Breeding and Genetics: Application and methods—Dairy I

373   Montbéliarde × Holstein and Viking Red × Holstein crossbreds compared with pure Holsteins during first lactation in eight high-performance dairies in Minnesota: I. Production. A. R. Hazel*[1], B. J. Heins[2], and L. B. Hansen[1], *[1]University of Minnesota, St. Paul, MN, [2]West Central Research and Outreach Center, Morris, MN.*

Montbéliarde × Holstein crossbred cows (MH, n = 484) and Viking Red × Holstein crossbred cows (VH, n = 510) were compared with pure Holstein cows (HO, n = 887) for 305-d milk, fat, and protein production and somatic cell score (SCS) during first lactation. A designed cross-breeding study was initiated in 8 commercial dairy herds in Minnesota in 2008. The first generation cows (MH, VH, and HO) calved for the first time from December 2010 to November 2013. Best Prediction was used to calculate production and SCS for 305-d lactations with adjustment for age at calving, and records less than 305 d were projected to 305 d. Independent variables for statistical analysis of all traits included the fixed effects of herd-year-season of calving, breed, interaction of herd-year-season and breed group, and random sire effect nested within breed. The MH, VH, and HO did not differ significantly for age at first calving (23.8 mo, 23.7 mo, and 23.8 mo, respectively). The MH and HO did not differ significantly ($P = 0.81$) for milk volume (11,304 kg vs. 11,272 kg, respectively); however, VH had significantly less ($P < 0.01$) milk volume (−495 kg) than HO. Fat solids production was similar ($P > 0.17$) for MH (429 kg) and VH (423 kg) compared with HO (423 kg). However, the MH had significantly greater ($P < 0.01$) protein production (355 kg vs. 344 kg) and fat plus protein production (784 kg vs. 767 kg) compared with HO. The protein production and fat plus protein production of VH (344 kg and 767 kg, respectively) were similar ($P > 0.94$) to pure HO. The MH (2.2), and VH (2.2) were also similar ($P > 0.27$) to HO (2.1) for SCS. The results have potential effect on the calculation of lifetime profit of cows because revenue from milk solids is the largest component of total revenue in many regions of the world.

Key Words: crossbreeding, Montbéliarde, Viking Red

374   Montbéliarde × Holstein and Viking Red × Holstein crossbreds compared with pure Holsteins during first lactation in eight high-performance dairies in Minnesota: II. Fertility, survival, and conformation. A. R. Hazel*[1], B. J. Heins[2], and L. B. Hansen[1], *[1]University of Minnesota, St. Paul, MN, [2]West Central Research and Outreach Center, Morris, MN.*

Montbéliarde × Holstein crossbred cows (MH) and Viking Red × Holstein crossbred cows (VH) were compared with pure Holstein cows (HO) for fertility, survival, and conformation during first lactation. A designed crossbreeding study was initiated in 8 commercial dairy herds in Minnesota in 2008. The first-generation cows (MH, VH, and HO) calved for the first time from December 2010 to November 2013. Cows (n = 451, 487, and 794 for MH, VH, and HO, respectively) were required to have at least 250 DIM for days open (DO), and cows with DO greater than 250 d were truncated to 250 d. For survival to second calving (n = 415, 450, and 697 for MH, VH, and HO, respectively), cows had at least 20 mo of opportunity to calve a second time. Conformation was scored once between 4 and 150 d on a linear, 9-point scale. Independent variables for the analysis of DO and conformation traits included herd-year-season, breed, interaction of herd-year-season and breed, and random sire effect nested within breed. Chi-squared was used to test survival to second calving. The MH (116 d) had significantly fewer DO ($P < 0.05$) than

HO (126 d); however, VH (122 d) were similar to HO for DO. The MH (86%) had significantly greater ($P < 0.01$) survival to second calving compared with HO (80%), but VH (83%) were similar to HO. The MH and VH had greater udder depth than HO (Table 1); however, culling for udder conformation did not differ for breed groups. The MH and VH had less stature, angularity, and body depth than HO (Table 1), indicating they had smaller body size with more body condition.

Table 1 (Abstr. 374). Least squares means of conformation scores for Montbéliarde × Holstein crossbred cows (MH) and Viking Red × Holstein crossbred cows (VH) compared with pure Holstein cows (HO) in 8 high-input dairies in Minnesota

Trait	HO (n = 1,137)	MH (n = 523)	VH (n = 564)
Stature (9 = tall)	5.4	4.7**	3.9**
Angularity (9 = angular)	5.6	2.6**	4.2**
Body depth (9 = deep)	5.1	4.1**	4.4**
Foot angle (9 = steep)	5.6	6.6**	5.5
Udder depth (9 = shallow)	6.9	5.4**	6.2**

**Difference from HO ($P < 0.01$).

Key Words: crossbreeding

375   Milk production and fertility performance of Holstein, Friesian, Jersey, Holstein x Jersey, and Friesian x Jersey crossbred cows on commercial Irish farms. E. L. Coffey*[1,2], B. Horan[1], R. D. Evans[3], K. M. Pierce[2], and D. P. Berry[1], *[1]Teagasc Moorepark, Fermoy, Co. Cork, Ireland, [2]School of Agricultural and Food Science, UCD, Dublin, Ireland, [3]Irish Cattle Breeding Federation, Bandon, Co. Cork, Ireland.*

There is renewed interest in dairy crossbreeding as a means to further augment farm productivity and profitability. Research experiments have demonstrated the benefits of crossbreeding on animal performance and financial efficiency, exploiting both additive and non-additive genetic effects. The objective of this study was to compare the biological performance of Holstein, Friesian, Jersey, Holstein × Jersey and Friesian × Jersey crossbred cows using commercial dairy herds practicing crossbreeding over a 5-year period. Milk production and fertility information from the national database on 11,808 cows from 40 spring calving dairy herds that adopted crossbreeding between Holstein and Jersey breeds from 2008 to 2012 inclusive were available. Obvious data errors were removed. Least squares means for traits of interest were estimated for purebred and crossbred animals using linear mixed models. Holstein-Jersey first cross cows produced more ($P < 0.001$) milk solids (heterosis = 6.5%), calved earlier ($P < 0.001$) as heifers (heterosis = 1.6%), had a shorter ($P < 0.001$) calving interval (heterosis = 2.1%) and had a higher ($P < 0.05$) submission rates in the first 21 d of the breeding season (heterosis = 4.5%) relative to their purebred parent breeds. Friesian-Jersey first cross cows had a lower ($P < 0.001$) somatic cell count (heterosis = 4%), a shorter ($P < 0.05$) calving interval (heterosis = 2.5%) and a higher ($P < 0.01$) submission rate in the first 21 d of the breeding season (heterosis = 1.2%) relative to their purebred parent breeds. Results were consistent with findings from controlled experiments. Breed complementarity and heterosis attainable from crossbreeding resulted in superior performance in crossbreds relative to their purebred parents.

Key Words: crossbreeding, Jersey, heterosis

376 Fertility and production of 3-breed and third-generation Holstein-sired crossbreds compared with pure Holstein cows in a seasonal pasture production system. Bradley J. Heins*[1,2], Amy R. Hazel[2], and Leslie B. Hansen[2], [1]University of Minnesota, West Central Research and Outreach Center, Morris, MN, [2]University of Minnesota, Saint Paul, MN.

Three-breed crossbred cows (Montbéliarde × Jersey × Holstein (HO) and Jersey × Montbéliarde × HO, n = 64); and HO-sired crossbred cows HO × Montbéliarde × Jersey × HO and HO × Jersey × Montbéliarde × HO, n = 87) were compared with pure HO cows (n = 138) for 305-d milk, fat, and protein production; SCS; and days open (DO) during their first 3 lactations. Cows were housed at the University of Minnesota West Central Research and Outreach Center, Morris, Minnesota, a grazing herd, and calved from March 2007 to May 2014. Best Prediction was used to calculate actual production (milk, fat, protein, and SCS) for 305-d lactations with adjustment for age at calving, and records less than 305 d were projected to 305 d. The DO was measured as actual DO for cows and cows were required to be at least 250 d in milk and those with greater than 250 DO were truncated to 250 d. Independent variables for statistical analysis were the fixed effects of season of calving, genetic group (HO, versus 3-breed crossbred versus Holstein-sired crossbred), parity nested within genetic group, and cow nested within genetic group, which was a random effect. Across the first 3 lactations, the 3-breed crossbred (485 kg) cows and Holstein-sired crossbred (499 kg) cows were not different (P > 0.05) from pure HO (495 kg) cows for fat plus protein production. Across lactations, 3-breed crossbred cows (2.78) and HO-sired crossbreds (2.92) were similar to pure HO cows (2.90) for SCS. The 3-breed crossbred cows (111 d) and HO-sired crossbreds (125 d) had significantly (P < 0.05) fewer DO than pure HO (150 d) cows during first lactation. During second lactation, the DO for the pure HO cows increased to 162 d, and the 3-breed crossbred (P < 0.05) and Holstein-sired crossbreds (P < 0.10) had a fewer DO (130 d and 136 d, respectively) compared with the pure HO cows. Mating 3-breed crossbreds to HO bulls may have advantages in a rotational crossbreeding system. Three distinct breeds is likely optimum for a rotational crossbreeding system.

Key Words: crossbreeding, days open, pasture

377 Relationships between yield, fitness, and type traits in US Brown Swiss. Keith D. Gibson* and Chad D. Dechow, *The Pennsylvania State University, State College, PA.*

Genetic parameters have often been estimated for the US Holstein population, but infrequently for Brown Swiss. The objective of this research was to evaluate heritabilities and correlations of fitness with yield and type traits for Brown Swiss cattle born in 2000 and later. The data consisted of 105,164 first through fifth lactation yield and somatic cell score (SCS) records from 45,464 cows with 82,761 d open (DO) and 31,105 productive life (PL) records. Approximately 52,250 of the records had values for 17 type traits and 41,074 had values for milking speed. These data were analyzed using a series of 3 trait models in ASREML that included fixed effects for lactation, age, and herd-calving cluster. Random effects were animal, permanent environment, and residual. The heritabilities of milk, fat, and protein yield were 0.30, 0.20, and 0.20, respectively. The heritabilities of PL, DO, SCS, and milking speed were 0.11, 0.03, 0.12, and 0.26, respectively. Yield traits had strong positive correlations with PL (0.63 to 0.71), whereas DO (−0.69) and SCS (−0.60) had strong negative correlations with PL. Milking speed had a moderate positive correlation with PL (0.26) and DO (0.19) and a slight negative correlation with SCS (−0.10). Yield traits had a slight unfavorable genetic correlation with DO (0.11 to 0.18). However, rear udder width (0.55), final score (0.45), body depth (0.43), dairy form (0.43), rear udder height (0.32), and stature (0.27), were more unfavorably correlated with DO than was yield. Yield was positively correlated with rear udder height (0.19 to 0.25) and rear udder width (0.34 to 0.48), and negatively correlated with udder depth (−0.40 to −0.24) and fore udder attachment (−0.21 to −0.04). However, udder depth (−0.26) and fore udder attachment (−0.14) were more favorably correlated with SCS than rear udder height and rear udder width (−0.02 and 0.18, respectively). Of the udder traits, fore udder attachment, rear udder width, rear udder height, and udder cleft were most favorably correlated with PL (0.31 to 0.44). These updated genetic parameters will allow for improved genetic selection in the Brown Swiss breed.

Key Words: Brown Swiss, correlation, productive life

378 Genetic disorders in Indian dairy cattle. Prasad Dinkar Deshpande*, Marimuthu Swaminathan, Jayant Ramchandra Khadse, Hemant Dasharath Kadam, Ashok Bhaskarrao Pande, Sumit Prakashrao Totade, and Priyanka Shivaji Garad, *BAIF Development Research Foundation, Central Research Station, Urulikanchan, Pune, Maharashtra, India.*

The advancements in cattle genetics and genomics have widened the scope of understanding number of hereditary diseases in cattle, leading to the development of early diagnostic techniques to detect presence of lethal or mutant allele for a specific phenotype. Bovine Leukocyte Adhesion Deficiency decreases host resistance and increases susceptibility to fatal illnesses. Citrullinemia is a disorder of urea cycle and this condition leads to increase levels of ammonia accumulation in blood and tissues, and subsequent death. Deficiency of uridine monophosphate synthase (DUMPS) causes prenatal embryonic mortality before d 40 of gestation. Factor XI results in a bleeding disorder and the affected animals (homozygotes) have hemophilia-like disorder. Although the frequency of these alleles in the population is usually very low, it can be easily increased if heterozygous (carrier) sires are used for large scale breeding through artificial insemination program resulting in increase in the proportion of lethal alleles. As per minimum standard protocol laid down by Government of India, it is mandatory to screen each stud bull before its entry to semen collection to rule out genetically transmitted diseases. All the stud bulls were screened by single nucleotide polymorphism (SNP) genotyping for BLAD, citrullinemia, DUMPS by Custom Designed Assays from Life Technologies (a brand of Thermo Fisher Scientific) and temperature melting curve for Factor XI. BAIF Development Research Foundation has a regular genetic disorder-screening program for its own stud bull farm. To date, 400 stud bulls have been screened and not a single male carrier for such genetic disorders has been found (Table 1).

Table 1 (Abstr. 378). Screening for disorders in Indian stud bulls

Sr. No.	Breed	Tests carried out	No. of stud bulls screened
1	Indigenous cattle and buffaloes	Factor XI, BLAD, citrullinemia	150
2	HF and HF crossbreeds	Factor XI, BLAD, citrullinemia, DUMPS	150
3	Jersey and Jersey crossbreeds	Factor XI, BLAD, citrullinemia	100

Key Words: genetic disorder, stud bull

J. Anim. Sci. Vol. 93, Suppl. s3/J. Dairy Sci. Vol. 98, Suppl. 2

515

380 SNP-analysis solves questions on the genetic background of the rare Dutch breed of Red Friesian cattle.

Kor Oldenbroek*[1], Ina Hulsegge[2,3], Jack Windig[2,3], and Mario Calus[2,3], [1]Centre for Genetic Resources the Netherlands, Wageningen, the Netherlands, [2]Animal Breeding and Genomics Centre, Wageningen, the Netherlands, [3]Wageningen UR Livestock Research, Wageningen, the Netherlands.

The Red Friesian cattle population went through a severe bottleneck around 1990. It revived due to the availability in the Dutch genebank of semen from bulls born between 1960 and 1970. Nowadays, it counts approximately 500 females and together with the bulls in the genebank, some 50 bulls are available for breeding. Three questions were put forward by the breeding organization: (1) is the Red Friesian cattle a unique breed or is it strongly related to the Black and White Dutch Friesian? (2) Is it relevant to distinguish the 5 different sire lines within the breed? (3) Are 2 herds of non-registered Red Friesian Cattle related to the registered population? DNA samples were extracted from 25 genebank bulls and 43 females from the 5 sire lines and 2 non-registered herds from semen and hair roots. These were analyzed with the BovineSNP50 BeadChip. After editing 42552 SNP's remained from the 54609 observed. Genetic relationships were evaluated by analyzing admixture using STRUCTURE and analyzing the average relatedness within and between lines. These revealed that (1) the Red Friesian Cattle is a breed in its own right, strongly related to the Black and White Dutch Friesian, (2) a large overlap in genetic variation exists between the 5 sire lines, and (3) the 2 non-registered herds although highly related to the registered population, contain genetic diversity not present in the 5 lines. For one of these herds this diversity originated from some Holstein Friesian sires used in the past. The other herd had been bred in isolation from the rest of the breed leading on the one hand to a high amount of inbreeding (25%) and associated loss of diversity, but on the other hand to conservation of diversity not present in the rest of the breed.

Key Words: SNP, genetic variation, genetic relatedness

381 Genetic variation and breeding values of casein in Holstein cattle using novel FTIR predictive modeling.

Herwin Eding[1], Gerben de Jong*[1], Hiemke Knijn[1], Jan Rademaker[2], and Nisha Shetty[2], [1]CRV, Arnhem, the Netherlands, [2]Qlip, Zutphen, the Netherlands.

Based on reference method measurements and Fourier transform infrared (FTIR) spectra, prediction equations for casein in raw milk were calculated. Subsequently casein content was predicted from multiple milk samples of 1.3 million cows from March 1, 2012, until February 23, 2013. After editing 8.5 million test-day records were available for analysis. The average casein content observed in milk was 2.77% (m/m), 77 percent of the total milk protein, with a standard deviation of 0.37% (m/m). Genetic parameter estimation was carried out on 61 000 Holstein cows, with 480 000 test days. The found heritability was 0.30, 0.34 and 0.39 for first, second and third lactation, respectively. The genetic correlation among the lactations ranged from 0.52 to 0.60. Genetic correlation with overall protein was 0.982. The genetic standard deviation for casein:protein ratio was 1.36 percent, with an heritability of 29 percent. The genetic correlation between casein:protein ratio and casein and protein yield was 0.23 and 0.35 respectively, while the phenotypic correlation was 0.01 lower, showing the ratio trait is independent from the yield traits. A genetic evaluation for protein yield and content, casein yield and content and casein:protein ratio was carried out on the whole population. This showed that selection for casein:protein ratio increases casein content but decrease casein and protein yield. In conclusion, casein yield showed to be a promising parameter in a cheese merit index.

Efficient assessment of casein using the novel FTIR prediction equation allowed for access to sufficient data being available. This research was supported by the EU and the province of Gelderland, the Netherlands.

Key Words: dairy cattle, FTIR, infrared

382 Use of infrared spectroscopy to enhance technological and nutritional quality of milk: Genetic components of FTIR spectra and breeding values estimates in Italian Simmental cattle.

Valentina Bonfatti*[1], Daniele Vicario[2], Lorenzo Degano[2], Andrea Lugo[3], and Paolo Carnier[1], [1]Department of Comparative Biomedicine and Food Science, University of Padova, Legnaro, Italy, [2]National Simmental Cattle Breeders Association, Udine, Italy, [3]Friuli Venezia Giulia Milk Recording Agency, Codroipo, Italy.

The aim of this study was to develop a general procedure for routine estimation of breeding values in the Italian Simmental cattle population for several innovative FTIR-predicted traits, using a direct prediction method, where breeding values estimation is directly conducted on milk FTIR spectral variables instead of FTIR-predicted traits. Breeding values for all new traits are then derived from the genetic component of the spectra. The investigated traits were: detailed milk fatty acid composition measured by 2D-GC, milk coagulation properties assessed by renneting meter analysis, pH, contents of major casein and whey protein fractions measured by RP-HPLC, cheese yield, curd composition and recovery rates of protein and fat in the curd, measured in individual micro-cheese making procedures, contents of major minerals by ICP-OES and of lactoferrin quantified by ELISA. FTIR calibrations were developed using more than 1,000 milk samples for all traits, with the exception of minerals (820 samples) and lactoferrin (635 samples). The calibration set included approximately 90% Simmental and 10% Holstein Friesian cows. A total of 100,272 milk spectra from 11,216 Italian Simmental cows were collected during the routine milk recording and stored. Principal component analysis of the unprocessed spectral data resulted in 8 latent traits that explained 99% of the total spectral variability. Restricted maximum likelihood was used to estimate (co)variance components of the latent variables. Heritability for these 8 latent traits ranged from 0.09 to 0.40. Variance ratios of the permanent environmental effect were between 0.10 and 0.25 and residual variance ratios ranged from 0.39 to 0.81. Variance components and the breeding values of original spectral transmittances were obtained by back transformation. Breeding values for the new milk traits were then predicted through FTIR calibrations as values correlated with the genetic component of the FTIR spectra. The procedure yielded estimates of breeding values for all the investigated traits for more than 10,000 Simmental animals.

Key Words: spectroscopy, breeding value, milk quality

383 Association between *INHA* A192G polymorphism and dairy traits in Holstein cattle of Antioquia-Colombia.

Stephania Madrid*, Albeiro López, and Julián Echeverri, Universidad Nacional de Colombia, Medellín, Antioquia, Colombia.

Productive and reproductive performance are some of the most important parameters in dairy cattle because they affect profitability of these systems. Marker-assisted selection is a useful tool to improve efficiency of dairy herds, because it allows identification of genetic differences related to a higher productive potential. Inhibin protein belongs to the transforming growth factor β super family, and its function is to modulate the secretion and action of the FSH. The goal of this research was to determine the effect of A192G polymorphism on productive and reproductive traits in Antioquia Holstein cows. The PCR-RFLP technique

was used to amplify a segment of 249bp of the bovine inhibin α gene (*INHA*), and then digested with the enzyme *Msp*I. It was analyzed 1240 lactations from 356 dairy cows. The effect of the INHA genotypes on the traits was determinate by a mixed linear model and Tukey test was used to establish significant differences between means for the 3 genotypes. The effect of allelic substitution was made through a linear regression model where the genotypes AA, AG and GG were transformed into a quantitative scale of 0, 1 and 2, according to the number of G alleles. In Antioquia Holstein cattle the most common genotype was AG (0.529), followed by AA (0.269) and GG (0.201). Allele frequencies were 0.534 for A and 0.466 for G. The INHA genotypes did not exerted a significant effect on the principal productive parameters, except for fat percentage, where GG animals presented the highest value for this trait. Despite it was not a significant effect of this polymorphism on reproductive parameters, Tukey test showed that G allele tended to have a detrimental effect on female fertility, increasing the calving interval and the number of services per conception, decreasing the reproductive efficiency of the herds. Further studies are required to determine whether this SNP may be used as a molecular marker.

Key Words: inhibin, PCR-RFLP, SNP

384   Genome-wide association studies for fertility traits in Brown Swiss cattle using single SNP regression and Bayesian approaches applied to high-density SNP array information.
Beat Bapst*[1], Christine F. Baes[1,2], Franz R. Seefried[1], Marlies A. Dolezal[5], Christine Flury[2], Heidi Signer-Hasler[2], Dorian Garrick[3], Christian Stricker[4], Johann Sölkner[7], Alessandro Bagnato[6], Ingolf Russ[8], Klemen Potocnik[9], and Birgit Gredler[1], *[1]Qualitas AG, Zug, Switzerland, [2]Bern University of Applied Sciences, Zollikofen, Bern, Switzerland, [3]Iowa State University, Ames, IA, [4]agn Genetics, Davos, Graubünden, Switzerland, [5]University of Veterinary Medicine Vienna, Vienna, Austria, [6]Dept. Vespa University of Milan, Milan, Italy, [7]University of Natural Resources and Life Sciences, Vienna, Austria, [8]Tierzuchtforschung e.V. (TZF), Poing, Bavaria, Germany, [9]University of Ljubljana, Ljubljana, Slovenia.*

Large-scale, in-depth, genome-wide analyses of various economically important traits are now possible due to the availability of medium (50K; 54,609 SNP) and high-density (HD; 777,962 SNP) SNP arrays. Genome-wide association studies (GWAS) provide a powerful tool for identifying associations between phenotypes and variants in the underlying genome. Here we present GWAS results for 5 fertility traits in Brown Swiss cattle. Traits analyzed included non-return-rates in heifers (NRR_H) and cows (NRR_C), days to first service (DFS), and intervals between first and last insemination in heifers (IFL_H) and in cows (IFL_C). Imputation from 50K to HD was carried out with FImpute. After filtering out SNPs with minor allele frequency <0.05, a total of 654,847 imputed SNPs on 29 bovine autosomes remained. Deregressed breeding values of 1,502 (IFL_H) to 3,379 (NRR_C) progeny-tested bulls were used as phenotypes. Single SNP GWAS (M1) were conducted with the SNP & Variation Suite package GoldenHelix. The Efficient Mixed-Model Association expedited (EMMAX) algorithm was applied to account for population stratification. Additionally, bulls with more than 75% Original Braunvieh pedigree background were excluded. Significance levels were determined by false discovery rates. Multi-SNP GWAS (M2) using Bayesian methodology implemented in GenSel were also conducted. In those analyses, all SNPs were fitted simultaneously. A 1 Mb non-overlapping window approach that accumulated contributions of adjacent SNPs was used to identify associated genomic regions. The M1 analyses using genome-wide significance levels showed that regions on BTA3, 17, and 25 were associated with NRR_C, a region on BTA29 was associated with DFS, and a region on BTA8 was associated with IFL_C. The significant SNPs in these regions were also represented in the 1 Mb windows accounting for the largest proportion of genetic variance in the corresponding traits from M2. The promising results presented here provide evidence that specific regions of the genome are associated with fertility traits in Brown Swiss cattle.

Key Words: GWAS, fertility, dairy cattle

J. Anim. Sci. Vol. 93, Suppl. s3/J. Dairy Sci. Vol. 98, Suppl. 2

517