were highest in the AE data and were 22% and 5% respectively with r_g of -0.77. Corresponding values for GL were 25%, 5% and -0.14. The AE data was used for breeding value estimation with the AI data incorporated as predictors. Sire PTAs for AI bulls across breeds ranged from -7% to 12% serious difficulty for direct CD, from -3% to 4% for Maternal CD and from -8 to 4 days for GL

Key Words: Calving Traits, Genetic Parameters, Across Breed Evaluation

653 Effect of the bovine solute carrier/sulfate transporter (SLC26a2) gene on foot and leg traits in newborn calves.

A. M. Scholz*[1], S. Nueske[1], I. Medugorac[2], D. Seichter[3], J. Hampe[1], and M. Foerster[2,1], [1]*Experimental Farm of the Veterinary Faculty, University Munich, Oberschleissheim, Germany*, [2]*Institute of Animal Breeding of the Veterinary Faculty, University Munich, Munich, Germany*, [3]*Animal Breeding Research Munich e.V., Poing, Germany*.

Foot and leg problems are of concern for cattle breeders. In this study, different foot and leg traits of newborn calves (age 5-8 days) measured linearly or by dual energy x-ray absorptiometry (DXA) were compared between the homozygous 'normal' (AA, n=114) and the heterozygous genotype (AB, n=58) of the bovine SLC26a2 gene (BTA 7q23-q24). Due to a relatively low frequency of the B allele (q=.18), the homozygous 'mutated' genotype (BB, n=1) was not included in the analysis. A T1559/G1559 mutation in the SLC26a2 gene results in an isoleucine to serine amino acid exchange at position 520. Comparable mutations in humans are responsible for bone and cartilage deformations caused by decreased transmembrane sulfate transportation.

Purebred and crossbred calves originating from German Holsteins and Fleckvieh underwent a DXA scan under light sedation using a GE LUNAR DPX-IQ scanner. The medial and lateral claws of the fore and hind legs (including the pedal, distal sesamoid, short pastern, long pastern bones) were analyzed using the 'small animal whole body' scan mode for bone mineral density (BMD, g/cm^2), bone mineral content (BMC, g), and amount of fat tissue (g) within the region of interest. In addition, linear parameters as shown in the table were measured. A generalized linear model with the fixed effects SLC26a2 genotype, breeding line, gender, claw, SLC26a2×claw, and gender×claw was used for statistical analysis.

AA calves have significantly higher BMD, BMC, a larger wall diagonal, and heel angle than AB calves. But AA have a smaller sole width and heel height.

It is not exactly known yet, if a higher claw (bone) mineralization combined with a larger fat cushion, wall diagonal, and heel angle would be of an advantage for the foot health in the future life cycle of the calves. However, a DNA test for the SLC26a2 genotypes combined with exact phenotyping could provide a future tool to select for secondary traits, especially related to foot and leg health in cattle.

Least squares means ± standard errors of estimation for foot and leg traits measured by DXA and linearly

SLC26a2 Genotype	BMD	BMC	Fat Tissue	Wall Diagonal	Sole Width	Heel Height	Heel Length	Heel Angle
	g/cm^2	g	g	cm	cm	cm	cm	°
AA	.610±.003^{a}	10.38±.08^{a}	16.76±.28	6.14±.014^{a}	2.60±.008^{a}	3.18±.013^{a}	3.33±.020	113.7±.26^{a}
AB	.596±.004^{b}	10.02±.11^{b}	16.16±.38	6.07±.019^{b}	2.65±.010^{b}	3.24±.018^{b}	3.27±.027	112.5±.35^{b}

Different superscripts characterize significance (p£.05).

Acknowledgements: The DNA test for the bovine SLC26a2 gene has been patented under DE10155999C2 (BRENIG et al., 2003).

Key Words: Sulfate Transporter Gene, Foot and Leg Health, Dual Energy X-Ray Absorptiometry

654 Inheritance of hair whorl characteristics in Holstein cattle.

A. VanCise*, T. Grandin, D. Garrick, and R. Enns, *Colorado State University, Fort Collins*.

A hair whorl is a follicular hair pattern on the forehead of most cattle. There are conflicting opinions as to whether hair whorl characteristics, such as height and asymmetry, are associated with scrotal circumference and spermatozoal characteristics such as motility and morphology. It has been hypothesized that an association between hair whorl characteristics and spermatozoal characteristics exists due to the fact that hair follicle pattern and testicular development occur at approximately the same time during fetal development. Hair whorls are visible from birth and if correlated with spermatozoal characteristics may be used as a selection criterion in cattle. Due to this possible relationship it was of interest to determine if hair whorl characteristics have a genetic basis. Using whorl characteristic data on Holstein bulls (n=414), whorl height and asymmetry were analyzed together to determine their heritabilities. MTDFREML was used to estimate the genetic correlation (r_g=0.10) between the two traits and their individual heritabilities. Both whorl height and asymmetry were found to be highly heritable (0.42±0.17 and 0.51±0.15, respectively). This high heritability would indicate that genes have a larger effect on whorl characteristics than environmental factors. If it were proven that a genetic correlation exists between hair whorl and spermatozoal traits, this would contradict the idea that the relationship between hair whorl and spermatozoal characteristics is due to an environmental correlation. If a genetic correlation were determined through further research, the high level of heritability in whorl height and asymmetry would make facial hair whorls a beneficial indicator trait on which to select young bulls to increase fertility.

Key Words: Hair Whorls, Heritability, Spermatozoal Characteristics