

and displaced abomasum were associated with early lactation culling risk. Serum associations with culling were treated in a similar manner as clinical disease. Initially a series of 2X2 tables at various serum cutoff values for non-esterified fatty acids (NEFA), calcium and beta-hydroxybutyrate (BHBA) versus risk of culling were created. The most significant cutoff values were then submitted to final modeling with the previously identified culling models. Precalving serum NEFA ≥ 0.4 in the last week precalving was associated with 2.0 X (P=0.002) increased risk of culling in the 1999 study. Both studies identified a cutpoint of 1.8 mmol/L of serum calcium in the first week postcalving being associated with a 3X increased risk (P < 0.05) of culling after removing

all of the clinical milk fever cows. Finally, BHBA ≥ 1400 umol/L was associated with a two-fold increased risk of early lactation culling in both studies. This suggests that high precalving NEFA and both subclinical hypocalcemia and subclinical ketosis are important predictors for the subsequent risk of early lactation culling.

Monitoring and intervention strategies using this information may be helpful in reducing early lactation culling risk.

Key Words: Subclinical, Disease, Culling

Beef Species: Vertical Coordination in the Beef Industry

243 National Animal Identification: An update. V. E. Ragan*, *USDA APHIS, Washington, DC.*

A key to safeguarding the Nation's livestock herds from both endemic diseases and the drastic effects of diseases such as BSE, Foot and Mouth Disease and other potential emerging diseases, is to have a national plan in place to identify livestock in a way that will provide rapid traceability. As some disease eradication programs, especially brucellosis, are nearing completion, fewer animals are being identified. Current world conditions which include the possibility of intentional or accidental introduction of foreign animal diseases make it essential that potentially exposed animals can quickly be traced. USDA, APHIS has been working closely with State and industry partners to develop a National Animal Identification System (NAIS). Once fully developed and operational, the goal of the national identification system will be to help USDA and our State and industry partners quickly identify any livestock or agricultural premises exposed to a foreign animal disease or disease of concern so that the disease can quickly be contained and eradicated. The goal of the system is to be able to identify an exposed animal, the herd of origin and all contact herds within 48 hours. An update on the premises behind the development of the system and the current status of the system will be provided.

Key Words: Livestock, Disease, Identification

244 Implications of beef system vertical coordination on animal identification and data handling. D. A. Blasi*, *Kansas State University, Manhattan.*

Vertical coordination implies the skillful and effective interaction between the parts of a whole system. Many US Beef value chains were conceived with the initial objective of adding value by differentiating and ultimately creating a branded product. In retrospect, most if not all have encountered numerous challenging issues in pursuit of their quest for the effective interaction between the supply and the demand for their product(s). While integrating the regulatory capacity of animal health is the primary objective of the National Animal Identification System (NAIS), the use of animal identification systems for verifying conformance to a Bovine Export Verification Program set forth by AMS for regaining access to the Asian export market will be the value proposition which will further drive its implementation as a staple process requirement in all segments of US beef cattle production. This accelerated growth of individual animal identification systems will generate significant amounts of data which will need to be synchronized, filtered, analyzed, managed and acted upon in real-time by data mining software and individuals who possess a dual understanding of beef systems production and technology. Ultimately, the resulting information will be used seamlessly throughout a vertically coordinated production system to conduct management and animal health compliance audits, initiate product recall measures and reveal complex biological and economic relationships.

Key Words: Animal Identification, Beef Industry, Information Management

245 Creating systems to produce high quality beef. D. B. Faulkner* and L. L. Berger, *University of Illinois, Urbana.*

Changing calving seasons to match forage resources can dramatically reduce cow feed costs. Making this change often requires weaning calves earlier than the traditional 205 days of age. Early weaning can help producers manage forage and feed supplies when: 1) forage supplies are low, such as during a drought, 2) forage is of low-quality, such as pure fescue pastures in mid-summer, 3) winter feed supplies are limited, or 4) Summer calving is initiated to reduce winter feed cost for the cow. Cow reproductive advantages can also be obtained with early weaning. It makes it easier to get thin cows and/or first or second calf heifers bred and the cows enter the winter in good condition. Cow reproduction can be improved by up to 12% when calves were weaned prior to the breeding season. This would result in savings of \$15 for each cow in the herd. Early weaning also can offer marketing advantages because a producer may market cull cows that have calved on a better spring or summer market and this system can produce lean, tender, high quality beef to meet consumer demand. Creep feeding is an alternative to early weaning. Creep feeding research has demonstrated that source of creep feed, amount of creep feed consumed, and length of time calves consume creep feed all have an influence on carcass quality grade. Nutritional management had 6 times more influence on quality grade than the calf's genetic merit for marbling. However, the effects of high marbling EPDs have been additive with this management system, so both are important. Producers desiring to produce high-quality cattle for the marketplace should consider the breeds they use in their crossbreeding program, the marbling EPD in the bulls, and the management of their calves to get them on a high-energy diet as early as possible. Research shows that carcass fat can be reduced and quality improved by using appropriate management strategies.

Key Words: Systems, Beef

246 Managing a beef production unit as part of a vertically coordinated supply chain. W. L. Mies*, *eMerge Interactive, College Station, TX.*

The obvious benefits to being part of a vertically coordinated system have been demonstrated by the Strategic Alliances Demonstration project in 1993 and the growth of the various alliances that have been created in the beef industry. The structure is designed so that the various production units in the supply chain stop competing with each other for whatever profit is available, but rather share the profit that can be made through producing product better suited to consumer needs. This structure takes some of the hills and valleys out of the profit picture, but makes it a more stable vehicle in order to obtain financing. The decreased risk is thus easier to manage. It is the management of a unit of a vertically coordinated supply chain that is of interest today. When producers enter into a vertical supply chain, they are usually those producers with a vision of the future and they are committed to try to find a better way to be a beef producer. Idealism is very strong during the startup of such an effort and it drives many of the early negotiations. As production starts and decisions are made about how animals are bred, raised and marketed, the idealism melts away and pragmatic business concerns enter the relationships. Vertical supply chains will produce an increasingly larger percentage of the beef in the U.S.

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-