

over the next several years. These supply chains will be made up of producers who are willing to sacrifice some of their individuality for less stress, and more

profit. These producers need to enter into the supply chain arrangements with their eyes open and have realistic expectations for success.

Key Words: Supply Chain, Vertical Coordination, Beef System

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

247 Detection of QTL affecting mastitis resistance traits and SCS in Canadian Holsteins. J. Moro-Mendez* and J. F. Hayes, *McGill University, Ste-Anne-de-Bellevue, QC, Canada.*

The objective of this study was to test for associations of genetic polymorphisms of genes related to immune response (growth hormone (GH), growth hormone receptor (GHR), ornithine decarboxylase (ODC), insuline-like growth factor-1 (IGF-1), adrenocorticotropin hormone (ACTH), corticotropin releasing hormone (CRH), and prolactin (PRL)) with mastitis resistance traits (incidence of clinical mastitis (ICM), occurrence of clinical mastitis (OCM), culling due to mastitis (CDM), and somatic cell scores (SCS)) in first, second and third lactations. Using lactation records of cows enrolled in milk recording in Québec from 1980 to 1994 (411,291 first, 238,432 second, and 130,983 third lactations, respectively) estimated transmitting abilities of traits were generated with a model that included fixed effects of herd-year-season of calving, age at calving, and genetic group, and random effect of sire. 721 bulls which had daughters with lactation records were genotyped for twenty polymorphisms of the above genes located on autosomes (BTA) 5, 11, 14, 19, 20, and 23. Two types of analysis of associations were performed: across-population analysis with a model that included fixed effect of marker and random effect of bull, and within-family analysis with a model that included fixed effects of grandsire, marker nested within grandsire, and random effect of son nested within marker and grandsire. Permutation tests were performed to reduce Type I error probability. Significant associations were found within families for markers of IGF-1 (BTA5), ODC (BTA11), GH (BTA 19), GHR (BTA 20), and PRL (BTA 23) for ICM, OCM, CDM, and SCS in different lactations. Some of these putative quantitative trait loci (QTL) are located on BTA where other authors have reported QTL affecting SCS and udder conformation. The results from this study may contribute to efforts to dissect the genetic basis of mastitis resistance in dairy cattle.

Key Words: QTL Mapping, Mastitis, Dairy Cattle

248 Characterization of FEZL effects on SCS in a sample of North American Holsteins. T. S. Sonstegard*, C. P. Van Tassell, and R. Li, *USDA, ARS, Bovine Functional Genomics Laboratory, Beltsville, MD.*

Previous mapping studies using overlaid daughter designs had identified a putative quantitative trait nucleotide (QTN) affecting somatic cell count within the coding region of the forebrain embryonic zinc finger-like (FEZL) gene. Cows inheriting the variant of FEZL with a glycine stretch of amino acids reduced from 13 to 12 amino acids tended to have lower somatic cell counts during first lactation. In order to validate the utility of this potential QTN in selection for dairy health, we conducted a substitution analysis on a sample of North American dairy sires. Bovine sequence traces were obtained for regions of FEZL flanking the QTN. PCR amplicons from genomic DNA were sequenced to design primers to assay QTN genotypes. FEZL QTN genotypes were generated for 2,379 dairy bulls. The deletion variant of FEZL was not identified in a group of influential Jersey sires (N=49). In Holsteins, the allele frequency of the deletion variant was less than 3% (N=2,325). Estimates of allele substitution effect were obtained using MTDFREML with a model that included a polygenic effect and a FEZL genotype effect with daughter deviations for somatic cell score as the phenotypic data. The estimates were based on the differences between estimated genotypic effects of the heterozygote and the common homozygote because only six homozygotes for the deletion variant were observed. The heritability of the trait was estimated to exceed 90%, because the deviations have been adjusted for all non-genetic effects and accumulated across daughters. The estimated allele substitution effects were 0.006, 0.005, 0.018, 0.026, and

0.043 units of SCS for heritabilities of 0.95 (REML estimate), 0.50, 0.10, 0.05, and 0.01, respectively. Previous analyses of the DGAT1 QTN showed allele effects that were much more robust to heritabilities using a similar analysis model. The extreme allele frequency of FEZL may be partially responsible for this phenomenon. Further analysis of this QTN is necessary before selection based on FEZL variants can be recommended.

Key Words: Quantitative Trait Nucleotide, Somatic Cell Score, Cattle

249 Danish Holstein show inbreeding depression for udder health. A. C. Sørensen*^{1,2}, P. Madsen¹, M. K. Sørensen¹, and P. Berg¹, ¹*Danish Institute of Agricultural Sciences, Tjele, Denmark,* ²*Royal Veterinary and Agricultural University, Frederiksberg C, Denmark.*

Inbreeding depression for udder health was estimated using records on clinical mastitis incidence and somatic cell count. Data were selected based on a pedigree completeness index so inbreeding coefficients were reliable. Average inbreeding was above 3%. Four binary mastitis traits were defined. In first lactation the occurrence or not in two overlapping periods were recorded. The first period was from ten days prior to the first calving to 50 days after (CM1S). The second period was from ten days prior to the first calving to 305 days after (CM1L). In second (CM2) and third (CM3) lactations the period was from ten days prior to calving to 100 days after calving. Somatic cell count (SCC) was also included and analysed on the log-scale. At least 140,000 cows with records were included per trait. REML estimates of (co)variance components were obtained in linear sire models. The models were the ones currently used in routine evaluations augmented by linear and quadratic regressions on inbreeding coefficient. Heritabilities of the traits were all in the range of previously published results. Inbreeding significantly affected all traits investigated. Three traits, CM1L, CM3, and SCC, showed a non-linear relationship between phenotype and inbreeding coefficient. Comparing cows with 5% inbreeding to cows with 2% inbreeding (with standard errors in brackets), SCC increased with 1500 (290) cells/ml in first lactation, well in the range of previously published estimates, and the incidence of mastitis increased by 1.08 (0.26), 0.55 (0.14), and 0.98 (0.48) percentage points in first, second, and third lactation, respectively. The corresponding reduction in net return over three lactations comprised to approximately 10 USD under Danish production conditions.

Key Words: Inbreeding Depression, Mastitis, Somatic Cell Count

250 Effects of ancestral consanguinity on inbreeding depression for yield traits and somatic cell score in Jersey cows. D. Gulisija*, D. Gianola, and K. A. Weigel, *University of Wisconsin, Madison.*

Inbreeding depression can be reduced (purged) via selection against deleterious mutants. Inbreeding exposes recessive or semi-recessive mutants, giving an opportunity for selection to act. Therefore, inbreeding depression may be lesser in descendants of inbred ancestors than in inbred contemporaries without inbred ancestors. An Index of Opportunity for Purging (*I*) was developed to evaluate whether or not ancestral inbreeding attenuates inbreeding depression for a quantitative trait. In *I*, each instance of ancestral inbreeding, measured by the inbreeding coefficient (*F*), is weighted using an estimated genetic contribution of an ancestor to an animal's genome. *I* ranged between 2.8 and 25.6, with a mean of 8.65. First-lactation milk, fat, protein and somatic cell score (SCS) records from 59,778 US Jerseys were used in a two-stage analysis. First, predicted re-

iduals from an animal model (EBLUP) were calculated for each trait; the linear model included fixed herd-year-season, age at calving and days in milk effects, and random additive genetic effects. Second, models with F and I of each animal as predictor variables were fitted to the EBLUP residuals, for each trait. Statistical tests indicated that ancestral inbreeding, as measured by I, significantly reduces the negative effect of inbreeding by 4.13 kg for milk and 0.16 kg for protein yield per unit of I. No evidence of purging was found for fat yield, and SCS was not affected by inbreeding.

Key Words: Inbreeding Depression, Purging

251 Between-founder heterogeneity in inbreeding depression for production and somatic cell score in Jersey cows. D. Gulisija^{*1}, D. Gianola¹, K. A. Weigel¹, and M. A. Toro², ¹Department of Dairy Science, University of Wisconsin-Madison, ²Departamento de Mejora Genética y Biotecnología, INIA, Madrid, Spain.

Severity of inbreeding depression depends on the genetic load carried by a population. If the load is distributed unevenly among founder genomes, descendants from different founders will be differentially affected by inbreeding. Between-founder heterogeneity in inbreeding depression for production traits and somatic cell score in milk (SCS) was studied using records from 59,788 Jersey cows. Inbreeding coefficients (F) were partitioned into components due to four founders, plus a remainder. A two-stage analysis was performed. First, empirical best linear unbiased predictions (EBLUP) of residuals for milk, fat and protein yield, and for SCS, were computed using linear models including fixed effects of herd-year-season, age at calving and days in milk, and random additive genetic effects of cows. Second, models with total and partial inbreeding coefficients as predictor variables were fitted to EBLUP residuals, by trait. Tests of differences between slopes indicated that regressions of milk, fat and protein yield on partial inbreeding coefficients were heterogeneous; SCS did not exhibit inbreeding depression. Hence, alleles contributing to inbreeding depression for production in this Jersey population seem to derive from specific founders. This indicates that a homogeneous effect of inbreeding on production may be an incorrect statistical specification in genetic evaluation models that attempt to account for inbreeding depression.

Key Words: Inbreeding Depression, Between-Founder Heterogeneity

252 Variance components of test-day milk, fat, and protein production, and somatic cell score from all parities of dairy cows in South-eastern Sicily estimated with a random regression model. A. P. W. De Roos^{*1}, M. H. Pool², M. Caccamo³, G. Azzaro³, J. D. Ferguson⁴, and G. Licitra³, ¹NRS, Arnhem, The Netherlands, ²Animal Sciences Group, Lelystad, The Netherlands, ³CoRFiLaC, Regione Siciliana, Ragusa, Italy, ⁴University of Pennsylvania, Kennett Square.

Consorzio Ricerca Filiera Lattiero-Casearia (CoRFiLaC) aims to develop management figures for dairy farmers with respect to milk production, nutrition, cow health, and farm economics. A proper statistical analysis of milk production records with a random regression test-day model may help to identify problems in herds and cows that need the farmer's attention. The aim of this study was to estimate the variance components of test-day milk, fat, and protein production, and somatic cell score (SCS) records of Sicilian dairy cows in the Ragusa area. The data set comprised 491,426 test-day records from 18,953 cows on 285 herds. Parity was between 1 and 13, and days in milk (DIM) between 5 and 450. Variance components were estimated with a multi-lactation, random regression, test-day animal model. The model comprised four fixed effects and a random herd x test date effect. Random regressions were included for herd x year of test, animal additive genetic effect, common permanent environment and lactation specific permanent environment, using fourth-order Legendre polynomials. The permanent environmental effect was split into a common and a lactation specific part to enable the inclusion of records from all parities. Parameters were estimated with a Bayesian analysis using Gibbs sampling. Heritabilities for test-day production increased from around 0.20 at DIM 5 to around 0.30 at DIM 365, whereas heritabilities of test-day SCS were between 0.12 and 0.20. The correlations of the herd effects between DIM 5 and DIM 365 were around 0.60, indicating differences in persistency across herds. In contrast with production traits, herd variances of SCS were much lower than variances of cow effects. The estimated variance components will be used for routine evaluation of Sicilian dairy cows, with the purpose to present management figures on the herd or cow level.

Key Words: Random Regression, Test-Day Production, Dairy Cattle

Forages and Pastures: Beef Cattle and Pastures

253 Timing of herbage allocation 1. Effect on daily grazing pattern of beef heifers. P. Gregorini^{*1,2}, M. Eirin¹, R. Refi¹, M. Ursino¹, R. Flores², and O. Ansin², ¹FCAYF Universidad Nacional de La Plata, La Plata, Buenos Aires, Argentina, ²University of Arkansas, Fayetteville.

Timing of grazing events (GE) determines how ruminants allot grazing to meet nutritional needs. Photosynthesis and respiration increases herbage DM and soluble carbohydrates concentrations daily, which may facilitate longer and intense GE at dusk. Linking the grazing pattern (GP) and the plant phenology with the time of herbage allocation (HA) emerges as an option to manipulate length and intensity of the GE. Herein, we analyzed the Spring daily GP of eight beef heifers in a crossover design. Heifers grazed annual ryegrass pastures using strip grazing. Behavioral activities of each heifer were recorded every 2 min, from 0600 to 1900 (total) and categorized into three intervals (morning, afternoon and evening) to determine time (minutes) of grazing (GT), rumination (RT), and idling (IT) along with bite rate (BR) at each time, when HA was allotted in the morning (0700; MHA) or afternoon (1500; AHA). An interval x HA affect was observed for GT, RT, IT and BR (Table). The AHA increased total IT (253 vs 213, P<0.01) and decreased GT (277 vs 331, P<0.01), concentrating GT in the evening, when BR was higher. The RT varied by time of the day, but total did not (166 AHA vs 152 MHA). With AHA, RT and IT were concentrated in the morning and afternoon. The time of HA alters the way heifers allot GT, RT and IT; AHA generates longer and more intense GE when herbage has higher quality.

Treatment/Time of the day ^a	AHA			MHA				
	GT	RT	IT	BR, bites/min	GT	RT	IT	BR, bites/min
Morning 0600 to 1000	80.5 ^b	84.2 ^b	95 ^b	26.4 ^b	119.2 ^c	44 ^c	75 ^d	34.5 ^d
Afternoon 1100 to 1400	57.2 ^c	63 ^c	108 ^c	32.7 ^c	80 ^b	76 ^d	76 ^d	30.3 ^c

^aMinutes ^{b,c}Means in the same rows or columns with different superscripts differ (P < 0.001).

Key Words: Herbage Allocation, Beef Heifers, Grazing Behavior