354 Meeting the changing needs of the dairy industry: perspective from an AI company. M. A. Faust*, A. Knuth, C. Marti, N. Michael, and A. Storch, *ABS Global, Inc.*, *DeForest, WI.*

Internal and external factors constantly influence the socioeconomic climate in which dairy farms operate. Successful dairy farms achieve sustainability and profitability within these dynamic conditions. The current result of changing socioeconomic conditions appears to be more distinct segmentation in dairy demographics with large, specialized dairies producing a commodity product and growth in importance of niche segments such as organic dairies, low input dairies, and cottage-industry operations. AI companies also are influenced by market forces, including industry success in generating genetic progress; thus high genetic merit is a customer expectation and it is difficult for AI companies to produce a differentiated product. Furthermore, semen expense represents <1% of dairy operating expense. The marketplace approach adopted by ABS Global which serves an international customer base has been to tailor products and services to individual market segments - using service and science to solve customer problems. Specifically, ABS sources and develops genetics appropriate for all market segments from three different continents. These genetics include elite breeder quality, mainline including a subset of European sourced bulls with higher milk components, show type, and grassland bulls. To further individualize sire selection, inbreeding, and breeding goals for dairies, sire selection and mate assignment programs are offered. Also, ABS and others offer specialized expertise and problem solving for herd reproduction management. Dairies can tailor the reproductive program further by selecting from a list of services such as heat detection, breeding and data entry, technical service consultation, performance monitoring, and evaluating measures of synchronization success. Acceptance of these programs by ABS customers has been great - during 2004, >2 million dairy cows were mated through the company's proprietary program while professionally trained reproductive management representatives walked behind >500,000 breeding eligible cows daily. Dairies expect products and services that meet their unique needs.

Key Words: Industry segmentation, Genetic improvement, Reproductive management

Breeding and Genetics: Genetics of New and Emerging Traits

355 Emerging traits of interest to the livestock industries: scrapie resistance in sheep. R. M. Lewis*[1] and B. Villanueva[2], [1]*Virginia Polytechnic Institute and State University*, *Blackburg*, [2]*Scottish Agricultural College*, *Edinburgh, UK.*

Many loci with major effects on performance, including fitness, have been identified in livestock. Where genotype tests characterizing polymorphisms at such loci are available, breeders have opportunity to use such information to increase the frequency of beneficial alleles. A clear example is the Prion Protein (PrP) locus in sheep, which is associated with resistance to the fatal transmissible spongiform (TSE) scrapie. Five main haplotypes have been identified for this locus resulting from polymorphisms at codons 136, 154 and 171. Animals homozygous for the ARR haplotype are considered resistant while animals carrying the VRQ haplotype are considered highly susceptible. Genetic strategies based on PrP genotyping have thus been adopted to eradicate scrapie in infected flocks while increasing the resistance of national flocks. The voluntary National Scrapie Plan (NSP) in Great Britain is one of the earliest PrP genotyping programs. It began in 2001 by genotyping rams registered with breed societies favoring rams with beneficial genotypes for breeding. Since other TSE diseases may be present in sheep, another aim of NSP is to remove the theoretical risk of bovine spongiform encephalopathy naturally affecting sheep. Although increasing genetic resistance to TSEs is clearly important, the path to achieving resistance requires care. For instance, limited evidence suggests ARR homozygosity may not unequivocally result in scrapie resistance, perhaps reflecting variable strains of scrapie. Semen banks designed to preserve alleles currently disfavored are needed to ensure flexibility to manage future TSEs. Furthermore, if favored alleles are antagonistic to other economically important traits or are sufficiently rare that selection increases inbreeding and reduces genetic variability, a focus on scrapie alone may prove risky. The careful integration of scrapie resistance into the overall breeding goal is thus central.

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Key Words: Scrapie, Genotyping, Risk

356 Effects of different strategies for breeding towards scrapie resistance in East Friesian milk sheep on inbreeding levels and production traits. F. de Vries*, H. Hamann, C. Drogemuller, and O. Distl, *University of Veterinary Medicine*, *Hannover, Germany.*

The European Union forces each member state to introduce a breeding programme for all sheep flocks of high genetic merit to breed towards scrapie resistance. The objective of the study was to assess the effects of different strategies to breed towards the scrapie resistant ARR/ARR homozygous genotype of the ovine prion protein gene in East Friesian milk sheep on inbreeding, drift variance, possible negative side effects, bottleneck effects and breeding costs. A simulation programme was developed, in which different population structures could be used. In this study the population structure of the region of origin of the East Friesian milk sheep was selected because of its low ARR allele frequency (10%) and an observed negative effect on withers height.

The simulation parameters were the allele frequencies of male and female founder animals, the population size, the age structure, the mating ratio, the effect of a QTL, a polygenic component associated or not with the QTL, the genetic distance between QTL and prion protein gene locus. Breeding strategies were optimized based on the mean inbreeding coefficients, the genetic distribution of founder rams to later generations, and the distributions of phenotypic and breeding values.

Based on the results, the strategy for East Friesian milk sheep should be to breed initially towards ARR heterozygous sheep until a threshold value of 30% for the ARR allele is reached in order to avoid a genetic bottleneck. After this the strategy should change and only ARR homozygous sheep should be selected. The higher cost of this strategy should be accepted in respect to minimal loss in genetic diversity. The developed simulation programme allows optimizing breeding schemes for other breeds.

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Key Words: Scrapie, Breeding Programme, Inbreeding

357 Association analyses between the prion protein locus and reproductive and weight traits in Ripollesa sheep. J. Casellas*[1], J. Piedrafita[1], G. Caja[1], R. Bach[2], and O. Francino[1], [1]*Universitat Autònoma de Barcelona*, *Bellaterra, Spain*, [2]*Associació Nacional de Criadors d'Ovins de Raça Ripollesa*, *Monells, Spain.*

The aim of this study was to analyze the association between the alleles of the prion protein locus (PrP) and performance traits in the Ripollesa sheep, an autochthonous breed of Catalonia (Spain). PrP genotypes were analyzed by the SnaPShot Multiplex technique in blood samples from 121 adult rams and ewes and 68 lambs from the experimental flock of the Universitat Autònoma of Barcelona. The genotype of 24 descendants of the genotyped adult individuals was also reconstructed, since both parents were homozygous for PrP alleles. Reproductive traits of ewes (n = 88) included conception rate (CR; n = 408) and litter size (LS; n = 364) whereas the lamb traits studied were birth weight

(BBW; n = 211) and 90 d BW (90BW; n = 164). Only three alleles were observed in the PrP locus of the Ripollesa flock: ARR (39%), ARQ (46%) and ARH (15%). The additive effect of PrP alleles was analyzed using the Bayesian threshold and linear models for reproductive and weight traits, respectively. No associations between PrP alleles and conception rate and weight traits were observed (Table 1). For litter size, the effect of the ARH allele was significantly greater than that of the ARQ allele. Difference between ARH and ARR alleles also suggested that ARH allele was superior for litter size. Our results indicate that the selection against the ARH and ARQ alleles, for which scrapie positive sheep have been observed in Spanish sheep breeds, might decrease litter size in the Ripollesa breed.

Table 1. Mode and 95% highest posterior density region bounds (HPD95) of the differences between additive effects of each pair of alleles.

Trait	ARR-ARQ Mode (HPD95)	ARR-ARH Mode (HPD95)	ARQ-ARH Mode (HPD95)
CR	-0.14 (-0.51 to 0.06)	0.01 (-0.41 to 0.44)	0.15 (-0.24 to 0.57)
LS	0.10 (-0.15 to 0.37)	-0.41 (-0.87 to 0.05)	-0.51 (-0.97 to -0.08)
BBW	0.03 (-0.14 to 0.19)	0.01 (-0.20 to 0.22)	-0.02 (-0.23 to 0.19)
90BW	0.33 (-0.60 to 1.26)	-0.51 (-1.66 to 0.81)	-0.84 (-2.03 to 0.53)

Acknowledgements: Conveni DARP-ANCRI-UAB

Key Words: Association Analysis, Prion Protein, Ripollesa Breed

358 QTL Scan for disposition in *Bos taurus* x *Bos indicus* cattle families. M. Wegenhoft*, J. Sanders, and C. Gill, *Texas A&M University*, *College Station*.

Disposition, or temperament, of cattle is important from both a commercial and purebred producer standpoint. Some studies suggest a correlation between an animalÃ¢â‚¬â„¢s disposition and meat tenderness. Others have suggested a relationship between behavior and circulating cortisol levels. However, relatively few groups have studied quantitative trait loci (QTL) for disposition in cattle, although heritability of the trait is moderate to high. The objective of this study was to detect QTL affecting disposition in a three-generation *Bos taurus* x *Bos indicus* reciprocal backcross population produced through embryo transfer. Disposition was scored prior to slaughter (n=567) on a scale of 1 (calm) to 5 (crazy). A sex-averaged map consisting of 313 markers and spanning 2796 cM was built for the 29 autosomes and the X chromosome. Disposition data were studied through analysis of covariance using the mixed model procedure of SAS. Independent variables included sire-type x dam-type (STxDT) interaction, the three-way interaction of sex x ST x DT, the regression of birth date within season-year combination, and family nested within ST x DT as a random effect. Residuals were used for interval mapping by linear regression under a line cross model to detect QTL segregating between breeds. Six QTL with suggestive evidence of linkage were detected on bovine chromosomes (BTA) 1, 4, 8, 9, 16 and 18. Four of these QTL were estimated to have dominance or overdominance effects, while two were estimated to have additive effects. Overdominance effects were detected for the QTL on BTA8 and BTA16 when evaluated under a Mendelian model and large imprinting effects were found when parent-of-origin effects were included in the model. The six putative QTL identified in this population provide a starting point for identification of positional candidate genes affecting disposition. None of these six putative QTL are on the same chromosome as the gene for cortisol.

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Key Words: Bovine, Disposition, QTL

359 Are time-budgets of dairy cows affected by genetic improvement of milk yield? P. Lovendahl* and L. Munksgaard, *Danish Institute of Agricultural Sciences*, *Tjele, Denmark*.

Time is a resource that the cow can spend on feed intake, walking between different loca-tions, waiting and resting. Our hypothesis is that components of dairy cows time budget have genetic variation and those parts closely connected with production traits may be affected by selection for improved yield. We studied time-budgets of 243 first lactation Holstein cows twice in early lactation (mean 86, range 50 to 123 DIM). Estimates of minutes spent eating, lying, standing or walking in alleys were obtained from scan sampling of the activities at 10 min intervals during 24 hours. Daily milk yield (ECM) was recorded at 3 week intervals. Data were analysed by AI-REML using two-trait repeatability models including relationship matrix. The heritability of daily ECM was $h^2 = 0.12 \pm 0.14$, and eating time had similar heritability (0.13 ± 0.13), but lying time had very low heritability (0.02 ± 0.15). Correlations between traits were calculated as individual animal correlations (r_i) based on permanent animal and additive genetic covariance components. Eating time was positively correlated with yield ($r_i = 0.23$), and lying time negatively correlated with yield ($r_i = -0.26$). Although eating time was negatively correlated with lying time ($r_i = -0.38$), the magnitude of this cor-relation decreased at higher yield. As restrictions on lying time are known to induce stress responses, further selection for higher yield may increase the liability to metabolic disease caused by deficits in time budgets of dairy cows.

Key Words: Behavior, Welfare, Cattle

360 Genetic variation of Johne's disease susceptibility in U.S. Holsteins. M. Gonda*, Y. Chang, G. Shook, M. Collins, and B. Kirkpatrick, *University of Wisconsin*, *Madison*.

Johne's disease infection, measured by serum antibodies (S/P ratio) and fecal culture of *Mycobacterium avium* subsp. *paratuberculosis,* is an enteric infection of ruminants causing weight loss, diarrhea, decreased milk production, and eventually death. Because the antibody and fecal tests have low false positive and high false negative error rates, cows positive for either antibody ($S/P \geq 0.10$) or culture test were classified as positive in a combined phenotype. Blood and fecal samples were collected primarily from daughters of twelve project bulls in their second or third lactation. These twelve sire families, which are part of a study to map major loci affecting Johne's disease susceptibility, were selected for their large family sizes and low relationships among sires. Approximately 92% of cows in this study were daughters of these twelve sires, although 46 sire families were represented in the edited dataset. Herds without a positive Johne's disease test and sire families with less than five daughters were removed from the dataset. The remaining 4655 cows from 241 herds were used for estimating heritability of susceptibility to Johne's disease with three traits: the antibody test, culture test, and combined tests. Overall disease prevalences were 0.248 with the antibody test and 0.0324 with the culture test. Mean prevalence with the combined phenotype for the twelve largest sire families was 0.259 (maximum sire prevalence = 0.324; minimum = 0.187). Analyses were carried out with a Bayesian linear sire model for log transformed antibody phenotypes and threshold sire models for culture and combined test phenotypes. Models included a fixed effect for parity and random effects for herd and sire using Markov chain Monte Carlo methodology. The posterior mean of across herd heritability was 0.211 (± 0.087) for the antibody test, 0.253 (± 0.135) for the culture test, and 0.148 (± 0.069) for the combined tests.

Key Words: Johne's Disease, Paratuberculosis, Heritability

361 Fine mapping of a QTL in a swine population selected for ovulation rate. M. Mousel*, G. Rohrer, K. Leymaster, and R. Christenson, *USDA-ARS; U.S. Meat Animal Research Center*, *Clay Center, NE.*

Fine mapping of a QTL located on chromosome 10 (SSC10) was conducted in a four-breed, white composite population of swine selected for ovulation rate (OR). Animals were selected for 11 generations for increased OR and compared to unselected controls (CO). The selection line had an increase of 3.0 corpora lutea (CL) and an increase of 0.3 pigs in total litter size as compared to controls. DNA was collected from 262 CO and 258 OR gilts and boars at generations 12 and 13. Six microsatellite markers, including two utilized in validation of the QTL, that spanned from 69cM to 96cM were genotyped. Utilizing SAS/Genetics, the marker which had showed the most significant ($P<0.001$) divergence between OR and CO lines was SW1041 (69cM). Significant differences ($P<0.001$) of SW1041 alleles on CL were identified with a model including allele, line, year born, season born, and sire as a random effect. The most frequent SW1041 allele in the OR line was associated with the second largest CL mean. Two markers (SWR1829, SW951) had the most frequent OR allele associated with greatest CL mean. An additional two markers (MRC1MS, GAD2) had an increase in the frequency of the OR line allele, compared to CO, which was associated with greatest CL mean for the marker. These data indicate that the divergence in allele frequencies on SSC10 between the OR and CO lines is likely due to a CL QTL and they refine the region in which a CL QTL is located. The selection line will be useful to identify genetic markers and causative genes for use in the industry.

Key Words: Swine, Fine Mapping, Ovulation Rate

362 Genetics of immune response in Canadian dairy cows and potential use in selection. R. Rupp[1], A. Hernandez[1], F. Miglior*[2,3], and B. Mallard[1], [1]*Ontario Veterinary College*, *Guelph, ON, Canada*, [2]*Agriculture and Agri-Food Canada - Dairy and Swine Research and Development Centre*, *Lennoxville, QC, Canada*, [3]*Canadian Dairy Network*, *Guelph, ON, Canada*.

In the last years selection goals for dairy cattle have evolved worldwide, with increasing interest for functional traits and special attention given to resistance to disease. As an alternative or complement to various indirect traits, improving immune response of animals is a promising mean to increase broad based resistance to disease. Recent progress has enabled characterization of both antibody (AMIR) and cell mediated (CMIR) immune responses, two complementary traits that indicate the general immune ability of the host. AMIR can be measured as serum concentration of specific antibody after immunization with an inert antigen. In addition, a delayed type hypersensitivity test based on the increase in skin-fold thickness following injection with test antigens has been developed to characterise CMIR. Accordingly, AMIR and CMIR were measured in 127 cows in an experimental farm. Heritability of CMIR varied from 0.27 to 0.50, showing a large genetic determinism of this trait although standard errors were high. Heritability of AMIR, relationships between both immune response traits and relationships with production traits are in progress. The indirect response of the selection based on the Canadian Lifetime Profitability Index (LPI) on both immune traits has been evaluated and showed that AMIR and CMIR may be deteriorating under current selection if their genetic correlations with protein and fat are antagonistic. A simulation study is in progress in order to assess the desirability, feasibility and modality of including AMIR and CMIR in an health index (as an alternative or together with other indirect traits such as somatic cell counts) to improve resistance to mastitis and other diseases.

Key Words: Disease Resistance, Immune Response, Genetic Parameters

363 Electrical conductivity of milk are genetically correlated to mastitis. E. Norberg*[1], G. W. Rogers[2], J. B. Cooper[2], and P. Madsen[1], [1]*Department of Genetics and Biotechnology, Danish Institute of Agricultural Sciences*, *Tjele, Denmark*, [2]*University of Tennessee*, *Knoxville*.

Electrical conductivity (EC) of milk was introduced as an indicator of mastitis several decades ago. Until now EC has solely been used for detection of bovine mastitis on the phenotypic level. However, EC may, if it shows genetic variation and is genetically correlated to mastitis, be used as an indicator trait in a breeding program. In this study, daily measurements of EC and mastitis on ~ 1500 first lactation Holstein cows, sired by 125 bulls, from 4 herds in Florida were used to estimate genetic parameters for EC and its relationship to mastitis. Electrical conductivity was measured in millimho (mmho) in composite milk from every milking with the Afikim computerized milking and management system (SAE Afikim, Kibbutz Afikim, Israel). Udder health status (mastitis or no mastitis) was recorded every day from DIM 6 to the last day of lactation. A bivariate analysis was carried out using a linear animal model with repeated measurements. Age at first calving, herd-test-day and DIM were included as fixed effects. Electrical conductivity was modeled with a constant additive genetic effect and a permanent environmental effect as a forth-order Legendre polynomial along the lactation trajectory. For mastitis, a simple repeatability model without random regressions was used. The permanent environmental variance of EC and mastitis was assumed to be uncorrelated. For EC, the estimated heritability ranged between 0.22 and 0.39 during the lactation. For mastitis, the heritability was as expected low (0.013). The genetic correlation between EC and mastitis was estimated to be 0.75, with a standard error of 0.13. These results show that electrical conductivity of milk has a high genetic correlation to clinical mastitis, and therefore has potential as an indicator trait in breeding programs were selection against mastitis is included.

Key Words: Dairy Cow, Electrical Conductivity, Mastitis

Dairy Foods: Cheese I—Cheddar, Mozzarella, and Kashar Cheeses

364 Effects of incorporation of probiotic *Lactobacillus acidophilus*, *Lb. casei*, *Lb. paracasei* and *Bifidobacterium* spp. on proteolytic patterns and production of organic acid in Cheddar cheese. L. Ong[1], A. Henriksson[2], and N. P. Shah*[1], [1]*Victoria University*, *Werribee Campus, School of Molecualr Sciences, PO Box 14428 melbourne City MC, Vic 8001 Australia*, [2]*DSM Food Specialties*, *Moorebank, NSW, Australia*.

Our objectives were to study i) the survivability of probiotic organisms in Cheddar cheeses and ii) the influence of these organisms on proteolytic patterns and production of organic acid.

Three types of Cheddar cheeses were made with lactococci starter (control) and a combination of probiotic bacteria. Probiotic, starter and non-starter lactic acid bacteria were enumerated using selective media. The compositional analysis was carried out as per AOAC. Concentration of organic acid was analysed using HPLC. Proteolytic patterns were examined using SDS-PAGE and soluble nitrogen method.

All probiotic adjuncts survived manufacturing process and maintained viability of >7.5 log10 CFU/g at the end of ripening for 6 months at 4°C. Lactococci counts decreased by one to two log cycles. No significant differences ($P>0.05$) were observed in fat, protein, moisture and salt contents, but acetic acid concentration was higher in probiotic cheeses. Primary proteolysis was not significantly different ($P>0.05$) between cheeses, but secondary proteolysis as indicated by concentration of free amino acids was significantly higher ($P<0.05$) in probiotic cheeses. Hydrolysis of casein after 6 months of storage was higher in probiotic cheeses with preference over α_s-CN than β-CN. As the concentrations of casein decreased, levels of lower molecular weight breakdown products of the caseins increased. Proteolytic activity, however, remained low for all cheeses.

Our results indicated that the addition of probiotic microorganisms in Cheddar cheeses increased proteolytic activity and changed flavour profile. Results also demonstrated that Cheddar cheese can be an effective vehicle for delivery of some health-promoting bacteria to the consumer.

Key Words: Probiotics, Proteolytic Patterns, Cheddar Cheese