USDA National Institute of Food and Agriculture.

Key Words: bovine respiratory disease complex, economics, epidemiology, genetics

0290 How might genomic information get translated into industry outcomes? A. L. Van Eenennaam*, *University of California, Davis.*

The 5-yr USDA-funded Bovine Respiratory Disease Complex Coordinated Agricultural Project (BRD CAP; USDA-AFRI 2011–68004–30367) aims to develop genetic markers associated with bovine respiratory disease (BRD) to enable the genetic identification of cattle that are less susceptible to BRD. Ultimately the aim of this project is to integrate predictive markers for BRD susceptibility into genetic tests and national cattle genetic evaluations. The research team is activity working to identify regions of the genome associated with BRD susceptibility in both dairy and beef cattle. Initial results have identified multiple genomic regions that were significantly associated with BRD susceptibility. Genomic selection has been introduced into dairy cattle breeding programs globally and within breed genomic estimated breeding values (GEBV) are published in a number of countries. Work is ongoing to integrate BRD information into dairy cattle evaluations at the appropriate economic weighting. However the incorporation of genomic information into beef cattle evaluations has been more problematic due to the presence of numerous breeds and the importance of crossbreeding in the commercial cattle population. Linkage disequilibrium between markers and quantitative trait loci (QTL) is not consistent across breeds, and so markers that were identified in one breed were frequently uninformative in other breeds. However, the sequencing of a large number of animals has opened up the possibility of identifying the actual SNP variations that are causing genetic variation. It is envisioned that by imputing the genotypes of reference animals collected by the BRD CAP up to full sequence and further fine mapping and analyses, the causative genetic variants associated with BRD susceptibility will be identified, and that inclusion of these markers on genotyping platforms will provide a reliable selection criterion to enable for the selection of both beef and dairy cattle that are less susceptible to BRD. There are several advantages associated with using causative SNP makers in selection panels including persistence of the marker effect across generations, and an increased likelihood that causative polymorphisms will be similarly associated with variation across multiple breeds. Ultimately, prospective marker panels will need to be tested in independent cattle populations to ensure they are predictive of BRD phenotype. Toward this end the BRD CAP is working in collaboration both breed associations and commercial feedlots to develop populations of BRD phenotyped animals. Ultimately selection against BRD susceptibility will depend on breeder inclusion of this disease trait in their breeding objective and selection decisions. See http://www.brdcomplex.org for more information.

Key Words: cattle, respiratory disease, extension

BREEDING AND GENETICS

0291 APY inverse of genomic relationship matrix–theory, analyses and questions. I. Misztal*, I. Pocrnic, D. Lourenco, and Y. Masuda, *University of Georgia, Athens.*

Genomic relationship matrix (GRM) can be inverted by Algorithm for Proven and Young (APY) based on recursion on a random subset of animals. While a regular inverse has a cubic cost, the cost of the APY inverse can be close to linear, allowing inexpensive computations with millions of genotyped animals. Theory proposed for APY assumes that optimal size of the subset (maximizing accuracy of genomic predictions) is due to a limited rank of GRM, which is a function of independent chromosome segments (Me) and subsequently of effective populations size (Ne). Simulation studies have shown that (1) the dimensionality is almost a linear function of Ne but for large Ne can be depressed by limited number of genotyped animals and SNP markers, (2) accuracy of predictions with APY inverse is higher than with a regular inverse, and (3) the distribution of independent chromosome segments is skewed. Tests using commercial data sets confirmed results by simulation. Comparisons of eigenvalue plots between simulated and commercial populations indicated an effective population size of 157 for Holsteins, 115 for Angus, 107 for Jerseys, 41 for broiler chicken and 30 for pigs. Experiences with the APY inverse raise a few questions. Can the rank provide information on the minimum SNP chip size that eliminates the polygenic component (or missing heritability)? Is the rank of GRM for a large two-breed population twice that of a single population? In simulation studies where QTL are on SNP markers, the best correlation of a simulated QTL effect is not with the actual SNP effect but with an average of adjacent SNPs. Is the optimum number (window size) of adjacent SNP a function of Ne and dictates the maximum resolution in GWAS? With all causative SNP are identified and their variances known, and appropriate weighted GRM (with APY inverse applicable) has the rank of the number of causative SNPs. Is the rank of weighted GRM with incomplete identification of QTLs (e.g., via GWAS or BayesB) smaller than that of a regular GRM? The APY inverse solves the problem of large-scale genomic computations and provides new insight into the genomic information.

Key Words: genomic selection, single-step GBLUP, APY inversion

0292 Dimensionality of genomic information and APY inverse of genomic relationship matrix. I. Pocrnic*[1], D. A. L. Lourenco[1], Y. Masuda[1], A. Legarra[2], and I. Misztal[1], [1]*University of Georgia, Athens,* [2]*INRA, UMR 1388 GenPhySE, Castanet-Tolosan, France.*

The objective of this study was to evaluate by simulation the dimensionality of genomic information in closed populations and its effect on genomic predictions using regular or sparse inverses of the genomic relationship matrices (GRM). Six datasets were simulated, representing populations with effective population sizes (Ne) approximately 20, 40, 80, 120, 160, and 200. Each population consisted of 10 non-overlapping generations, with 25,000 animals per generation and phenotypes available for generations 1 to 9. The last three generations were fully genotyped assuming genome length L = 30 Morgan, with 49,980 evenly allocated biallelic SNP markers and a total of 4980 biallelic and randomly distributed QTL affected the trait. The GRM was constructed for each population and analyzed for distribution of eigenvalues. The number of the largest eigenvalues explaining 90, 95, 98 or 99% of variation in GRM ranged from 814, 1611, 3701, 6253 (Ne≈20) to 5512, 9245, 15483, 20786 (Ne≈200), respectively. Genomic EBV (GEBV) were computed by single-step genomic BLUP (ssGBLUP) using either a direct inverse of GRM or a sparse inverse with the algorithm for proven and young (APY) that is based on recursion on a random subset of animals, where subset sizes were set to number of the largest eigenvalues explaining 90, 95, 98 or 99% of variation in GRM. APY inverse has approximately a linear cost as opposed to cubic for the regular inverse. Accuracies of GEBV for the last generation with APY inverse peaked at EIG98 and were slightly lower with EIG95, EIG99 or the direct inverse. In a situation with large number of SNP markers and genotyped animals, dimensionality of the SNP genomic information defined by the eigenvalues of GRM is approximately a linear function of effective population size, where most information is contained in about NeL largest eigenvalues, with no information beyond 4NeL. Genomic predictions with APY sparse inverse of GRM are more accurate and computationally inexpensive compared with regular inverse.

Key Words: genomic relationship matrix, genomic recursion, single-step genomic BLUP

0293 Accounting for discovery bias in genomic prediction. R. M. Thallman*[1], J. T. Parham[2], L. A. Kuehn[1], and J. P. Cassady[2], [1]*USDA-ARS, U.S. Meat Animal Research Center, Clay Center, NE,* [2]*South Dakota State University, Brookings.*

Our objective was to evaluate an approach to mitigating discovery bias in genomic prediction. Accuracy may be improved by placing greater emphasis on regions of the genome expected to be more influential on a trait. Methods emphasizing regions result in a phenomenon known as "discovery bias" if information used to determine influential regions is also used to predict genetic merit. Discovery bias causes genomic predictions to appear to be more accurate than they actually are. Generally, EBV of a population are conditional on as much information as possible and individual EBV are each conditional on exactly the same information. An analysis of simulated data (105 replicates) was conducted to test whether discovery bias could be reduced and true accuracy of prediction could be improved by relaxing the constraint that all EBV are conditional on the same information. In the default analysis, molecular breeding values (MBV) were computed from 2487 random SNP effects whose variances were estimated by REML. The 2600 phenotypes were simulated for non-parent animals only, which were progeny of 107 sires with number of paternal half-sibs per group ranging from one to 107. Corrected MBV (CMBV) were computed for each paternal half sib group by repeating the REML analysis on a data set that excluded records within that paternal half-sib group in an attempt to reduce discovery bias. True accuracy (correlation of MBV or CMBV with simulated breeding value) was lower for CMBV than for MBV. To recover the lost information without reintroducing discovery bias, a two-trait pedigree-based post-analysis was performed in which all 2600 phenotypes were fit as the first trait and the MBV (CMBV) were fit as the second trait. The solutions for the first trait are referred to as EBV and CEBV, respectively. True accuracy was greater for EBV than for MBV, suggesting the pedigree captured some genetic variance not accounted for by SNP. True accuracy was greater for CEBV than for EBV. Model derived accuracies were computed from prediction error variances of animals or functions of marker effects in the respective models. All model derived accuracies were greater than the corresponding true accuracies, indicating that discovery bias was present. Model

Table 0293.

	Model Derived Accuracy		True Accuracy		Discovery Bias
	Mean	SE	Mean	SE	Mean
MBV	0.960	7.11e-5	0.687	0.006	0.273
CMBV	0.954	7.59e-5	0.620	0.007	0.334
EBV	0.942	6.85e-5	0.716	0.006	0.226
CEBV	0.865	5.84e-5	0.721	0.007	0.144

MBV = Uncorrected molecular breeding value; CMBV = Corrected MBV; EBV = Uncorrected estimated breeding value; CEBV = Corrected EBV; Discovery bias = Model derived accuracy – True accuracy

derived accuracy was closer to true accuracy for CEBV than for EBV, indicating that the proposed correction was successful in reducing discovery bias, although it did not completely remove it. USDA is an equal opportunity employer.

Key Words: accuracy, discovery bias, genomic prediction

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294 Assessing genomic prediction accuracy for Holstein sires using bootstrap aggregation sampling and leave-one-out cross validation. A. Mikshowsky[1], K. A. Weigel[*2], and D. Gianola[3], *[1]University of Wisconsin, Madison, [2]Department of Dairy Science, University of Wisconsin, Madison, [3]University of Wisconsin, Madison.*

Since the introduction of genomic prediction for dairy cattle in 2009, genomic selection has dramatically changed many aspects of the dairy genetics industry and enhanced the rate of response to selection for most economically important traits. Young dairy bulls are genotyped to obtain their genomic predicted transmitting ability (GPTA) and reliability (REL) values. These GPTA are the main factor in most purchasing, marketing, and culling decisions until the bulls reach 5 yr of age and their milk-recorded offspring become available. At that time, daughter yield deviations (DYD) can be compared with the GPTA computed several years earlier. For most bulls, the DYD are similar to the initial predictions. However, for some bulls, the difference between DYD and corresponding GPTA is quite large, and published REL are of limited value in identifying such bulls. A method of bootstrap aggregation sampling (bagging) using genomic BLUP (GBLUP) was applied to predict the GPTA of 2963, 2963, and 2803 young Holstein bulls for protein yield, somatic cell score (SCS), and daughter pregnancy rate (DPR), respectively. For each trait, 50 bootstrap samples from a reference population comprised of 2011 DYD of 8610, 8405, and 7945 older Holstein bulls were used. Leave-one-out cross validation was also performed to assess the prediction accuracy when removing specific bulls from the reference population. The main objectives of this study were: (1) to assess the extent to which current REL values and alternative measures of variability, such as the bootstrap standard deviation (SD) of predictions, could detect bulls whose daughter performance will deviate significantly from early genomic predictions and (2) to identify factors associated with the reference population that can cause inaccurate genomic predictions. Correlations between bagged GBLUP predictions and 2014 DYD were lower than GBLUP predictions from the full reference population. The SD of bootstrap predictions was a useful metric for identifying bulls whose future daughter performance may deviate significantly from early GPTA for protein and DPR. Use of bootstrap predictions could prevent up to 50% of type I errors and roughly 10% of type II errors in sire selection decisions. The removal of certain reference population bulls indicated that testing set predictions for protein were robust overall, but some bulls negatively affecting prediction accuracy were identified.

Key Words: genomic prediction, bootstrap sampling, dairy cattle

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0295 The impact of call rate on genotype accuracy. D. C. Purfield[*1], M. C. McClure[2], and D. P. Berry[3], *[1]Animal & Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy, Co. Cork, Ireland, [2]Irish Cattle Breeding Federation, Bandon, Ireland, [3]Teagasc, Moorepark, Fermoy, Co. Cork, Ireland.*

Data quality of single nucleotide polymorphism (SNP) arrays plays a key role in the accuracy and precision of downstream data analyses. The use of low quality genotypes can lead to false-positive results and impair the accuracy of genomic predictions. One such quality control measure commonly used is individual animal call rate, defined as the proportion of SNPs per individual where a genotype was called. Currently, no consensus exits on the minimum individual call rate that should be imposed, with threshold call rates per individual varying from 0.80 to 0.95 across studies. The objective of the present study was to determine the minimum individual call rate that could be applied without jeopardizing data quality. A total of 144,672 samples genotyped on a custom Illumina genotype panel on 143,827 dairy and beef cattle were available. The genotyping panel includes 14,371 SNPs on either the Illumina Bovine SNP50 or high density genotyping panels. All genotypes were called using the Illumina GenCall method. Lab-dates ($n = 4$) where > 15% of the samples genotyped had a call rate < 90% were not considered further. Of the remaining 142,433 samples, 493 animals had both a poor call rate (< 90%) and a subsequent high call rate (> 99%) after re-sampling and re-genotyping. The mean call rate for all samples was 98.77% (range: 15.81%-99.97%). The genotype and allele concordance rate among the genotypes available for all 493 animals with both a low and subsequent high call rate was estimated. Genotype and allelic concordance between low- and high-call genotypes increased as call rate increased (Table 1.). Low minor allele variants (i.e., variants with a minor allele frequency < 0.05) were imputed with greatest accuracy for samples with a mean genotype and allelic concordance of 99.24% and 99.55%. Imputation algorithms often correct for genotyping error, therefore to test if imputation improved concordance, all 493 low call rate samples were imputed using FImpute. A reference population of 140,268 animals with call rates > 90%, excluding the 493 high-call rate samples, was used. Imputation marginally increased concordance rates for all SNPs with a called genotype, but overall genotype concordance per class slightly decreased because missing genotypes were often incorrectly imputed as heterozygous genotypes. However, if a direct relative (i.e., sire, dam or progeny) was included in the imputation reference population, mean genotype

Table 0295.

Table 1. Genotype and allele concordance rates (CR) prior and post imputation for all 493 animals with a poor (<90%) and subsequent high call rate (>99%).

	Pre Imputation		Post Imputation			
Call rate class	Genotype CR	Allele CR	Genotype CR Called SNPs	Allele CR Called SNPs	Genotype CR All SNPs	Allele CR All SNPs
<40	38.36	62.35	38.61	62.38	39.42	63.22
40-50	47.08	68.57	47.33	68.62	44.74	67.15
50-60	58.59	76.59	58.89	76.67	53.68	73.54
60-70	79.31	89.51	79.66	89.65	73.21	85.92
70-75	86.06	93.01	86.29	93.08	81.71	90.51
75-80	93.47	96.73	93.64	96.79	90.77	95.26
80-85	96.83	98.41	96.93	98.46	95.56	97.72
85-90	98.44	99.22	98.47	99.22	98.08	99.01

and allele concordance for samples with a call rate between 85 and 90% increased to 98.13% and 99.04%, respectively.

Key Words: call rate, quality-control, genotype panels

296 Strategy for incorporating newly discovered causative genetic variants into genomic evaluations. G. R. Wiggans*[1], P. M. VanRaden[1], D. M. Bickhart[2], and M. E. Tooker[1], *[1]Animal Genomics and Improvement Laboratory, USDA-ARS, Beltsville, MD, [2]Animal Genomics and Improvement Laboratory, USDA-ARS, Beltsville, MD.*

With sequence data available for an increasing number of dairy cattle, discovery of causative genetic variants is expected to be frequent. Current genomic evaluation systems require genotypes for all markers that contribute to an evaluation. A minimum number of animals with an observation for a new marker is required for accurate imputation. The SNP calls derived from sequence data from the 1000 Bull Genomes Project for 444 Holsteins were combined with SNP genotypes from bulls in the predictor population for U.S. national genetic evaluations to impute candidate variants from the full sequence. From this imputed data, the set of SNP used in genomic evaluation along with the newly discovered causative variants were selected and stored. Those genotypes replaced the original genotypes for the bulls when extracting genotypes for genomic evaluation. The time required for imputation is substantially reduced in routine evaluation by using the haplotype library and assignments from the previous evaluation. To create suitable prior information for the expanded SNP set, genotypes for approximately 100,000 animals (including the predictor bulls and many cows with genotyped progeny) were imputed without priors. This step took about 1 d; if the full set of animals had been used, it would have taken over a week. The accuracy of this approximation was tested using the December 2015 Holstein genomic evaluation of nearly 1 million animals. Genotypes from 978,987 bulls and cows were used to create the priors, which were used to impute the December 2015 Holstein genotypes. Of the nearly 60 billion comparisons, 97.7% were identical, 1% differed by 1 allele, and 1.2% differed by a missing allele. Efficient methods that result in higher concordance may be possible. Adding new highly informative markers to the evaluation process is expected to improve prediction accuracy. In addition, excluding other markers may further increase accuracy if they contribute more noise than value when highly informative markers are included. The procedure developed enables newly discovered causative variants to be added to genomic evaluation almost immediately, which saves the time previously required for a marker to be added to a new genotyping chip as well as the time required for sufficient animals to be genotyped with the new chip to achieve adequate imputation accuracy. With this strategy, the benefits from adding new markers to genomic evaluation can be realized sooner.

Key Words: causative variant, sequence data, genomic evaluation

0297 High density marker panels, SNPs prioritizing and accuracy of genomic selection. L. Y. Chang*[1], S. Toghiani[1], S. E. Aggrey[2,3], and R. Rekaya[1,3], *[1]Department of Animal and Dairy Science, University of Georgia, Athens, [2]NutriGenomics Laboratory, Department of Poultry Science, University of Georgia, Athens, [3]Institute of Bioinformatics, University of Georgia, Athens.*

Availability of high density (HD) SNP marker panels, genome wide variants and even sequence data create an unprecedented opportunity of dissect the genetic basis of complex traits and to enhance selection in livestock and plant species. The disproportional increase in the number of parameters in the genetic association model compared with the number of phenotypes has led to further deterioration in the statistical power, and increase in co-linearity and false positive rates. HD panels do not improve the accuracy of GS in any significant manner and could even lead to reduction in accuracy using both regression and variance component methods. As a result, HD panels at best they did not improve significantly the accuracy of genomic selection and at worst they led to a reduction in accuracy. This is true for both regression and

variance component approaches. To remedy this situation, either some form of SNP filtering or external information is needed. Current methods for prioritizing SNP markers (i.e., BayesB, BayesC) are sensitive to the increased co-linearity in HD panels which could limit their performance. In this study, the usefulness of F_{st}, a measure of allele frequency variation among populations, as an external source of information in genomic selection was evaluated. A simulation was performed for a trait with heritability of 0.4. Data was divided into three subpopulations based on trait distribution (top 5%, bottom 5% and in between). Marker data was simulated to mimic 770K SNP marker panel. A ten chromosome genome with 200K SNPs was simulated. Several scenarios with varying number of QTLs and their associated effects were simulated. F_{st} empirical cutoff values of 0.004, 0.008, 0.01, and 0.02 were used to prioritize markers resulting in 4579, 2288, 1745, and 650 selected SNPs, respectively. Using all 200K markers and no filtering, the accuracy of genomic prediction (correlation between true and predicted breeding values) was 0.48. When SNPs were pre-selected based on F_{st}, accuracy was 0.41, 0.48, 0.49, and 0.53 for F_{st} cutoff values of 0.004, 0.008, 0.01, and 0.02, respectively. It is clear that the accuracy obtained using all SNPs can be easily achieved using only 0.5 to 1% of all markers. These results indicated that SNP filtering using already available external information could increase the accuracy of genomic selection. This is especially important as next generation sequencing technology is becoming more affordable and accessible to animal and plant applications.

Key Words: SNP prioritizing, genomic selection, high density

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298 Selection of sequence variants to improve dairy cattle genomic predictions. M. E. Tooker*[1], P. M. VanRaden[1], D. M. Bickhart[1], and J. O'Connell[2], *[1]Animal Genomics and Improvement Laboratory, USDA-ARS, Beltsville, MD, [2]University of Maryland School of Medicine, Baltimore.*

Genomic prediction reliabilities improved when adding selected sequence variants from run 5 (July 2015) of the 1000 bull genomes project. High density (HD) imputed genotypes for 26,970 progeny tested Holstein bulls were combined with candidate sequence variants within or near genes for 444 Holstein animals. Variants with minor allele frequency (MAF) < 0.01, incorrect map locations, excess heterozygotes, or low correlations of sequence and HD genotypes for the same variant were removed. Individual genotype probabilities < 0.98 from Beagle and Mendelian conflicts between parents and progeny were set to missing. Test 1 included 481,904 candidate sequence SNP consisting of 107,471 exonic, 9422 splice, 35,242 untranslated regions at the beginning and end of genes, 329,769 SNP upstream or downstream of genes. Test 2 also included 249,966 insertions and deletions (indels). After merging sequence variants with 312,614 HD SNP and editing, Test 1 included 762,588 variants and Test 2 included 1003,453. Imputation quality was assessed by keeping 404 of the sequenced animals in the reference population and randomly choosing 40 animals as a test set. Their sequence genotypes were reduced to the subset in common with HD genotypes and then imputed back to sequence. Percentage of correctly imputed variants averaged 97.3% across all chromosomes in Test 1 and 97.2% in Test 2. Total time required to prepare, edit, and impute the sequence variants for 27,235 animals was about 5 d using < 20 processors. Computation of genomic predictions using deregressed evaluations from August 2011 for 33 traits and 19,575 bulls required about 3 d with 33 processors. Predictions were tested using 2015 data of 3983 U.S. bulls whose daughters were first phenotyped after August 2011. Many sequence variants had larger estimated effects than nearby HD markers, but prediction reliability improved only 0.6% points in Test 1 when sequence SNP were added to HD SNP, and only 0.4 higher than HD SNP in Test 2 when sequence SNP and indels were included. However, selecting the 17,000 candidate SNP with largest estimated effects and adding those to the 60,671 SNP used in routine evaluations improved reliabilities by 2.7% points (67.4% vs. 64.7%) on average across traits, compared with 35.2% parent average reliability. Accuracy of prediction can improve by adding selected sequence SNP to marker sets.

Key Words: causative variant, sequence data, genomic evaluation

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0299 Genomic prediction of crossbred performance. B. Harlizius*[1], M. S. Lopes[1], J. Vandenplas[2], C. A. Sevillano[2], and J. W. M. Bastiaansen[3], *[1]Topigs Norsvin Research Center, Beuningen, Netherlands, [2]Wageningen University, Netherlands, [3]Animal Breeding and Genomics Centre, Wageningen University, Netherlands.*

The majority of the commercial slaughter pigs are crossbred animals. However, breeding efforts have been mainly focused on increasing genetic progress of purebred populations. The aim of this work is to evaluate different strategies to improve genomic prediction of crossbred performance taking into account the breed origin of alleles in crossbred populations (breed-specific effects). Previous work showed that marker effects estimated in one breed cannot predict performance in another breed (across-breed prediction). This might be due to breed-specific effects caused by differences in linkage disequilibrium between the marker and the QTL, as well as differences in allele frequencies and in genetic background of the breeds. For prediction of crossbred performance, marker effects estimated in single-breed data showed some predictive value but training on crossbred data achieved higher accuracies, although the breed origin of alleles was ignored. In this study, prediction accuracies of breeding values from a traditional genomic selection model (GS) were compared

with prediction accuracies of breeding values from a model that accounts for breed-specific effects (BS). The population evaluated consisted of a two-way (Large White and Landrace) crossbred population. As both parents of all crossbred animals were known, the breed origin of alleles was easily determined after phasing of the data. The trait evaluated was gestation length (GL), for which a genetic correlation between purebred and crossbred performance (r_{pc}) of 0.90 was estimated. Prediction accuracy of BS breeding values was slightly greater than prediction accuracy of GS breeding values (0.53 and 0.52, respectively). Additional benefits of BS over GS are expected for traits with lower r_{pc} and when crosses of more distant purebred populations are evaluated. As a step further, a method based on long-range phasing for determining the breed origin of alleles in three-way crossbred data was developed. In a simulation study, the accuracy of breed of origin assignment was determined for 400 three-way crossbred animals with 95% correct assignments, 3% unassigned and < 2% incorrect assignments. Application of this method to real data, including 14,000 genotyped purebred animals and 1700 genotyped three-way crossbred animals, achieved 93% assignments of breed of origin of alleles without using pedigree information. Genotypic data from purebred animals was required to define the haplotypes of the three breeds contributing to the crossbreds. Currently, analyses are underway to use this breed origin information of the three-way crossbred population to estimate breed-specific effects for genomic prediction.

Key Words: pigs, crossbred performance, breed-specific effects

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0300 SNP filtering using Fst and implications for genome wide association and phenotype prediction. S. Toghiani[*1], L. Y. Chang[1], S. E. Aggrey[2,3], and R. Rekaya[1,3],[1]*Department of Animal and Dairy Science, University of Georgia, Athens,* [2]*NutriGenomics Laboratory, Department of Poultry Science, University of Georgia, Athens,* [3]*Institute of Bioinformatics, University of Georgia, Athens.*

Although genome-wide association studies (GWAS) detect single nucleotide polymorphism (SNP)-trait association, these SNPs explain only a small fraction of the variation. Genomic selection (GS), through the use of all available genetic information, tends to have a better dissection of the phenotypic variation, but its performance is still far from optimum. GWAS and GS are affected by lack of power is due to small sample size, large number of highly correlated markers, and the moderate to small effects of most QTLs. This situation could get even more complex with the continuous increase in marker density. Methods that internally try to prioritize SNPs (i.e., BayesB) tend to provide a certain relief when low to medium density panels are used but their advantages degrade with the increase of the number of markers. Thus, it is becoming a necessity to either perform a SNP filtering before conducting the association analysis or to enlist additional external sources of information. Knowledge of genetic diversity based on evolutionary forces is beneficial for tracking loci influenced by selection. F_{ST}, as measure of allele frequency variation among populations, provides a tool to reveal genomic regions under selection pressure. To evaluate its usefulness as an external source of information in association studies, a simulation was performed. A trait with heritability of 0.4 was simulated and three sub-populations were created based on the empirical phenotypic distribution (< 5% quantile; > 95% quantile and between 5 and 95% quantiles). Marker data was simulated to mimic 600K and 1 million SNP panels. Genetic complexity of the trait was modeled by the number of QTLs, their distribution, and magnitude of their effects. Using different empirical cut off values for F_{ST}, most QTLs were correctly detected using as little as 0.8% of SNP markers in the panels. Furthermore, the genomic similarity base on the selected SNPs was very high (> 0.80) for individuals with similar genetic and phenotypic values even that they have limited to no blood relationship. These results indicate that filtering SNPs using F_{ST}could be beneficial to GWAS and GS by focusing on genome regions under selection pressure. This could be relevant with the availability of next-generation-sequencing data. High functional genomic similarity based on selected markers indicates similarity in SNP signatures, regardless of blood relationships, and translates into high phenotypic correlation that could be used in decision making.

Key Words: GWAS, F_{ST}, genetic and phenotypic prediction

0301 A combined coalescence forward in time simulator software for pedigreed populations undergoing selection for complex traits. J. T. Howard[*1], F. Tiezzi[1], J. E. Pryce[2], and C. Maltecca[1], [1]*North Carolina State University, Raleigh,* [2]*Department of Economic Development, Jobs, Transport and Resources, Bundoora, Australia.*

The use of marker information in animal breeding has recently been an active area of research and has been incorporated in selection decisions and as a tool to control inbreeding across a variety of species. There is yet still much to be learned on the optimal way to use marker information to select animals and manage the genome of a population that is undergoing selection for complex traits that have a traditional quantitative basis (i.e., yield) and/or fitness basis (i.e., number of progeny). We have developed a combined coalescence and forward-in-time simulator for complex traits and populations. The simulator is performed in two stages. In the first stage whole-genome SNP data is read in ms format and is utilized to generate founder individuals and associated SNP marker panels ranging in size from thousands to millions of SNP. During this stage a wide variety of trait architectures can be generated with additive

and dominance effects for both a traditional quantitative trait and fitness along with genomic covariance among traits. The second stage generates new individuals across generations based on a variety of selection scenarios. The selection stage can be performed using a wide variety of relationship matrices including pedigree, independent markers, haplotypes, or run of homozygosity based haplotypes. Relationship matrices and their associated inverse are generated using computationally efficient algorithms based on updating matrices from previous generations. Complex population structures can be generated that allow for a differential contribution of gametes to the next generation as well as mating constraints. To demonstrate the program, we present a small application that mimics a dairy cattle and swine population to describe some of the metrics that are generated. Scenarios were generated based on a 12,000 SNP marker panel spread across 3 chromosomes and a population size of 650 animals (sires = 50; dams = 600) per generation. A scenario with selection on a quantitative trait occurring for 5 generations and breeding values estimated from pedigree or independent SNP had a running time for the dairy cattle scenario of 4.85 and 5.82 min, respectively. GenoDriver allows for a wide range of selection strategies to be evaluated in the presence of a fitness trait and is available at https://github.com/jeremyhoward/GenoDriver.

Key Words: genetic simulation, quantitative traits, genomic selection

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0302 Identifying and calling insertions, deletions, and single-base mutations efficiently from sequence data. P. M. VanRaden[*1], D. M. Bickhart[2], and J. R. O'Connell[3], *[1]Animal Genomics and Improvement Laboratory, USDA-ARS, Beltsville, MD, [2]Animal Genomics and Improvement Laboratory, USDA-ARS, Beltsville, MD, [3]University of Maryland School of Medicine, Baltimore.*

Whole-genome sequencing studies can identify causative mutations for subsequent use in genomic evaluations, but sequence alignment and variant identification are lengthy and sometimes inaccurate processes. Speed and accuracy of identifying small insertions and deletions (indels) of sequence can be improved by calling variants while aligning sequence reads. Previous algorithms separated alignment and calling steps, whereas program findmap stores previously known variants in memory, calls alleles for those variants, and identifies other potential new variants during alignment. The algorithm uses a string-pattern hash to store the reference genome in a rapidly accessed table. If both ends of a paired-end read do not align fully, the length of a potential indel within the read is calculated from the map location difference for two partial matches. The algorithm then finds the indel location and checks if the full read matches after accounting for the indel. Potential variants detected by findmap are checked and edited by program findvar for consistency across reads. New variants from findvar were compared with those from the Genome Analysis Toolkit (GATK) UnifiedGenotyper and from SamTools after Burrows-Wheeler Aligner (BWA) alignment. Detection accuracy was examined using reads simulated for 10 animals at 10X coverage from cattle reference map UMD3.1 with variants derived from run 5 (July 2015) of the 1000 bull genomes project that included 38,062,190 SNP, 532,179 insertions, and 1127,620 deletions. Half of variants were simulated as heterozygous, one-fourth as homozygous alternate, and one-fourth as homozygous reference. For homozygous alternate variants, findvar found 99.8% of SNP, 79% of insertions, and 67% of deletions; GATK found 99.4, 90, and 89%; and SamTools found 99.8, 12, and 18%, respectively. For heterozygotes, findvar found 99.1, 75, and 62%; GATK found 99.0, 90, and 88%; and SamTools found 98.2, 9, and 11%, respectively. False positives as percentages of true variants were 14, 0.4, and 0.3% from findvar; 12, 8.4, and 2.9% from GATK; and 37, 1.3, and 0.4% from SamTools, respectively. Read depth was 85.9 from findmap/findvar, 96.1 from BWA/GATK, and 84.4 from BWA/SamTools. With 10 processors, clock times were 106 h for BWA, 25 h for GATK, 11 h for SamTools, 3 h for findmap, and 1 h for findvar. The new software is freely available, with algorithms 10 to 30 times faster than current strategies for calling known and identifying new variants. Accuracy is improved by accounting for DNA variants while aligning sequence data.

Key Words: sequence alignment, variant calling, indel

0303 Issues in commercial application of single-step genomic BLUP for genetic evaluation in American Angus. D. A. L. Lourenco[*1], S. Tsuruta[1], B. D. Fragomeni[1], Y. Masuda[1], I. Pocrnic[1], I. Aguilar[2], J. K. Bertrand[1], D. W. Moser[3], and I. Misztal[1], *[1]University of Georgia, Athens, [2]INIA, Las Brujas, Uruguay, [3]Angus Genetics Inc., St. Joseph, MO.*

American Angus Association (AAA) has been using genomic information for genetic evaluations in a multistep approach since 2009. To improve accuracy while simplifying procedures, AAA is transitioning to single-step genomic BLUP (ssGBLUP) in the middle of 2016. Initial tests with ssGBLUP showed an increase in prediction accuracy of 25% for growth traits compared with traditional evaluations. Besides evaluation for growth traits, the goal of this study was to update the full pipeline for genetic evaluation with ssGBLUP methodology. The pipeline includes multi-trait models with linear and categorical traits, maternal effects, multibreed evaluations with external information, and a large number of genotyped animals but most of them with low EBV accuracy. Data included 9.7 M animals in the pedigree, 184,354 genotyped animals, and at most 8.2 M phenotypes for growth traits, calving ease (categorical), and carcass traits. The first issue during the implementation was the increasing number of genotyped animals. Single-step GBLUP requires the inverse of the genomic

relationship matrix (GRM), which had a high computing cost and required around 1 Tb of memory for this dataset. The algorithm for proven and young animals (APY) was used to approximate the inverse of the GRM. The number of core animals was set to 15,000, which was calculated as the number of eigenvalues of GRM explaining 99% of the variation. This algorithm reduced the memory usage to 40 Gb and required 10% of the computing time while slightly improving the accuracy. Another issue was the increase in computing time for calving ease evaluation, which uses a threshold model, from 12 h to 4.5 d. Resetting the preconditioned conjugate gradient iteration to solve the mixed model equations every 40 to 200 rounds helped decrease the time to 19 h. The inclusion of external EBV for Red Angus was required for evaluation of growth traits. We developed software to support genomic and external information, and the implementation of a genomic multibreed model increased the computing time only by 2.5 h. Current algorithm for approximation of accuracy of genomic EBV (GEBV) was too expensive for > 100,000 animals. A new algorithm was developed that does not require inverse of large GRM and accounts for multiple sources of information while avoiding double-counting. Correlations between accuracy from the new algorithm and true accuracy from PEV were higher than 0.85 for growth traits. Single-step GBLUP can be considered a mature methodology for commercial genomic selection in beef cattle.

Key Words: beef cattle, genomic selection

0304 Single-step GBLUP using APY inverse for protein yield in U.S. Holstein with a large number of genotyped animals. Y. Masuda*[1], I. Misztal[1], and P. M. VanRaden[2], [1]*University of Georgia, Athens,* [2]*Animal Genomics and Improvement Laboratory, USDA-ARS, Beltsville, MD.*

The objective of this study was to provide initial results in an application of single-step genomic BLUP with a genomic relationship matrix (G^{-1}_{APY}) calculated using the Algorithm of Proven and Young (APY) to 305-d protein yield for U.S. Holsteins. Two G^{-1}_{APY} were tested; one was from 139,057 genotyped bulls with 12,895 core animals (APY140K) and the other one was from 764,029 genotyped animals with 12,913 core animals (APY760K). The predictor data set consisted of phenotypes recorded after 1989 and pedigrees limited to 3 generations back from recorded or genotyped animals. Genomic predictions (GPTA2011) were calculated for predicted bulls that had no recorded-daughters in 2011 but had at least 50 such daughters in 2015. We used the official daughter yield deviations published in 2015 (DYD2015) for the predicted bulls (N = 3797). We also used the official GPTA published in 2011 with a multistep method as a comparison, although official methods have improved since then. Coefficient of determination (R^2) and slope (b_1) were calculated from a linear regression of DYD2015 on GPTA2011. Using APY140K, the R^2 was 0.50 compared with 0.51 from the official GPTA. The b_1 was much better (0.98) compared with 0.81 from the official GPTA. With APY760K, the R^2 was 0.46 and b_1 was 1.08. Incorporating effect of a SNP related to DGAT1 increased R^2 to 0.51 for APY140K and 0.48 for APY760K. The decrease in R^2 with APY760K compared with APY140K could be due to inclusion of lower quality genotypes, or biases caused with the use of all genotypes with incomplete phenotypes. All the computations finished within 11 h including 4.2 h to set up APY-inverse with APY760K. Based on the linearity of the computation cost, using 1 million genotyped animals with the same model would require 14 h of computations. Single-step GBLUP can provide genomic predictions for all genotyped bulls and cows while accounting for pre-selection. Further research will determine the impact of various factors affecting the reliability such as validation methodology, weighting SNP markers, and quality of genotyped data.

Key Words: genomic evaluation, Holstein, ssGBLUP

0305 Heteroskedastic extensions for genome-wide association studies. Z. Ou*[1], R. J. Tempelman[2], J. P. Steibel[3,4], C. W. Ernst[3], R. O. Bates[3], C. Chen[3], and N. M. Bello[1], [1]*Department of Statistics, Kansas State University, Manhattan,* [2]*Michigan State University, East Lansing,* [3]*Department of Animal Science, Michigan State University, East Lansing,* [4]*Department of Fisheries and Wildlife, Michigan State University, East Lansing.*

Bayesian multiple regression models based on genomic marker information are commonly used for genomic prediction and selection and are being increasingly utilized in genome-wide association (GWA) analyses to search for genomic regions associated with economical important traits in agriculture. These models jointly fit all markers, thereby circumventing the limitations of "one-marker-at-a-time" of traditional GWA inference. We have recently validated and tested extensions of genomic prediction models to account for residual heteroskedasticity, which is prevalent in livestock field data. Our objective was to evaluate the impact of not accounting for potential residual heteroskedasticity in GWA inference. Using simulated data scenarios that reflected a gradient of increasing residual heteroskedasticity, we fitted homoscedastic and heteroskedastic error versions of hierarchical Bayesian genomic prediction models assuming either normal (RR-BLUP) or heavy-tailed (BayesA) prior specifications on the effects of genomic markers. For each marker, we then constructed a posterior z-score using prediction error variance of the estimated marker effect to detect associations between genomic regions and phenotypes of interest. Under conditions of extreme heterogeneity of residual variances, heteroskedastic models showed an increase in power of up to 10% points for GWA discovery with little impact on false positive rate (i.e., change of 0 to 3% points), compared with the homoscedastic model counterparts.

Further, when heteroskedasticity was high, the absolute magnitude of the estimated signal for the most prominent QTL expressed as a posterior *z*-score was enhanced by 20% and 34% for heteroskedastic RR-BLUP and BayesA, respectively. The inferential advantages of heteroskedastic models over homoscedastic ones were particularly apparent under a BayesA specification. A data application involving three quantitative carcass and meat quality traits from a swine resource population representing high, mild and low levels of heteroskedasticity yielded proportionally enhanced differential detection signal for the heteroskedastic models relative to the homoscedastic ones, consistent with results from the simulation study. In conclusion, accounting for residual heteroskedasticity can be expected to enhance power in the identification of important genomic regions for traits of interest.

Key Words: genome-wide association, residual heteroskedasticity, genomic prediction model

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0306 Exploring the feasibility of using copy number variants as genetic markers through large-scale whole genome sequencing experiments.

D. M. Bickhart*[1], L. Xu[2], J. L. Hutchison[3], J. B. Cole[4], D. J. Null[4], S. G. Schroeder[5], J. Song[6], J. F. Garcia[7], T. Sonstegard[8], C. P. VanTassell[5], R. D. Schnabel[9], J. F. Taylor[9], and G. E. Liu[5], *[1]Animal Genomics and Improvement Laboratory, USDA-ARS, Beltsville, MD, [2]Department of Animal and Avian Sciences, University of Maryland, College Park, [3]Animal Improvement Programs Laboratory, USDA-ARS, Beltsville, MD, [4]Animal Genomics and Improvement Laboratory, USDA-ARS, Beltsville, MD, [5]Animal Genomics and Improvement Laboratory, USDA-ARS, Beltsville, MD, [6]University of Maryland, Animal Science and Avian, College Park, [7]UNESP Univ Estadual Paulista, Araçatuba, Brazil, [8]Recombinetics Inc., St Paul, MN, [9]University of Missouri, Columbia.*

Copy number variants (CNV) are large scale duplications or deletions of genomic sequence that are caused by a diverse set of molecular phenomena that are distinct from single nucleotide polymorphism (SNP) formation. Due to their different mechanisms of formation, CNVs are often difficult to track using SNP-based linkage disequilibrium inference. This can result in decreased reliabilities of prediction for CNV causal mutations tracked by SNP genotyping arrays. To test if CNVs can serve as suitable genetic markers, we sequenced 75 individual bulls from eight different breeds and two subspecies of cattle (*Bos taurus taurus*: Angus, Holstein, Jersey, Limousin, Romagnola; *Bos taurus indicus*: Brahman, Gir, Nellore) to 11X coverage. We identified 1853 non-redundant CNV regions (CNVR) that comprise ~3.1% (87.5 Megabases) of the cattle genome, which represents an increase over previous cattle genome variability estimates (~2%). With the discrete genome copy number values identified in our analysis, we selected the top 1% (n = 80) of CNV sites found to be variable among the sequenced breeds by a modified F statistical measure to perform population structure analyses. We were able to distinctly separate breeds of cattle based on genomic copy number, suggesting that CNVs may have utility as genetic markers. Further analysis revealed that 77.5% (62/80) of our selected CNV windows could reliably be assessed for variability and that 54 of these loci were, in turn, located near tandem duplications. CNV genotyping remains a difficult endeavor and suffers from several obstacles related to their detection and mechanisms of formation; however, these initial results suggest that our current methods can be refined and may provide suitable utility for genomic evaluation in the future.

Key Words: sequence data, genetic markers, genotyping

0307 Use of marker × environment interaction whole genome regression model to incorporate genetic heterogeneity for residual feed intake, dry matter intake, net energy in milk, and metabolic body weight in dairy cattle.

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Feed efficiency in dairy cattle has gained much attention recently. Due to the cost prohibitive measurement of individual feed intakes, combining data from multiple countries is usually necessary to ensure a large enough reference population. It may then be essential to model genetic heterogeneity when making inferences about feed efficiency or selecting efficient cattle using genomic information. In this study, we constructed a marker × environment interaction model that decomposed marker effects into main effects and interaction components that were specific to each environment. We compared environment-specific variance component estimates and prediction accuracies of the interaction model analysis, an across-environment analysis ignoring population stratification, and a within-environment analysis on the feed efficiency data set. Phenotype traits included residual feed intake (RFI), dry matter intake (DMI), net energy in milk (MilkE), and metabolic body weight (MBW) from 3656 cows measured

in 3 broadly defined environments: North America (NAM), the Netherlands (NLD), and Scotland (SAC). Genotypic data included 57,574 single nucleotide polymorphisms per animal. The interaction model gave the highest prediction accuracy for MBW, which had the largest estimated heritabilities ranging from 0.37 to 0.55. The within-environment model performed the best when predicting the trait of RFI which had the lowest estimated heritabilities, ranging from 0.13 to 0.41. For traits (DMI and MilkE) which had intermediate estimated heritabilities (0.21 to 0.50 and 0.17 to 0.53), performance of the 3 models was comparable. Genomic correlations between environments were also computed using the variance component estimates from the interaction model. Averaged across all traits, genomic correlation was the highest between NAM and NLD, and was the lowest between NAM and SAC. In conclusion, the interaction model provided a novel way to evaluate traits measured in multiple environments in which genetic heterogeneity may exist. It offered the capability of estimating environment-specific parameters and performed either the best or nearly the best in the genomic prediction.

Key Words: genomic selection, interaction model, feed efficiency

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0308 Imputation of medium density genotypes from custom low density genotype panel in sheep.

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A custom low density genotype panel has been developed with 16,351 single nucleotide polymorphisms (SNPs), 12,118 of which are on the medium density Illumina Ovine50 Beadchip which has 51,135 SNPs. The objective of the present study was to quantify the accuracy of imputation from the low density to medium density panel in five different sheep breeds. Medium density genotypes were available on 2375 sheep from the breeds Suffolk (n = 566), Texel (n = 318), Vendeen (n = 461), Charollais (n = 559) and Belclare (n = 471). The youngest 75 animals per breed were used as the validation population; the 37,278 autosomal SNPs on the medium density panel that are not on the low density panel were masked for the validation population. Imputation was undertaken across the entire genome simultaneously using both family and population wide linkage (disequilibrium) information. Concordance rates and the correlation between the true and imputed genotypes were estimated for the validation animals which included the low density SNPs in the calculation. Across all genotypes, the correlation between the actual and imputed genotype was 0.983; the mean genotype (allele) concordance rate was 0.979 (0.989). The mean genotype and allele concordance rate per individual varied from 0.864 to 0.997 and from 0.929 to 0.999, respectively. The individual with the poor concordance rate was an outlier and the minimum genotype (allele) concordance rate excluding this individual was 0.920 (0.958). Mean genotype concordance rate per breed was 0.984, 0.972, 0.982, 0.969 and 0.989 for Belclare, Charollais, Suffolk, Texel and Vendeen, respectively. Imputation accuracy not accounting for pedigree was marginally better than when pedigree was accounted for in the imputation process. Imputation accuracy with a reference population of only the breed of animal to be imputed was also marginally better than when multiple breeds were included in the reference population; imputation accuracy of breeds not represented in the reference population were considerably worse. The low density panel is therefore a useful, lower cost, strategy to achieve genomics evaluations in these sheep breeds.

Key Words: imputation, sheep, genomic, low density

0309 Systematic profiling of short tandem repeats in the cattle genome.

G. E. Liu*[1], L. Xu[1], R. Haasl[2], J. Sun[3], Y. Zhou[1], D. M. Bickhart[4], J. Li[5], J. Song[6], T. Sonstegard[7], C. P. VanTassell[1], and H. Lewin[8], *[1]Animal Genomics and Improvement Laboratory, USDA-ARS, Beltsville, MD, [2]University of Wisconsin, Platteville, [3]South China Agricultural University, Guangzhou, [4]Animal Genomics and Improvement Laboratory, USDA-ARS, Beltsville, MD, [5]Institute of Animal Science of Chinese Academy of Agricultural Sciences, Beijing, China, [6]University of Maryland, Animal Science and Avian, College Park, [7]Recombinetics Inc., St Paul, MN, [8]University of California, Department of Evolution and Ecology, Davis.*

Short tandem repeats (STRs), or microsatellites (MS), are genetic variants with repetitive 2–6 base pair motifs in many genomes. Using high-throughput sequencing and experimental validations, we systematically profiled STRs in five Holsteins. We identified a total of 60,106 microsatellites and generated the first high-resolution STR map, representing a substantial pool of polymorphism in cattle. We observed significant STR overlaps with RefSeq genes and quantitative trait loci (QTL). We performed evolutionary and population genetic analyses using over 20,000 common dinucleotide STRs. Besides corroborating the well-established positive correlation between allele size and variance in allele size, these analyses also identified dozens of outlier STRs based on two anomalous relationships that counter expected characteristics of neutral evolution. And one STR locus overlaps with a significant region of a summary statistic designed to detect STR-related selection. Additionally, we showed that only 57.1% of STRs are located within SNP-based linkage disequilibrium (LD) blocks while the other 42.9% are not. Therefore, a substantial number of STRs are not tagged by SNPs in the cattle genome, likely due to STR's distinct mutation mechanism and elevated polymorphism. This study provides the foundation for future

STR-based studies of cattle genome evolution and selection.

Key Words: cattle genome, short tandem repeat (STR), whole genome sequencing (WGS)

0310 Assessing genetic diversity in Canadian beef cattle populations using Illumina BovineSNP50 chip.

M. K. Abo-Ismail*[1,2], E. C. Akanno[1], R. Khorshidi[1], J. Crowley[1,3], L. Chen[1], B. K. Karisa[4], X. Li[1], Z. Wang[1], J. Basarab[1,5], C. Li[1,6], P. Stothard[1], and G. Plastow[1], *[1]Livestock Gentec, Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Canada, [2]Animal and Poultry Production, Damanhour University, Egypt, [3]Canadian Beef Breeds Council, Calgary, AB, [4]Alberta Livestock and Meat Agency Ltd, Edmonton, Canada, [5]Lacombe Research Centre, Alberta Agriculture and Forestry, Lacombe, Canada, [6]Lacombe Research and Development Centre, Agriculture and Agri-Food Canada, Edmonton, AB, Canada.*

The main objective of this study was to utilize genomic profiles to assess genetic diversity within and between Canadian beef cattle populations to gain insights on population admixture and dynamics. Individuals (n = 2831) were genotyped for Illumina BovineSNP50 for 9 populations (Gelbvieh (GVH, n = 488), Charolais (CHA, n = 396), Angus (AAN, n = 492), Simmental (SIM, n = 404), Limousin (LIM, n = 205), Hereford (HER, n = 591), Hays Converter (HC, n = 208), Kinsella composites (KC, n = 15) and Lacombe Research Centre (LRC, n = 33). A total of 2828 individuals with 43,172 SNPs across 29 autosomes passed quality control and were used for further analyses. To study population structure between populations, a principal component analysis (PCA) was performed using SNP1101 software. Genomic inbreeding coefficients for each individual were estimated using 4 methods; VanRaden 2008 (F_v), Leutenegger 2003 (F_l), excess of homozygosity (F_h) and GCTA software (F_g) method implemented in SNP1101 software. The PCA analysis reported clear divergence between GVH, CH, AAN, SIM, LIM, HER and HC populations where 7 clusters were well defined, illustrated in Fig. 1. The KC and LRC populations are distributed between the other clusters confirming their genetic architectures as crossbred. The most genomically divergent breeds were CHA, AAN, GVH and HER. The correlations between inbreeding coefficients F_v with F_l and F_g were strong; 0.98 and 0.93, respectively. The average estimate of genomic inbreeding coefficients (F_v, Fl, and Fg) were highest for the HER ranged from 12.8 ± 0.1to 18.5 ± 0.2% followed by AAN ranged from 10 ± 0.1 to 12.7 ± 0.1%. In addition, the genomic inbreeding coefficients for composites/crossbreds ranged from 2.0 ± 1.0 to 4.0 ± 1.0% and from 1.0 ± 0.7 to 7.0 ± 1.0% for KC and LRC, respectively, where these inbreeding levels were low across all methods compared with purebred cattle. In conclusion, the genomic assessment of inbreeding using different methods indicated that HER and AAN breeds had the highest inbreeding level and thus inbreeding depression should be assessed for their traits at the genome level. Information on specific regions that are fixed for deleterious alleles allows directed introgres-

Fig 0310.

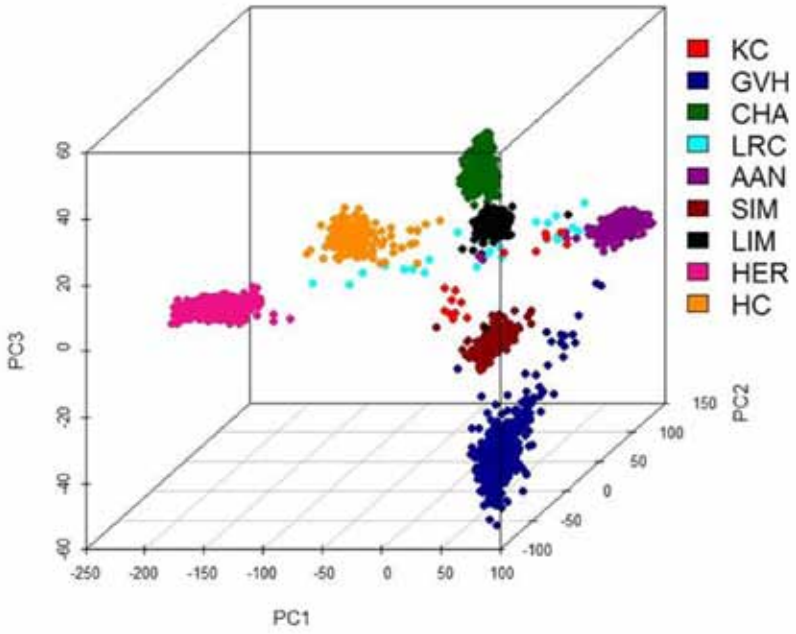

Figure 1. Population structures identified by principal component analysis. The plot shows the first three principal components (PCs) using Illumina BovineSNP50 (43,172 SNPs) across the 29 autosomes. KC is Kinsella composites, LRC is Lacombe Research Centre, GVH is Gelbvieh, CHA is Charolais, ANG is Angus, SIM is Simmental, LIM is Limousin, HER is Hereford, HC is Hays Converter.

sion between breeds to help address performance.

Key Words: genetic diversity, inbreeding, single nucleotide polymorphism, Canadian beef cattle

0311 Joint association analysis of additive and non-additive genomic effects for growth and carcass traits of beef cattle. E. C. Akanno*[1], M. K. Abo-Ismail[1,2], L. Chen[1], C. Li[1,3], J. Basarab[1,4], and G. Plastow[1], *[1]Livestock Gentec, Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Canada, [2]Animal and Poultry Production, Damanhour University, Egypt, [3]Lacombe Research and Development Centre, Agriculture and Agri-Food Canada, Edmonton, AB, Canada, [4]Lacombe Research Centre, Alberta Agriculture and Forestry, Lacombe, Canada.*

The biological dominance effects of genes have been suggested as one of the genetic mechanism explaining heterosis. We performed a joint association analysis using genotypes from Illumina BovineSNP50 (50K) BeadChip to evaluate the contributions of additive and dominance genomic effects to the variance of growth and carcass traits in beef cattle and to identify genomic regions that potentially harbor genes or quantitative trait loci underlying the variation. A total of 6794 multi-breed and crossbred beef cattle with phenotype and 50K genotypes were used. Traits studied included birth weight (BWT), weaning weight (WWT), pre-weaning daily gain (PDG), average daily gain (ADG), yearling weight (YWT), hot carcass weight (HCW), back fat thickness (BFT), rib-eye area (REA), marbling score (MS), lean meat yield (LMY) and yield grade (YG). Additive and dominance genomic relationships were created based on 42,610 single nucleotide polymorphism (SNP) markers that passed the quality control. The model used accounted for fixed contemporary group effects (herd, year, data source, and sex), covariates of genomic breed composition, age of dam, weaning age, age at start of feedlot test, and slaughter age, and random maternal and maternal permanent effect depending on the trait analyzed. A single SNP analysis that partitions the SNP effects into additive and dominance components was used for genome-wide association. The proportions of total phenotypic variance explained by additive and dominance effects for the studied traits are presented in Table 1. After applying a false discovery rate at a 5% significance level, a total of 66, 20, 2, 36, 66, 22, 9, 15, 10, and 3 SNPs were significantly associated with BWT, WWT, PDG, ADG, YWT, HCW, BFT, REA, LMY, and YG, respectively, for the additive component. For the dominance component, three SNPs (rs110564527, rs110361335, and rs41663796) and one SNP (rs43624164) were significantly associated with MS and WWT, respectively. The SNP rs110361335 located on chromosome 4 was found to be within *islet cell autoantigen 1* (*ICA1*) gene which is involved in insulin regulation. In addition, SNP rs43624164 on chromosome 10 found to be near the gene *ribosomal protein L10-like* (*RPL10L*) had significant additive and dominance effects on WWT. Although, the proportions of phenotypic variance explained by dominance were moderate for growth traits with known heterosis effects, the results of this study suggest that dominance effects are polygenic.

Key Words: beef cattle, dominance genetic effect, genomic prediction

0312 Investigation of genomic imprinting through allelic expression analysis of mRNA in chicken embryonic brain and liver. Z. Zhuo[1], S. J. Lamont[2], and B. Abasht*[1], *[1]Department of Animal and Food Sciences, University of Delaware, Newark, [2]Department of Animal Science, Iowa State University, Ames.*

Genomic imprinting refers to the epigenetic phenomenon that some autosomal genes are exclusively expressed from either the maternal or paternal allele whereas, based on Mendelian inheritance, expression of alleles are expected to be in

Table 0311.

Table 1. Proportions of phenotypic variance explained by additive and dominance effects in purebreds, crossbreds and overall populations[1]

	Purebreds (n = 2060)		Crossbreds (n = 4734)		Overall (n = 6794)	
Traits	Additive	Dominance	Additive	Dominance	Additive	Dominance
Birth weight, kg	0.54±0.053	0.21±0.066	0.56±0.034	0.10±0.043	0.51±0.026	0.08±0.028
Weaning weight, kg	0.21±0.052	0.25±0.081	0.34±0.031	0.03±0.039	0.30±0.024	0.06±0.027
Pre-weaning daily gain, kg/d	0.31±0.055	0.21±0.069	0.35±0.035	0.04±0.049	0.27±0.026	0.07±0.031
Average daily gain, kg/d	0.27±0.048	0.01±0.078	0.33±0.029	0.01±0.038	0.30±0.023	0.02±0.026
Yearling weight, kg	0.47±0.050	0.12±0.073	0.56±0.029	0.10±0.038	0.47±0.023	0.08±0.026
Hot carcass weight, kg	0.29±0.066	0.05±0.125	0.44±0.042	0.00±0.000	0.43±0.035	0.00±0.000
Back fat thickness, mm	0.48±0.070	0.00±0.000	0.23±0.039	0.01±0.070	0.31±0.036	0.01±0.054
Rib eye area, cm^2	0.40±0.069	0.11±0.133	0.40±0.041	0.00±0.000	0.41±0.036	0.00±0.000
Marbling score	0.32±0.066	0.00±0.000	0.35±0.041	0.13±0.067	0.32±0.035	0.00±0.000
Lean meat yield, %	0.45±0.070	0.03±0.125	0.30±0.040	0.03±0.067	0.37±0.036	0.05±0.053
Yield grade	0.43±0.071	0.10±0.129	0.32±0.041	0.05±0.068	0.39±0.036	0.03±0.053

[1]Purebred individuals have > 90% of their representative breeds (Angus, Hereford and Charolais); Crossbred individuals included beef-dairy hybrids, Beefbooster composite (www.beefbooster.com), and two and three way crossbreds involving Angus, Hereford, Charolais, Gelbvieh, Simmental, Limousine, and Piedmontese

equal amount and independent of their parental origin. DNA methylation in *cis*-acting manner is the major mechanism for genomic imprinting. Imprinted genes have been identified in several animal species and are frequently associated with embryonic growth and survival functions. Yet whether genomic imprinting exists in chickens is still debatable, as previous studies reported conflicting evidence regarding the topic. Albeit no genomic imprinting has been found in the chicken embryo as a whole, we investigated whether certain embryonic tissues exhibit genomic imprinting. In this study we interrogated the existence or absence of genomic imprinting in chicken embryonic brain and liver by examining the mRNA expression of parental alleles in an F1 generation. Eggs from two highly inbred chicken lines (Fayoumi and Leghorn) and their reciprocal crosses were collected and incubated for 12 d; then brain and liver were harvested from embryos for cDNA library preparation. To establish the genotypes of the inbred lines and the F1 hybrids and to minimize reference bias of RNA-seq sequence alignment, genomic DNA from inbred Fayoumi and Leghorn chickens was pooled separately and each pool was sequenced at 20X coverage. The SNP loci identified from DNA-Seq data were masked to create a customized reference genome (based on Ensembl Galgal4) for RNA-seq reads mapping. Of 65 million RNA-seq reads per sample generated using the Illumina HiSeq 2000 sequencer, 88% were mapped to the customized reference genome. The genome-wide ratio of mapped reads containing reference allele was reduced by 1.5% when comparing with the results from the original reference genome. Our analyses indicated that genomic imprinting is absent in chicken 12-d embryonic brain and liver. In genome-wide and chromosome-wide scales, we observed a balanced expression of maternal and paternal alleles. About 9.2% of the heterozygous loci showed allele specific expression independent of their parental origin (binominal test, p value $\leq$ 0.05). Certain alleles showed consistent expression pattern across all 8 F1 individuals indicating possible presence of *cis*-acting regulatory mutations or epigenetic modifications influencing expression of these alleles.

Key Words: genomic imprinting, chicken, RNA-seq

0313 Identification of causative genomic region for carcass weights of cattle. H. Chung*, *National Institute of Animal Science, Wanju, Korea (The Republic of)*.

The present analysis was designed to find causative genomic regions for carcass weights according to the recent requirements of farms. A total of 5000 Hanwoo cattle, which were registered in the national database, were slaughtered to measure carcass weights and extract DNA samples. Animals were genotyped with customized 56K Affymetrix SNP chips to identify genomic regions regarding carcass weight. The chip contained previously reported genetic variants, including QTL analyses from the literature reviews for meat quality traits from various cattle breeds in the world. Genome-wide association studies (GWAS) found significant genotypic effects for carcass weights in the genomic region (26254142 to 26274142 Mb) on the bovine chromosome 14 based on UMD3.1. To confirm significance for the identified SNP, 3700 animals were additionally slaughtered and genotyped, and as results, the 20 SNP presented extreme significant associations for carcass weights. The identified genomic regions with SNP may be used in marker-assisted selection programs to improve carcass weights in beef cattle.

Key Words: SNP, carcass weight, QTL

0314 Introgression of the Belgian Blue Myostatin variant into Nellore cattle: Effects of double muscling on birth weight and calving ease. G. Nogueira*[1], K. S. Paulussi[2], A. T. H. Utsunomiya[3], Y. T. Utsunomiya[3], A. Almeida[4], A. Tanuri[5], T. Santos[4], and R. Alonso[6], *[1]UNESP, Aracatuba-SP, Brazil, [2]UNESP, Araçatuba, Brazil, [3]UNESP Univ. Estadual Paulista, Jaboticabal, Brazil, [4]Deoxi, Aracatuba-SP, Brazil, [5]UFRRJ, Rio de Janeiro-RJ, Brazil, [6]Deoxi, Aracatuba-SP, Brazil.*

Introgression and backcrossing are powerful strategies to insert a specific segment of the genome expressing a desirable trait from a population to another and recover the original genetic background, respectively. The aim of this work is to present the effect of introgression of myostatin mutation on birth weight in Nellore cattle (*Bos indicus*). We evaluated 92 calves 15/16 Nellore, offspring of one purebred Nellore and two 7/8 crossbred (Nellore x Belgian Blue) bulls. All animals were genotyped to identify the ones carrying the myostatin mutation (BN– heterozygous for the mutation, NN– homozygous for the absence of mutation). The birth weight was analyzed in a mixed model framework, fitted by restricted maximum likelihood (REML) using lme4 package in R, including sex, biotechnology of reproduction (FTAI-fixed-time artificial insemination x FTET-fixed-time embryo transfer) and myostatin mutation as fixed effect and sire as random effect. Thirty-nine calves were identified as heterozigous for the mutation (BN) and 53 as homozygous for absence of mutation (NN). Heterozygous calves were born 4.92 ± 0.998 kg heavier (p-value = 1.6e-6) compared with the homozygous. No differences were found comparing FTAI (34.12 kg) and FTET (35.50 kg) (p-value = 0.126). Although not significant, males were born 1.76 ± 1.01 kg heavier than females (p-value = 0.083). Considering the random term of the mixed model, only 0.34% of the phenotypic variance was explained by sire effect. In summary, these results show that the effect of the myostatin mutation is the main factor regulating differences in birth weight. Despite to be expected, dystocia was not an issue in this study. Future analysis will comprise homozygous individuals for the presence of myostatin mutation (BB) and

its impact on birth weight and parturition.

Key Words: Nellore, double muscling, birth weight

0315 Genomic-polygenic and polygenic parameters and prediction trends for growth and reproduction traits in an Angus-Brahman multibreed population. M. A. Elzo*[1], R. Mateescu[1], M. G. Thomas[2], D. D. Johnson[1], D. O. Rae[1], J. D. Wasdin[1], M. D. Driver[1], and J. D. Driver[1], *[1]University of Florida, Gainesville, [2]Department of Animal Sciences, Colorado State University, Fort Collins.*

The objectives of this research were to estimate genomic-polygenic and polygenic parameters and to evaluate prediction trends as Brahman fraction increased from 0% to 100% in an Angus-Brahman multibreed population for 305-d yearling weight (YW), yearling reproductive tract score (RTS), age at first calving (AFC), and first calving interval (FCI) using single-step genomic-polygenic (GPM) and polygenic models (PM). Phenotype records were 1758 for YW, 381 for RTS, 1385 for AFC, and 985 for FCI. The pedigree file had 6845 calves, sires, and dams, and the genotype file contained 115,711 actual and imputed Illumina150k SNP markers from 1547 animals. The 4-trait GPM and PM included contemporary group, age of dam (YW only), sex of calf (YW only), direct heterosis, maternal heterosis (YW only) as fixed effects, and animal and residual as random effects. Genetic parameters were estimated using REML procedures and computed using AIREMLF90. Heritabilities were somewhat higher for GPM than for PM (0.47 vs. 0.45 for YW, 0.31 vs. 0.30 for RTS, 0.14 vs. 0.12 for AFC, and 0.31 vs. 0.29 for FCI). Genetic correlations were positive between YW and RTS (GPM: 0.55; PM: 0.60), negative between RTS and AFC (GPM: −0.22; PM: −0.55) and between AFC and FCI (GPM: −0.68; PM: −0.67), and near zero for all other trait pairs. The similarity between GPM and PM heritabilities and genetic correlations indicated that the 115,711 Illumina150k SNP markers added little additional information to that contained in the pedigree. Regression coefficients of breed group EBV means on Brahman fraction were negative ($P < 0.0005$) for YW, RTS, and FCI, and positive ($P < 0.0001$) for AFC as Brahman fraction increased. This indicated that heifers with higher Brahman percentages tended to be lighter and less mature as yearlings, older at first calving, and have shorter FCI than heifers with higher Angus percentages in this population. Regression coefficients of individual animal EBV on Brahman fraction showed similar trends, but were smaller, guaranteeing the existence of animals with high, medium, and low EBV across all Brahman percentages.

Key Words: cattle, genomic, reproduction

0316 Genome-enabled prediction of genetic values of growth traits using artificial neural networks. S. O. Peters*[1], M. Sinecen[2], M. G. Thomas[3], I. G. Imumorin[4], and K. Kizilkaya[2], *[1]Department of Animal Science, Berry College, Mount Berry, GA, [2]Adnan Menderes University, Aydin, Turkey, [3]Department of Animal Sciences, Colorado State University, Fort Collins, [4]Animal Genetics and Genomics Laboratory, Cornell University, Ithaca, NY.*

Data from Brangus heifers (3/8 Brahman-*Bos indicus* × 5/8 Angus-*Bos taurus;* n ≈ 743) registered with International Brangus Breeders Association were analyzed to predict genetic parameters of growth traits. Phenotypes included body weights collected at birth (birth weight), ~205 (weaning) and 365 (yearling) days of age. Genotypes were from BovineSNP50 (Infinium BeadChip, Illumina, San Diego, CA; 53,692 SNP). Artificial neural networks (ANN) have been used for marker-based genomic predictions of complex traits in animal and plant breeding. In this study, ANN was used to estimate the genetic values of growth traits of birth weight, weaning weight and yearling weight of Brangus heifers with all genome-wide marker data set and chromosome-base genome-wide marker data set. ANN provide nonlinear relationships between inputs and outputs with the interplay among variables learned adaptively. For the ANN model, 95% of the animals were randomly allocated to a training set, 5% to a test set. In the training phase of ANN with the scaled conjugate gradient method, 52,640 SNP as the genomic covariates of 706 individuals are linearly combined with a vector of weights. The resulting linear score were then transformed using an activation function to produce the output of ANN. Different ANN architectures were examined to assess the best predictive ANN. Up to 30 neurons in the hidden layer were tested for their influence on predictive quality. ANN models with 13, 15, and 1 neurons in the hidden layer were used for birth weight, weaning weight and yearling weight of Brangus heifers. ANN model including chromosome-base genome-wide markers achieved predictive correlations of $r = 0.96$ for birth weight using chromosome 23, $r = 0.94$ for weaning weight using chromosome 17 and $r = 0.92$ for yearling weight using chromosome 1. ANN model including all genome-wide markers achieved predictive correlations of $r = 0.93$ for birth weight, $r = 0.91$ for weaning weight and $r = 0.91$ for yearling weight. Results suggest that neural networks may be useful for predicting complex traits using high-dimensional genomic information.

Key Words: artificial neural network, genomic prediction, growth traits, SNP

0317 Molecular breeding values distribution in slick male and female Senepol cattle differing in musculature. C. L. González-Berríos*[1], A. Rivera-Serrano[1], A. Casas-Guérnica[1], T. Sonstegard[2], and M. Pagán-Morales[1], [1]*Department of Animal Science, University of Puerto Rico, Mayaguez, Puerto Rico,* [2]*Recombinetics Inc., St. Paul, MN.*

Recently, the polymorphisms responsible for double muscling [MSTN: exon 3 11bp indel (NT821)] and slick coat phenotype (PRLR: exon 10 cytosine indel) in Senepol cattle were described. However, the genomic implications of segregating animals according to PRLR and MSTN genotypes have not been elucidated for economically relevant traits (ERTs), especially in tropically adapted beef cattle. Thus, purebred Senepol cattle (males/females) were genotyped for both indel and molecular breeding values (MBV) were obtained through a commercially available marker panel (Igenity, Neogen Corp.). Three MBV categories were established: low (L), intermediate (I) and high (H) based on standard deviations of +1 (L), +2 (I) or +3 (H) from the average MBV for 12 ERTs. Statistical differences were determined using the Chi^2 test [sex, genotype (MSTN; PRLR) and double and triple combinations]. Genotypic proportions observed were: double muscle (DM): 6/NT821-NT821, 95/NT821-WT, and normal musculature (NM): 273 WT-WT ($P < 0.0001$) and slick coat (SC): 256/BB, 99/BA, and normal coat (NC): 4 = AA ($P < 0.0001$). Proportional differences were observed within BB for MBV-average daily gain between MSTN genotypes: NT821/WT: (11.76 H, 72.06 I, 16.18 L) and NM: (26.06 H, 53.72 I, 20.21 L) ($P < 0.05$). Also, within BB, differences in MBV categories distribution were: males: (20.90 H, 79.10 I, 0.00 L)/females: (33.33 H, 56.08 I, 10.58 L) and females: (16.93 H, 68.78 I, 14.29 L)/males: (4.48 H, 77.61 I, 17.91 L) for average daily gain and calving ease, respectively ($P < 0.05$). Significant differences in MBV-tenderness were observed within females for: NT821/WT (7.46% H, 68.66% I, 23.88% L) and NM: (14.22% H, 73.04% I, 12.75% L) ($P < 0.05$). Moreover, females BB ($n = 189$) significantly differed in MBV category distribution depending on musculature for: residual feed intake [NT821/WT: (26.83 H, 68.29 I, 4.88 L)/NM: (18.92 H, 60.14 I, 20.95 L), yield grade [NT821/WT: (24.39 H, 70.73 I, 4.88 L)/NM: (14.19 H, 66.89 I, 18.92 L)], backfat thickness [NT821/WT: (57.14 H, 38.10 I, 4.76 L)/NM: (27.70 H, 50.0 I, 22.30 L)], pregnancy rate [NT821/WT: (4.88 H, 78.05 I, 17.07 L)/NM:(25.00 H, 66.22 I, 8.78 L)] and Stayability [NT821/WT: (9.76 H, 63.41 I, 26.83 L)/NM: (18.24 H, 70.27 I, 11.49 L)] ($P < 0.05$). In the present study, a higher proportion of Senepol cattle with SC and NM were observed and intermediate MBV for all ERTs were predominant, with the exception of backfat thickness (NT821/WT-BB-Females). Therefore, genomic selection in slick Senepols segregating MSTN alleles are needed to improve their ERTs-MBV.

Key Words: slick, myostatin, Senepol

0318 PRUNE2 gene has a potential effect on residual feed intake in Nellore cattle. A. O. D. Lima[1], P. S. N. Oliveira*[2], P. C. Tizioto[2], A. L. Somavilla[3], W. J. S. Diniz[1], J. V. D. Silva[1], S. C. S. Andrade[4], C. Boschiero[5], A. S. M. Cesar[6], M. M. Souza[7], M. I. P. Rocha[1], J. Afonso[1], C. E. Buss[1], M. A. Mudadu[8], G. B. Mourao[5], L. L. Coutinho[6], and L. C. A. Regitano[9], [1]*Federal University of São Carlos, São Carlos, Brazil,* [2]*Embrapa Southeast Livestock, São Carlos, Brazil,* [3]*Universidade Estadual Paulista "Júlio de Mesquita Filho," Jaboticabal, Brazil,* [4]*Genetics and Evolutionary Biology Department-IB, University of São Paulo, Brazil,* [5]*Department of Animal Science, University of São Paulo/ESALQ, Piracicaba, Brazil,* [6]*Animal Biotechnology Laboratory-ESALQ, University of São Paulo, Piracicaba, Brazil,* [7]*Federal University of São Carlos, Brazil,* [8]*Embrapa Pecuária Sudeste, São Carlos, Brazil,* [9]*Embrapa Southeast Livestock, São Carlos, Brazil.*

Residual feed intake (RFI) can increase the profitability of producers, reduce methane emission and land allocation to livestock production. However, this trait has late and costly measurements. Identifying gene expression changes combined with polymorphisms that affect residual feed intake variation is important for identify target regulatory polymorphisms that can be used in animal breeding programs. Diverse studies performed by our research group in a Nellore population, such as genome-wide association (GWA), association weight matrix (AWM) and RNA-seq analysis of liver tissue have been pointed *Prune homolog 2 (Drosophila) (PRUNE2*) as a potential candidate gene influencing feed efficiency. For this reason, we select this gene for a more detailed analysis considering haplotypes consisting of SNPs presented in the *Illumina Bovine HD Bead Chip.* For this, we used a population consisted of 591 steers with genotypes and RFI estimates available. After quality control filtering, performed by PLINK and Bioconductor/R, we used a total of 449.203 SNPs in our haplotype analysis. Genotype phasing and missing genotype imputation were performed using BEAGLE and the LDexplorer software was used for haplotype block recognition. After adjust the RFI estimates for fixed effects of contemporary group, which included type of pen, birth place, feedlot location and age of the animal effect as covariate, the genetic effects of haplotypes in *PRUNE2* gene was estimated by PLINK using a linear regression method. We identified 1 haplotype constituted of 4 SNPs: rs136298898 (C/T); rs133593644 (C/T); rs137799737 (A/C); rs132675549 (C/T), for which two out of 4 haplotype combinations had significant effect ($P \leq 0.05$) on RFI. Haplotype variation (1111) (p-value

= 0.0345) with 35.29% frequency was associated to lower RFI ($\beta = -0.0776$). On the other hand, haplotype variation (1112) (p-value = 0.0351) presenting 11.13% frequency was associated with high RFI ($\beta = 0.0846$). The *PRUNE2*gene has a potential role in biological processes, such as oxidation–reduction, metal ion and polyphosphate catabolic. Our findings indicated that this gene influence genetic variation of RFI, it is a strong candidate gene to be incorporated in Nellore breeding programs, nevertheless more studies considering this gene should be realized to understand better its biological role on feed efficiency in beef cattle.

Key Words: haplotype, feed efficiency, functional gene enrichment

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0319 A genome-wide association study for changes in dry matter intake due to temperature variation in an admixed beef cattle population. R. Ghebrewold[*1] and M. L. Spangler[2], *[1]University of Nebraska, Lincoln, [2]University of Nebraska, Lincoln.*

Environmental conditions, such as changes in ambient temperature, can cause changes in animal behavior and performance. In general it is believed that as ambient temperature increases, dry matter intake (DMI) of beef cattle decreases. However, our hypothesis was that the degree to which animals adjust their daily DMI due to changes in ambient temperature is partially controlled by underlying genetic effects. Consequently, the objective of this study was to estimate the genetic component of the regression of DMI on ambient temperature using an admixed beef cattle population consisting of various crosses of Angus, Simmental, and Piedmontese (n = 207). Ambient temperatures were received from a local weather station and DMI was collected via Calen gates. The feeding period averaged 155 d with a range of 114 d to 189 d depending on the management group. Individual animal regressions of DMI on ambient temperature were performed using either daily high or low temperatures over the entirety of the feeding period. Daily high temperatures (°C) averaged 15.07 with a range of −17.21 to 38.25. Daily low temperatures (°C) averaged 2.37 with a range of −28.33 to 15.26. The corresponding intercept and regression coefficient for each animal were used as phenotypes for a genome-wide association study (GWAS). Animals were genotyped with the BovineSNP50 Beadchip. Data were analyzed using GenSel software and a BayesC model fitting contemporary group (n = 4) and initial body weight (IBW) as fixed effects. A MCMC chain of 100,000 iterations was used with the first 40,000 samples discarded as burn-in. The proportion of SNPs having null effect (π) was set to 0.995. Posterior mean heritability estimates (SD) for the analysis when daily high temperature was considered in the regression were 0.64 (0.07) and 0.46 (0.08), for the intercept and slope, respectively. Similarly, posterior mean heritability estimates (SD) for the intercept and slope when the daily low temperature was considered in the regression were 0.69 (0.06) and 0.52 (0.07), respectively. These results suggest that changes in DMI due to changes in ambient temperature are under genetic control. Admittedly the population under study is small and admixed, suggesting that the genomic heritability estimates contained herein are potentially biased upward. However, the concept of applying this same procedure in larger populations warrants further investigation as a means of identifying animals that are less sensitive to environmental extremes.

Key Words: beef cattle, GWAS, feed intake

0320 An international effort to improve feed efficiency and reduce methane emissions in dairy cows through genomics. A. M. Wilson[*1], A. M. Butty[1], C. Baes[1], A. Cánovas[1], M. P. Coffey[2], E. E. Connor[3], M. De Pauw[4], B. Gredler[5], E. Goddard[4], G. Hailu[6], V. R. Osborne[7], J. E. Pryce[8], M. Sargolzaei[1,9], F. S. Schenkel[1], P. Stothard[10], E. Wall[2], Z. Wang[4], T. C. Wright[7,11], and F. Miglior[1,12], *[1]Centre for Genetic Improvement of Livestock, Department of Animal Biosciences, University of Guelph, ON, Canada, [2]SRUC, Edinburgh, UK, [3]USDA-ARS, Animal Genomics and Improvement Laboratory, Beltsville, MD, [4]University of Alberta, Edmonton, Canada, [5]Qualitas AG, Zug, Switzerland, [6]Department of Food, Agricultural and Resource Economics, University of Guelph, ON, Canada, [7]University of Guelph, ON, Canada, [8]Department of Economic Development, Jobs, Transport and Resources, Bundoora, Australia, [9]Semex Alliance, Guelph, ON, Canada, [10]Livestock Gentec, Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Canada, [11]Ontario Ministry of Agriculture, Food and Rural Affairs, Guelph, ON, Canada, [12]Canadian Dairy Network, Guelph, ON.*

Increasing international demand for high quality dairy and meat products as well as greater awareness of climate change has put pressure on the livestock industry to deliver quality products while reducing its environmental impact. Enteric methane from cattle is a major contributor to greenhouse gas emissions and is a target of reduction through improving cow feed efficiency (FE) and reducing methane emissions (ME). The overall goal of this project is to produce genomic predictions for FE and ME that are ready for breeding application in the dairy cattle industry. Breeding for improved FE and less methane emitted will lower feed costs and reduce the industry's environmental footprint. Collecting phenotypes required for genetic improvement is presently very difficult and expensive, and to date, there has been limited to no direct selection for these traits in dairy cattle breeding. Recent genomic approaches provide the opportunity to finally select for these traits, but require a large reference population with accurate phenotypes. Data of individual feed intake and ME are being

collected from dairy cows and heifers, and whole DNA (Genome) and RNA (Transcriptome) sequence information will be used to identify new markers or mutations that influence the traits. The expanded Canadian database will be combined with international data from the United States, UK, Australia and Switzerland to create the world's first database to routinely validate genomic predictions for FE and ME. Milk spectral records will also be used to further develop predictions of FE and ME. In addition, research will be conducted to analyze the economic, environmental and social costs and benefits of the two traits, as well as the economic and social factors affecting the adoption of the technology at farm, industry and national levels.

Key Words: feed efficiency, methane emissions, dairy cattle

0321 Effect of diet energy level and genomic residual feed intake on dairy heifer performance.

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The objective of this study was to determine growth, feed intake, and feed efficiency of dairy heifers with different genomic residual feed intake (RFI) predicted as a lactating cow and offered diets differing in energy density. Post-bred Holstein heifers (128, ages 14–20 mo), were blocked by initial weight (high, medium-high, medium-low, and low weight) with 32 heifers per block. Each weight block was sorted by RFI (high, low) to obtain 2 pens of high and 2 pens of low predicted RFI for each block (8 heifers per pen). Low RFI heifers were expected to have greater feed efficiency than high RFI heifers. Dietary treatments were (1) a control diet with corn silage and alfalfa haylage (CON; 62.7% TDN, 11.8% CP, and 45.6% NDF, DM basis), and (2) a similar diet diluted with straw to reduce energy density (STR; 55.9% TDN, 11.7% CP, and 50.1% NDF, DM basis). Each treatment was randomly allocated to blocks to obtain a 2x2 factorial treatment arrangement of 2 RFI levels and 2 dietary energy levels. Diets were offered in a 120-d trial. Statistical analyses were performed using a MIXED procedure in SAS 9.3 with pen as experimental unit. Dry matter intake was affected by diet (11.0 vs. 10.0 kg/d for CON and STR, respectively; $P < 0.01$) but not RFI or the interaction of main effects ($P > 0.10$). Average daily gain was affected by the interaction of RFI and diet with low RFI heifers having higher gains than high RFI when fed STR (0.94 vs. 0.84 kg/d for low and high RFI, respectively, $P = 0.02$), but no difference for RFI groups when fed CON ($P = 0.25$). Feed efficiency was better for low RFI than high RFI heifers when fed STR (10.6 vs. 11.8 kg feed/kg gain for high and low RFI, respectively; $P < 0.01$), but no effect of RFI found when fed CON ($P > 0.10$). Body condition score increased when fed CON (3.8 vs. 3.5 for CON and STR, respectively; $P = 0.02$). Diet digestibility was greater for CON (58.4 vs. 50.8% DM digestibility for CON and STR, respectively; $P = 0.01$), which likely caused greater intake and gains for heifers fed CON. Based on these results, feed efficiency of heifers having different RFI is dependent on diet energy level with heifers having low RFI using the moderate energy (STR) diet more efficiently. The straw diet reduced intake and also maintained more desirable heifer weight gains.

Key Words: dairy heifer, residual feed intake, diet energy

0322 Genomic prediction for feed efficiency traits based on 50K and imputed high density SNP genotypes in multiple breed populations of Canadian beef cattle.

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Phenotypic data of difficult and/or costly to measure traits, such as feed efficiency, are usually available for a small number of beef cattle in each breed/population, resulting in low accuracy when within-breed/population genomic selection is attempted. Investigation of different strategies to combine data has the potential to improve the genomic prediction accuracy. In this study, we consolidated data of residual feed intake (RFI), average daily gain (ADG) and daily feed intake (DMI) from 7479 animals. These animals consisted of Canadian Angus ($N = 1158$), Charolais ($N = 707$), and four crossbred populations including Kinsella (UofAlberta, $N = 1487$), Elora (UofGuelph, $N = 746$), commercial animals PG1 ($N = 1885$) and TX ($N = 1496$). SNPs from the Illumina Bovine SNP50 Beadchip (50K SNP chip) and imputed Affymetrix high density (HD) (~428K SNPs) were employed to evaluate the genomic prediction accuracy at five-fold cross-validation using single-task Bayesian, simple data pooling Bayesian, and multitask Bayesian methods. The single-task Bayesian method estimates the SNP effects within a breed/population. The simple data pooling Bayesian method assumes the same SNP effect across breeds/populations and estimates the SNP effects based on the training data set that are simply combined from

all breeds/populations. The multitask Bayesian method estimates the SNP effects for each breed/population by also utilizing SNP effect information from other breeds/populations. The results showed that realized prediction accuracy of the single-task Bayesian method with the 50K SNP chip for RFI ranged from 0.22 ± 0.04 for Elora to 0.65 ± 0.03 for Angus. For ADG and DMI, the realized prediction accuracy of the single-task Bayesian ranged from 0.21 ± 0.03 for ADG in the Kinsella and TX populations to 0.57 ± 0.03 for DMI in Angus. The genomic prediction accuracies were improved by 0.02 to 0.17 with the simple data pooling Bayesian method except for RFI, in which the prediction accuracies were similar or slightly reduced by 0.02 to 0.07. The multitask Bayesian method yielded better prediction accuracy than the single-task Bayesian for most of the traits but did not perform better than the simple data pooling Bayesian method. Genomic prediction based on the imputed HD SNPs resulted in similar accuracies to that of the 50K SNP chip under all three methods. Further studies that include SNP functional information and/or intermediate phenotypes are underway to improve the genomic prediction accuracy for feed efficiency traits in Canadian beef cattle.

Key Words: beef cattle, genomic prediction, feed efficiency

0323 Use of multivariate statistical analyses to preselect SNP markers for GWAS on residual feed intake in dairy cattle. C. Dimauro[*1], E. Manca[2], A. Rossoni[3], E. Santus[3], M. Cellesi[4], and G. Gaspa[5], *[1]Università di , Italy, [2]Università di Sassari, Italy, [3]ANARB, Italian Brown Cattle Breeders' Association, Bussolengo (VR), Italy, [4]Università di Sassari, Italy, [5]Dipartimento di Agraria, University of Sassari, Italy.*

An index currently used to evaluate feed efficiency in cattle is the residual feed intake (RFI) whose heritability is around 0.20–0.40. Genome wide association studies (GWAS) can contribute to breeding programs aimed at improving RFI by detecting genomic regions and candidate genes that regulate it. However, the detection of significant SNP in GWAS with high density SNP platforms is often hampered by the severity of Bonferroni's *p*-value correction for multiple testing, due to huge number of tests. The pre-selection of markers could be an option to mitigate this problem. In the present research, a multivariate approach was used to select a pool of markers that could have any chances to be associated with RFI. Data consisted of 1092 Brown Swiss young bulls genotyped with the Illumina's 50K BeadChip. Animals were divided into two groups, according to RFI: high RFI (HRFI) for RFI > 0.5 standard deviations from the mean RFI; low RFI (LRFI) for animals with RFI < – 0.5 standard deviations from the mean. The two groups consisted of 266 and 280 animals, for LRFI and HRFI, respectively. Individuals that did not belong to the two groups were discarded.Three multivariate discriminant techniques were applied to data. The stepwise discriminant analysis was used to select 152 genome-wide most discriminant markers that were retained for the further analyses. The canonical discriminant analysis significantly separated the LRFI from the HRFI group, and the extracted canonical function was able to correctly assign 92% of animals to the correct group. Canonical coefficients associated to the 152 SNP in the canonical function were useful to rank markers according to their discriminant power. The ability of the selected SNP in depicting the RFI profile of calves was tested by developing a k-means cluster analysis that correctly classified 84% of individuals. For instance, a GWAS was also developed by regressing RFI phenotypes on SNP covariates. After *p*-values were corrected for multiple testing, no significant marker was obtained by using all original variables (41,183). When only the selected 152 SNP were used, 5 significant markers were obtained.

Key Words: SNP preselection, discriminant analysis, RFI

0324 Breed base representation in dairy animals of five breeds. H. D. Norman[*1], P. M. VanRaden[2], J. H. Megonigal[1], J. W. Dürr[1], and T. A. Cooper[2], *[1]Council on Dairy Cattle Breeding, Bowie, MD, [2]Animal Genomics and Improvement Laboratory, USDA-ARS, Beltsville, MD.*

Inheritance of DNA from different dairy breeds can be determined by genotyping, just as individual ancestors such as parents, grandparents, or even great grandparents can be identified correctly in a high percentage of cases by genotyping even if not reported or reported incorrectly in pedigrees. Numbers of crossbreds in the U.S. dairy herd have increased by about 400% in the last decade. A procedure developed to determine the extent that alleles of various breeds appear in these crossbreds and in apparent purebreds was used to document breed composition in animals genotyped. The procedure constructed purebred reference groups (PRG) containing registered AI bulls (with milking daughters) chosen to represent 5 different breeds: Ayrshire (AY), Brown Swiss (BS), Guernsey (GU), Holstein (HO), and Jersey (JE). Any bull with an ancestor of another breed in his recorded 5-generation pedigree was excluded from the PRG. An exception was made for AY, for which other red breeds were permitted. The procedure was termed breed base representation (BBR) and estimated the similarity of alleles present in the 5 PRG to those of genotyped individuals. To measure BBR, the percentages of DNA contributed to a genotyped animal by each of the 5 breeds were calculated, summed, and then restricted to be between 0 and 100%. The more an animal's alleles resembled those in a PRG, the higher its BBR for that breed. The BBR help reveal the presence of either outcross bloodlines or crossbreeding, which are difficult to separate. Because animals vary even within breeds, the true source of the various breed alleles differs somewhat from BBR. Numbers of AI bulls in the reference populations in March 2016 were 442 AY, 5464

BS, 550 GU, 19,209 HO, and 3147 JE. Primary-breed BBR for those bulls were 97.2, 97.6, 97.8, 99.2, and 98.0%, respectively, which implies that they are purebreds; SD were 1.9, 1.2, 2.7, 1.2, and 1.0%, respectively. Mean primary-breed BBR were 94.8 for AY, 97.0 for BS, 97.8 for GU, 99.0 for HO, and 96.5% for JE for all genotyped males (201,283) and 95.0, 97.1, 96.9, 98.9, and 96.5%, respectively, for all genotyped females (994,949); SD ranged from 1.2 for males and 1.5% for females (HO) to 5.6 and 4.4% (AY), respectively. Genetic predictions for animals with crossbred genetics in their pedigrees could be obtained in the future by weighting marker effects from each breed by BBR.

Key Words: allele, genomics, purebred

0325 Estimation of the composition of four U.S. swine breeds using genomic data. S. A. Funkhouser[*1], R. O. Bates[2], C. W. Ernst[2], D. W. Newcom[3], and J. P. Steibel[2,4], *[1]Genetics Program, Michigan State University, East Lansing, [2]Department of Animal Science, Michigan State University, East Lansing, [3]National Swine Registry, West Lafayette, IN, [4]Department of Fisheries and Wildlife, Michigan State University, East Lansing.*

Lines of purebred pigs are essential for use in crossbreeding systems within the commercial industry. However, verification of breed purity can be challenging, and using color test matings to confirm white color in the Yorkshire or Landrace breeds is time-consuming and costly. Alternatively, advances in the availability and analysis of genomic data may enable rapid and precise determination of breed composition. Here, we have refined methods for determination of breed composition in U.S. populations of four swine breeds, and white color in Yorkshire or Landrace breeds using SNPs present on the GeneSeek Genomic Profiler for Porcine LD platform. These methods use a linear model in which unknown animal genotypes are regressed on a panel of allele frequencies, derived from reference Duroc, Landrace, Hampshire and Yorkshire purebred animals. Only SNPs that are not fixed across all reference animals and have a genotyping call rate of 90% or greater were used in the model. Model coefficients were constrained to be non-negative and to sum to 1.0, facilitating their interpretation as breed composition coefficients. By simulating 1000 admixed animals of known composition, a strong correlation was observed between the actual and estimated breed proportion of the simulated animals ($R^2 = 0.94$) so long as the actual breed of the simulated animals was reflected in the reference panel. Among a real dataset consisting of 920 Yorkshire sires, 95% of the animals were evaluated to have a Yorkshire breed proportion of 0.825 or greater. Determining that an animal may be highly purebred genome-wide does not preclude from failing a color test mating, in which alleles at particular genes such as *KIT* play a major role in color segregation patterns. Using seven SNPs flanking *KIT* (spanning chr8:43Mb– 44Mb), we have demonstrated that SNP haplotypes derived from the reference animals may be used to compute breed composition probabilities for a genomic segment flanking *KIT* of an unknown test animal. From the real Yorkshire sire dataset, 95% of the animals were estimated to have at least a 0.439 KIT-based breed composition probability of being a white breed. Dual use of genome-wide breed proportions and gene-based breed probabilities has great potential to inform swine breeders of the overall purity of an animal, as well as breed characteristics around particular key genes. Such knowledge may reduce the need to perform color test matings or other time-consuming and expensive procedures for breed verification.

Key Words: breed composition, swine, SNPs

0326 Genome-wide association study and accuracy of genomic prediction for teat number in Duroc pigs using genotyping by sequencing. C. Tan[*1,2], Y. Da[2], Z. Wu[3], D. Liu[3], X. He[2,3], N. Li[1], and X. Hu[1], *[1]State Key Laboratory for Agrobiotechnology, China Agricultural University, Beijing, [2]Department of Animal Science, University of Minnesota, St. Paul, [3]College of Animal Science, South China Agricultural University, Guangzhou.*

Swine teat number is related to a sow's ability to rear piglets to weaning age. The objective of this study was to identify genetic factors affecting swine teat number, evaluate the accuracy of genomic prediction, and evaluate the contribution of significant genes and genomic regions to the total genomic heritability and prediction accuracy using 84,151 autosome single nucleotide polymorphism (SNP) markers from genotyping-by-sequencing on 2936 Duroc boars. Heritability of teat number estimated using genomic restricted maximum likelihood estimation was 0.397 ± 0.033 for additive heritability and was 0.055 ± 0.027 for dominance heritability. Observed prediction accuracy calculated as the average correlation between the genomic best linear unbiased prediction and the phenotypic observations of validation individuals in a 10-fold validation study was 0.44 ± 0.04. Genome-wide association study (GWAS) and heritability estimates of individual SNPs identified a cluster of SNPs in or near the *PTGR2*, *FAM161B*, *VRTN* and *AREL1*genes in the 102.5–104.3 Mb region of chromosome 7 to have highly significant SNP effects on teat number. Fitting 10 SNPs in or near these four genes as fixed non-genetic effects in the model eliminated the significant effects in this region, reduced the additive heritability by 5.9% and reduced the prediction accuracy by 6.88%. Chromosomes 1, 2, 11, 12, 14, and 17 also had significant effects on teat number or substantial SNP heritabilities, and removal of those significant effects by fitting them as fixed non-genetic effects in the model reduced the prediction accuracy by 0.74–2.59% and reduced the total SNP additive heritability by 0–2.69%. The results indicated that swine teat number was

affected by genes with relatively large effects and that many more genes were also relevant to the accuracy in predicting teat numbers using the approach of genomic prediction.

Key Words: teat number, GWAS, genomic prediction, heritability

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0327 Genome-wide association study for supernumerary teats in Swiss Brown Swiss Cattle reveals LGR5 as a major gene on chromosome 5.

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Supernumerary teats (SNT) are any teats present on a cow's udder other than the regular four. In Swiss Brown Swiss cows, 19.9% carry SNT. Different stages of development of SNT are observed from rudimentary appendices to functional and possibly lactating teats. SNT may promote mastitis, impeach good placement of the milking machine and lower the market price of the animals. No genetic analysis of the trait has been done in this cattle population, although SNT have been routinely recorded with other conformation traits since 1995 in Switzerland. This study aimed to investigate the genetic architecture of this trait through genome-wide association studies (GWAS) performed with imputed whole-genome sequence.

Two trait definitions were used: Udder Clearance (UCT) considering whether a cow is carrier of any SNT or has a clear udder and Presence of Supernumerary Mammary Gland (PMG) opposing animal carrier of completely developed and possibly functional SNT with animals with a clear udder or carrier of a rudimentary SNT. Breeding values were estimated for Brown Swiss sires of at least 20 daughters with SNT records using an animal model including the random effects expert-by-year, farm-by-year and animal. The animal's dam life stage—heifer or cow—during its parity was fitted as a fixed effect in the same model. Single SNP regression using deregressed proofs of 1519 bulls with genotypes imputed to the variant list of the 5thRun of the 1000 Bulls Genome Project permitted discovery of three important regions on BTA5, BTA17 and BTA20 associated with the presence or the development of SNT.

Regions on BTA17 and BTA20 reached clearly lower *p*-values (10^{-7} vs. 10^{-4}) when associated to PMG than UCT, while variants on BTA5 were significantly linked to both trait definitions. No candidate genes on BTA 17 and BTA20 were found after functional analysis. On BTA5, however, the *leucine-rich repeat-containing G protein coupled receptor 5* (*LGR5*) can be considered as the major gene for our trait. Encoding a protein known as an up-regulator of the Wnt pathway and having an expression level impacting the mammary gland development, *LGR5* also carries a synonymous mutation that is highly associated to SNT.

To conclude, GWAS in the Swiss Brown Swiss population revealed *LGR5* on BTA5 as a candidate gene influencing the presence and development stage of supernumerary teats.

Key Words: dairy cattle, genome-wide association, supernumerary teats

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0328 Genomic and polygenic evaluations for milk and fat yields in Holstein upgraded Thai dairy cattle.

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The objectives of this study were to compare variance components, genetic parameters, prediction accuracies, and ranking of animals for 305-d milk yield (MY) and 305-d fat yield (FY) in a Holstein upgraded Thai dairy population using two genomic models and a polygenic model (PM). One genomic model utilized 7656 SNP (GM7K) and the other one used 74,144 actual and imputed 80K SNP (GM80K). Phenotypic and pedigree data were from 8361 first-lactation cows located in 810 farms that had their first calving between 1989 and 2014. Variance components and genetic parameters were estimated using REML procedures. Fixed effects were contemporary group (herd-year-season), calving age and heterosis. Random effects were animal additive genetic and residual. Estimates of variance components and heritabilities for MY and FY from GM80K were the highest, followed by those from GM7K, and PM had the lowest values. Correlations estimates between MY and FY were similar across models. The GM80K yielded higher prediction accuracies (38.8% for MY and 31.9% for FY) than GM7K (36.7% for MY, and 31.4% for FY) and PM (31.5% for MY, and 24.4% for FY). Different MY and FY EBV rankings existed across models. The highest rank correlations were between GM80K and GM7K (0.90 for MY, and 0.91 for FY), followed by those between GM80K and PM (0.84 for MY, and 0.83 for FY), and the lowest ones were between GM7K and PM (0.80 for MY, and 0.80 for FY). Animal rankings from GM80K should be preferred because its EBV had higher accuracy than EBV from GM7K and PM. Faster selection responses for MY and FY would be expected from GM80K than from GM7K and PM in this Holstein upgraded population.

Key Words: dairy cattle, genomic evaluation, imputation

0329 Genome-wide association study for loci associated with digital dermatitis and pododermatitis circumscripta in Holstein cattle. A. M. Oberbauer*[1], A. L. Danner[1], J. M. Belanger[1], T. R. Famula[1], and J. M. Heguy[2], [1]*Department of Animal Science, University of California, Davis,* [2]*UCCE Stanislaus and San Joaquin Counties, Modesto, CA.*

Estimates of dairy cattle lameness range up to 50% of individuals in a herd being lame at any one time. The economic costs associated with lameness include premature culling, treatment, reduced reproductive fertility, and decreased milk while there are welfare concerns associated with the pain caused by lesions. Two of the most common lameness disorders are digital dermatitis and sole ulcers (pododermatitis circumscripta). Though the etiology of the two conditions differs greatly, heritability estimates for digital dermatitis and sole ulcers have been determined to be 0.4 and 0.3, respectively, signifying moderate heritability and amenable to genetic selection programs designed to reduce prevalence. To determine loci associated with each condition, genome wide association studies (GWAS) were conducted. Using diagnostic hoof trimming records, as well as digital dermatitis and sole ulcer sire EBVs from two commercial dairy farms in California, blood samples were taken from 150 selected Holstein cows representing 56 cases and 94 controls. DNA extracted from each cow was genotyped with the Illumina BovineHD BeadChip. Derived SNP genotypes were filtered such that only SNPs having call rates ≥ 0.8, minor allele frequencies < 0.5, Hardy-Weinberg equilibria (HWE) p < 0.05, and Fisher's HWE p < 0.05 were included in the GWAS using Golden Helix SNP and Variation suite. Association testing using an additive, recessive, and dominant model for inheritance for each condition was performed using a correlation/trend test. Population stratification was corrected for using a principle component analysis. Haplotype block detection with linkage disequilibrium and association testing were also performed. Significant associations ($P <$ sup > genome < /sub > ≤ 0.05;-log 10≥ 1.3) were noted on chromosomes 3, 8, and 29 for digital dermatitis and a highly significant haplotype (Χ < sup > 2 < /sup > -log10 P ≥ 7.00, 95% CI) was noted on chromosome 29. Genome wide significance was reached on chromosomes 3 and 5 for sole ulcers though significant haplotype blocks were located on chromosomes 17, 25, and 28. An immune mediating candidate gene, *TIRAP*, on chromosome 29 was sequenced in three digital dermatitis cases and three controls, but no significant variations were noted. Future work will focus on further exploring the associated regions with the objective of identifying potential markers to aid in selecting breeding stock to reduce the incidence of both conditions.

Key Words: digital dermatitis, dairy cattle, genome-wide association

0330 Genome-wide associations study for somatic cell score in Russian Holstein cattle population. A. A. Sermyagin*, E. A. Gladyr', and N. A. Zinovieva, *L. K. Ernst Institute of Animal Husbandry, Moscow, Russian Federation.*

The cattle health traits are one of the most important selection features but their improvement in short term is limited by low heritability. For the Russian Holsteins the utilization of fitness traits such as metabolic disorders, genetic diseases and especially udder health became the main goals. The developing new methods in dairy cattle have prompted us to find out associations between SNPs and sires' genomic enhanced breeding values (GEBV) for somatic cell score (SCS) to understand the additive genetic contribution to potential mastitis resistance. According to the first step for implementation of genomic selection in Russia we genotyped 256 bulls using Illumina BovineSNP50 BeadChip. The field records for somatic cell count (SCC) in the milk of 3419 first-calving daughters of 141 Holstein sires from 26 herds were included in the dataset. For sires with daughters' records we calculated the deregressed estimated breeding values (EBV) using BLUP AM. For the sires without SCC daughters' records we got the direct genomic values (DGV) calculated through GBLUP. The DGVs with the EBVs or parents' averages were combined using weight 0.8 to get GEBV as pseudo-phenotypes for common dataset. After quality check in Plink 1.9, the 41383 SNPs were taken for further analysis. The heritability coefficients for SCC and SCS were 0.202 and 0.142, respectively. We detected 10, 67, and 289 significant SNPs using Bonferroni ($P < 1.21 \times 10^{-6}$), permutation procedure (1×10^6 numbers per SNP) and FDR ($P < 0.05$) tests, respectively. The most of the closest and functional related genes involved for cellular, metabolic and immune functions were signed to SNPs: rs41981595 (*TRNAC-ACA*, $P = 2.7 \times 10^{-10}$), rs109696042 (*TCIRG1*, $P = 1.3 \times 10^{-7}$), rs109799695 (*ACO1*, $P = 1.6 \times 10^{-7}$), rs29026486 (*UQCC*, $P = 7.5 \times 10^{-7}$) and rs43298370 (*CERS6*, $P = 1.2 \times 10^{-6}$). Additive genetic variances for these genes ranged from 9.0 to 14.9%. The most of considerable polymorphisms were identified on chromosomes 2, 4, 8, 9, 13, 20, 21, and 29. Some SNPs without a clear causal mutation for SCS were identified (rs109186647, rs110041812, rs41633009, rs110507090 and rs41589293). Our knowledges of gene distribution and quantitative trait loci for SCC combined with the bulls' mating strategy allow decreasing the incidence of mammary gland infection in Russian Holstein population. Supported by the Russian Scientific Foundation, project number 15–16–00020.

Key Words: genome-wide associations, Russian Holstein cattle, somatic cell score

0331 Genome-wide association study of milk coagulation properties in dairy sheep. G. Gaspa[1], J. Serdino[1], M. G. Manca[1], S. Sorbolini[1], R. Negrini[2], C. Dimauro[3], and N. P. P. Macciotta[*1], *[1]Dipartimento di Agraria, University of Sassari, Italy, [2]Associazione Italiana Allevatori, Roma, Italy, [3]University of Sassari, Italy.*

The objective of this work was to seek genomic regions associated with milk coagulation (MCP) properties of ovine milk. A total 478 Sardadairy breed ewes were genotyped with the 60K SNP ovine beadchip (Illumina Inc., San Diego, CA). Individuals and SNPs with > 2.5% missing data were discharged. The remaining missing genotypes were imputed using BEAGLE 4.1 and checked for quality control (QC): SNPs that did not map on any chromosome, with minor allele frequency < 0.1% or statistically deviating from the Hardy-Weimberg equilibrium ($P < 0.01$) were removed. Individual milk samples from mid-late lactating ewes (45–249 d postpartum) added with preservatives (bronopol, 62,5 μL/100 mL) were analyzed to determine MCP by using Formagraph Instrument (Foss Electric A/S, Hillerød, Denmark) The three classical MCP were measured: rennet coagulation time (RCT), curd firming time (k_{20}) and curd firmness (a_{30}). Individual laboratory cheese yield (ILCY, % w/v) was also measured. A GWAS was performed with the GRAMMARgenomic control (GC) approach, that accounts for genetic substructure in the population, as implemented in the Genabel R package. MCP were pre-corrected for the systematic effects of flock-test date, days in milk, parity, lambing month, rack position and the random polygenic additive effect. The genetic (co)variance between animals was structured using the genomic relationship matrix. Environmental residual of the model were analyzed with a linear model including SNP genotype as covariate and statistical significance of the SNP effects were adjusted using the Bonferroni correction on the effective number of independent tests estimated on haplotype blocks bases. A total of 474 individuals and 47,202 SNPs pass the QC. Ten SNP passed the significance threshold in chromosomes 3, 7 10, 12, 13, and 25. Of interest s69172.1 (90,362,719 bp) in OAR7 was close to a QTL affecting fat and protein yield in Sheep. In chromosome 12 one SNP was both associated with RCT and k_{20} (OAR12_80896495.1) and another SNP (OAR12_39255725.1) affected significantly ILCY. Unexpectedly, no significant association were found on OAR6 where casein cluster maps.

Key Words: milk coagulation, GWAS, sheep milk

0332 Genetic markers identification and genotyping for resistance to internal parasites in sheep and goat infected with *Haemonchus contortus*. Z. M. Estrada Reyes[*1], A. L. Goetsch[2], T. A. Gipson[3], Z. Wang[4], M. Rolf[5], T. Sahlu[3], R. Puchala[3], S. Zeng[4], and R. Mateescu[1], *[1]University of Florida, Gainesville, [2]American Institute for Goat Research, Langston University, Langston, OK, [3]American Institute for Goat Research, Langston University, Langston, OK, [4]Langston University, Langston, OK, [5]Oklahoma State University, Stillwater.*

Gastrointestinal nematode infections (GNI) have a great economic impact for small ruminant production in humid areas. In these regions, *Haemonchus contortus* is the most important gastroenteric nematode. Unfortunately, the indiscriminate use of anthelmintic drugs to control GNI has generated resistance to these chemical compounds. Among the alternative strategies proposed, the genotypic and phenotypic variability of the small ruminants have encouraged the identification of the most resistant animals. To identify genetic markers associated with the control of nematode populations within the host, the detection of single nucleotide polymorphisms (SNPs) OLA-DRA20 gene was performed in sheep and goats experimentally infected with *H. contortus*. Animals from 3 different breeds of sheep and goat were used for the study during 3 yr of evaluation. Individuals were selected by using positive assortative mating of the most resistant individuals each year and received a complete diet (15% Crude Protein) ad libitum for the duration of the trial. Animals were treated with levamisole (7.5 mg/kg of live weight) 3 wk before the start of the trial. After deworming,

Table 0332.

Table 1. General Linear Model using SQRTFEC as dependent variable

Source	DF	Type III SS	Mean Square	F Value	Pr > F
Genotype	2	1504.089791	752.044895	3.57	0.0318
Species	1	503.004815	503.004815	2.39	0.1255
BREED(Species)	4	2451.739709	612.934927	2.91	0.0252
ADG	1	1609.890360	1609.890360	7.64	0.0068
MPCV	1	2003.812646	2003.812646	9.51	0.0026

Parameter	Estimate		Standard Error	t Value	Pr > |t|
Intercept	103.3585848	B	15.80079300	6.54	<.0001
Genotype AA	-10.6063506	B	4.07398853	-2.60	0.0106
Genotype GA	-9.7173711	B	4.83175843	-2.01	0.0469
Genotype GG	0.0000000	B	.	.	.
Species 1	8.1320130	B	6.54058182	1.24	0.2166
Species 2	0.0000000	B	.	.	.
BREED(Species) Dorper 1	7.6681621	B	5.61469332	1.37	0.1750
BREED(Species) Katahdin 1	5.1096637	B	5.59148000	0.91	0.3630
BREED(Species) St.Croix 1	0.0000000	B	.	.	.
BREED(Species) Kiko 2	-3.0964142	B	5.12691557	-0.60	0.5472
BREED(Species) LBoer 2	17.0954108	B	6.29246453	2.72	0.0077
BREED(Species) Spanish 2	0.0000000	B	.	.	.
ADG	-0.0855908		0.03096787	-2.76	0.0068
MPCV	-1.8844031		0.61112131	-3.08	0.0026

each experimental animal was infected with 10,000 L_3 of *H. contortus* per kg of body weight per oral route. Fecal samples were obtained to determine fecal egg count using the modified McMaster technique. Blood samples were collected from the jugular vein with sterile vacuum tubes with sodium heparin to evaluate blood package cell volume (PCV) and levels of IgA, IgM and IgG. DNA was purified from blood samples using DNeasy Blood & Tissue Kit (Qiagen). One SNP in the OLA-DRA20 segregating in this population was analyzed using High Resolution Melting assays and three genotypes were observed (AA, GA, GG). A GLM was fitted with MPCV, DMI, ADG, RFI, IgM, IgG, IgA levels and genotype as predictors and the square root of the mean of FEC as the response variable. According the results, the best significant predictors to fit the model were Genotype, Breed (Species), MPCV, DMI, ADG and genotype ($p < 0.05$). In conclusion, the polymorphism in the OLA-DRA20 gene could have an important role in the immune mechanisms against *H. contortus* infections in sheep and goats. Indeed, these results provided evidence that there is a significant effect among the square root of the mean of FEC and production traits between breeds within species.

Key Words: *Haemonchus contortus*, small ruminants, OLA-DRA20 gene

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0333 Genomic analysis of lactation persistency in four breeds of dairy cattle.

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The objectives of this study were to determine gains in reliability from the addition of genomic information to genetic evaluations for best predictions of lactation persistency in U.S. Ayrshire (AY), Brown Swiss (BS), Holstein (HO), and Jersey (JE) cattle, and to identify genomic regions with large effects on those traits. Data consisted of lactations initiated by calvings on or after January 1, 1997, stored in the national dairy database (NDDB) at the Council on Dairy Cattle Breeding (Bowie, MD). Persistencies were computed by multiple-trait best prediction for milk (PM), fat (PF), and protein (PP) yields. Genetic analyses were conducted on a within-breed basis using identical repeatability animal models and breed-specific (co)variance components. Traditional and genomic PTA and reliabilities were computed by GBLUP using the national genomic evaluation system. Gain in reliability from the addition of genomic information was calculated as the difference between the realized genomic reliability and the reliability of traditional PA using a cutoff study. Predictor populations consisted of animals with traditional genetic evaluations in April 2014, and validation sets included animals with traditional genetic evaluations in August 2009. Allele effects were converted to additive genetic standard deviations, and closestBed 2.17.0 was used to obtain a list of genes that contained SNP or were within 25 kbp of a genotyped SNP. Gene names and coordinates were those published in Cow Ensembl Release 79. Reliability gains averaged 8% in AY, 5% in BS, 12% in HO, and 12% in JE. The SNP ARS-BFGL-NGS-4939 at 1801,116 bp on BTA14, downstream of the *DGAT1* gene, had the largest effects on PM and PF in HO and PM in JE of any marker in the analysis. BovineHD1600000386 at 1554,597 bp on BTA16 had largest effect on PF and PP in JE, in a region previously reported to effect fat and protein yields and percentages. The SNP with the largest effects in AY were located on the X chromosome in regions reported to affect fat and protein yields and percentages in HO. The largest effect for PM in BS was in a region of BTA19 associated with MY in Chinese Holsteins, while the largest PF and PP effects were in regions of the X chromosome reported to affect fat and protein yield in U.S. Holsteins. Genetic correlations of yield with persistency range from −0.32 to 0.26, so loci with large effects on yield also can affect persistency.

Key Words: association analysis, best prediction, reliability

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0334 Genome-wide association study for tick count and infection level of *Babesia bovis* traits in Angus cattle.

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Tick and tick-borne diseases, including babesia (*B. bovis*), constitutes a major drawback to improve productivity of beef cattle in the tropics, especially for systems where *Bos taurus* cattle animals and their crosses are used. To identify highlight regions highly associated with the studied traits, genome-wide association studies (GWAS) were performed. Tick counts and blood sample were taken in two occasions from each of 355 Angus cattle at a farm located at Rio Grande do Sul State, Brazil. Blood samples were collected, in tubes containing EDTA for DNA extraction. *B. bovis* quantification was performed using both qPCR technique from genomic DNA of each animal with specific primers for this protozoary and the absolute quantification method. Animals were genotyped by using Illumina GeneSeek GGP Bovine 150K. Quality control criteria were: MAF < 2%, call rate < 92%, and animal call rate (with less than 90% of SNPs called). After edits, 144,924 SNPs and 350 animals were available. Fixed effects in the model included contemporary groups and effect of data collection period, as well as additive genetic direct and permanent environmental effects as random. Variance components and genetic parameters were estimated by Bayesian inference in a bivariate analysis using GIBBS2F90 software, and the effect of each SNP was estimated using methods Bayes C as implemented in the GS3 software. Also, it was

used de-regressed EBV. The mean h^2 were 0.207 and 0.059 for tick count (TC), and infection level of *Babesia bovis* (IB), respectively. The genetic correlations were 0.079 between TC and IB. Variances were calculated for windows of 1-Mb SNP. The results showed that the top 10 SNP windows for each trait explained a total of 51.45%, and 3.09% of genetic variance for TC, and IB, respectively. The 10 most significant markers for TC were located on chromosomes 4, 5, 6, 10, 12, 16, 19, 22, 29, and 30. The 10 most significant markers for IB were located on chromosomes 3, 5, 7, 8, 14, 20, and 24. There are others studies that indentified QTLs located in regions of top SNP associated with TC. Therefore, genomic regions identified may be important for the variation of tick count, but less important for infection level of *Babesia bovis* traits in Angus cattle. Acknowledgment: Grant provided by São Paulo State Foundation (FAPESP), São Paulo, Brazil.

Key Words: *Bos taurus,* GWAS

0335 Identification of loci associated with susceptibility to bovine paratuberculosis using imputed genotypes based on whole genome sequencing.

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Johne's disease or bovine paratuberculosis is a contagious bacterial infection in cattle caused by *Mycobacterium avium* ssp. *paratuberculosis* (*Map*). Previous genome wide association studies (GWAS) to identify loci associated with susceptibility to *Map* infection in Holstein and Jersey cattle have been performed using the Illumina BovineSNP50 BeadChip which consisted of approximately 54,000 SNPs in three released BeadChip versions. Although uniform SNP spacing was a design objective, a number of genomic regions were under-represented by markers. The objective of this study was to determine if there were loci associated with susceptibility to *Map* tissue infection located within these under-represented areas of the Bovine SNP50 BeadChip that would be identified using genotypes imputed to whole genome sequence (WGS). To do this, BovineSNP50 genotypes of 409 Holstein cows (162 cases and 247 controls) were first imputed using Beagle 4.1 to the density of the Illumina BovineHD BeadChip using 2703 previously genotyped Holstein cattle as a reference. The imputed BovineHD data were then imputed to WGS level (35,431,201 indels and SNPs) with FImpute using phased Run 4 WGS data for 1147 previously sequenced cattle from the 1000 Bull Genomes Project as a reference. Genotype quality control was performed using the same parameters as for the BovineSNP50 data and any SNP with a call rate < 90% or MAF < 1% was removed. After quality control, 16,063,342 indels and SNPs remained for analysis. A GWAS was performed with Efficient Mixed Model Association expedited (EMMAX) additive and allelic models and the most highly significant 500 loci were compared with the BovineSNP50 GWAS results. With the imputed genotypes, 13 and 5 new QTL were identified with the allelic and additive models, respectively, and 14 new QTL were identified by both models ($p = 4.17\text{x}10^{-6}$ to $p = 4.45\text{x}10^{-5}$). In addition, 81, 18, and 67 previously identified QTL were identified under the allelic, additive or by both models and were more precisely finely mapped using the imputed genotypes. In conclusion, imputation of BovineSNP50 data to WGS was effective for identifying new QTL and fine-mapping previously identified QTL.

Key Words: paratuberculosis, imputation, GWAS

0336 Joint SNP-haplotype analysis for genomic selection based on the invariance property of GBLUP and GREML to duplicate SNPs.

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Haplotype analysis of SNP markers in genomic prediction and estimation may utilize haplotype effects unaccounted for by single-SNP analysis, whereas haplotype analysis alone may not account for all single-SNP effects. The objective of this study was to establish a theoretical model by mathematical derivation and validation studies to show why haplotype analysis and the joint SNP-haplotype analysis may improve the accuracy of genomic prediction. We first modeled the genotypic value of a two-haplotype genotype as the summation of the single-SNP effects and the haplotype effects unaccounted for by the single SNPs within the haplotype block plus a potential loss of single-SNP effects of the haplotypes. Then we established an invariance property to duplicate SNPs. Assume that a set of SNP markers is duplicated r times in the mixed model. Genomic best linear unbiased prediction (GBLUP) of genetic values (additive, dominance and genotypic values) of individuals and SNP genetic variance components as well as the associated heritability estimates by genomic restricted maximum likelihood estimation (GREML) are invariant to the duplication of SNPs, and GBLUP of SNP additive, dominance and genotypic effects differ from those without duplicate SNPs by the square root of r. Based on this invariance property, adding single SNPs to the haplotype analysis would recover any loss of single-SNP effects of haplotype-only analysis and maintain the haplotype effects not utilized by single-SNP analysis without overestimating single-SNP effects. Validation studies using 6000 individuals with 423,131 SNPs from the Framingham Heart Study showed that heritability estimates under the joint SNP-haplotype model were lower than those from the haplotype-only model, confirming that adding SNPs to the haplotype model did not result in overestimation

of the total genetic contribution. In most validation samples, haplotype analysis was at least as accurate as single-SNP analysis, and the joint SNP-haplotype analysis had further improvement in prediction accuracy over the SNP-only or haplotype-only models. These validation results provided a confirmation of the benefit predicted by our theoretical model for the joint SNP-haplotype analysis of genomic prediction based on the invariance property of duplicate SNPs.

Key Words: genomic selection, haplotype, GBLUP, GREML, SNP

0337 Practical approximation of accuracy in genomic breeding values for a large number of genotyped animals. S. Tsuruta[*1], D. Lourenco[1], Y. Masuda[1], D. W. Moser[2], and I. Misztal[1], *[1]University of Georgia, Athens, [2]Angus Genetics Inc., St. Joseph, MO.*

Accuracy defined as the squared correlation between true and genomic EBV (GEBV) is required in genomic evaluations and it can be approximated by contributions from phenotypes, pedigrees, and genotypes. In single-step genomic BLUP, contribution from genotypes is based on inverses of genomic (G) and pedigree (A22) relationship matrices for genotyped animals. The objective of this study was to develop a less expensive formula to calculate accuracy in GEBV for a large number of genotyped animals. As alternative contributions from genotypes, we considered the mean square difference between off-diagonals for G and A22 (GmA22) and the number of genotyped animals or the number of effective SNP markers (ESM) as well as parent average accuracy (ACCPA). The ESM was calculated as the number of the largest eigenvalues of G explaining 99% of variation. The following three formulas were proposed: F1 = heritability × ESM × GmA22 × (1 + ACCPA); F2 = 1 + heritability × ESM × ACCPA × GmA22; and F3 = 1 + ACCPA. Phenotypes for birth weight (BW) and post weaning gain (PWG), pedigrees, and genotypes were provided by American Angus Association. The BW dataset consisted of 20K records and 91K animals with 20K genotyped animals. Two PWG datasets consisted of 30K records and 122K animals with 30K genotyped animals, and 35K records and 202K animals with 60K genotyped animals, respectively. The three formulas were compared with the accuracy calculated from prediction error variances (PEV) obtained from the inverse of the left-hand side of the mixed model equations. For direct GEBV on BW, correlations of PEV with F1 and F2 were the highest (0.86), but F1 was overestimated and the MSE was larger. For maternal GEBV on BW, correlations between PEV and F1 and F2 were the highest (0.85). For GEBV on PWG with 30K genotyped animals, correlations of PEV with F1 and F2 were the highest (0.82), but the MSE for F2 was larger. With 60K genotyped animals, correlations between PEV and F1 and F2 were also high (0.79 and 0.78, respectively), but F2 was underestimated and the MSE was larger. Both F1 and F2 gave reliable approximations of accuracy in GEBV. For each data set, the mean accuracy can be adjusted to reduce the bias. The new formula can calculate approximations of accuracy in GEBV for a large number of genotyped animals at a low cost.

Key Words: genomic breeding values, accuracy, Angus

0338 Comparison of transcriptome profiles in longissimus dorsi muscle between bulls and steers of Korean cattle. M. Baik, S. J. Park*, and N. Sang Weon, *Department of Agricultural Biotechnology, College of Agriculture and Life Sciences, Seoul National University, Korea (The Republic of).*

Castration of bulls improves beef quality including intramuscular fat (IMF) content and tenderness. Studies have revealed that castration changes expression of many genes associated with beef quality and IMF deposition in longissimus muscle (LM). Limited information is available for global gene expression changes in the LM following castration. Objectives of this study were to understand global transcriptome changes following castration in the LM of beef cattle and to identify new genes associated with beef quality. By using RNA-sequencing (RNA-seq) technique, transcriptome profiles were compared in the LM between bulls and steer of Korean cattle. LM tissues samples of ten bulls and ten steers were prepared, and LM RNA samples from three bulls and three steers were used for the RNA-seq. Among total 18,027 genes identified by RNA-seq and subsequent read mapping analysis with TopHat software, total 1146 transcriptomes (521 upregulated and 625 downregulated genes following castration) were differentially expressed genes (DEGs) in the LM between bulls and steers with false discovery rate at < 0.05 and log fold change above 1.5. Pathway analysis with the 1146 DEGs showed significant ($P < 0.05$) changes in 9 KEGG pathways, including complement and coagulation cascade and peroxisome proliferator-activated receptor signaling. We conducted quantitative PCR (qPCR) with ten genes of the complement and coagulation cascades using LM tissue samples of ten bulls and ten steers. The qPCR data were analyzed using GLM of SAS. The qPCR analysis confirmed differential ($P < 0.05$) expression patterns of all genes including coagulation factor III and mannan-binding lectin serine peptidase 1. In conclusion, global transcriptome analysis using RNA-seq reveals for the first time that castration changes expression of many genes involved in complement and coagulation cascade pathway, which may be linked to beef quality.

Key Words: castration, complement and coagulation cascade, beef cattle

0339 Gene network regulated by microRNAs suggests modulation of fat deposition in cattle.
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Meat quality depends on many factors such as nutrition, management system and genetic. The mainly attributes of meat quality besides tenderness are juiciness and flavor, which are associated with intramuscular fat (IMF) content. In this study microRNAs expressed in Longissimus dorsi muscle from *Bos indicus* were identified to better understand the biological processes related to IMF deposition in skeletal muscle. MicroRNAs are small non-coding regulatory RNAs that play an important role in post-transcriptional gene regulation in many tissues and are associated with numerous biological processes. Total RNA was extracted from Longissimus dorsi muscle of 30 steers with extreme values of genomic estimated values (GEBV) for IMF content, classified into High (H) and Low (L) IMF content groups. MicroRNA libraries were constructed and sequenced using NGS technology (MiSeq-Illumina) generating 1 million reads/sample. MicroRNAs were filtered by FastX, annotated by miRDeep2 and, differentially expressed (DE) microRNAs were identified by DESeq2 package. A total of 463 known microRNAs were identified and six of them were DE (FDR < 0.1). MicroRNAs bta-let-7f, bta-let-7a-5p and bta-miR-423 were downregulated, while bta-miR-100, bta-miR-143 and bta-miR-146b were upregulated in the L group. MicroRNAs target genes were identified by Ingenuity Pathways Analysis (IPA®) MicroRNA Target Filter tool and filtered by muscle RNA-Seq data obtained in previous studies, creating a list with 2520 target genes. The metabolic pathways and gene networks were constructed and analyzed by IPA® software, to identify enriched biological processes and genes regulated by microRNAs that were associated with lipid metabolism. Important genes for fatty acid metabolism were related in three gene networks: "Gene Expression, Cell Cycle, Cancer," involving 32 target genes; "Drug Metabolism, Lipid Metabolism, Molecular Transport," with 32 target genes and "Lipid Metabolism, Small Molecule Biochemistry, Vitamin and Mineral Metabolism," with 30 target genes. This last network involved genes such as PPARGC1A, MYCN, ESR2 and ARL4D, targets of downregulated microRNAs; MED1, SMAD4, NEDD4 and MBOAT2, targets of upregulated microRNAs in the L group. These results indicate that gene regulation by microRNAs in this gene network influences lipid homeostasis, principally by PPARα signaling pathway activation and can modulate fat deposition in muscle.

Key Words: smallRNA, functional enrichment, lipid metabolism

0340 Differentially expressed miRNAs in skeletal muscle related to feed efficiency in Nellore cattle.
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Feed efficiency (FE), also referred as residual feed intake (RFI), is a production trait that can have a major impact on production costs, reduction of pasture area, and pollutants. Bovine transcriptomic studies have shown that the expression of many miRNAs are tissue specific and have potential roles in some biological mechanisms. In this study, Nellore steers genetically divergent for RFI (kg/d) were selected based on BLUP (Best Linear Unbiased Prediction) estimates and ranked to select the most extreme values for additive genetic merit. Sequencing of small RNA libraries from Longissimus dorsi (LD) muscle tissue of eight Nellore steers (N = 4 High RFI, N = 4 Low RFI) was conducted on a MiSeq using the Miseq Reagent Kit V3 150 cycles. After quality control, the miRDeep2 software was used to identify and quantify novel and known miRNAs using *Bos taurus* UMD3.1 as reference genome. Differentially expressed (DE) miRNAs (FDR = 10%) were identified by DESeq2 R package and potential regulatory target transcripts were predicted by TargetScan software. The bta-miR-486 (padj = 0.0072) was DE in LD muscle tissue. This miRNA was also identified as DE in a transcriptome analysis in skeletal muscle for differential RFI in pigs. The genes *PKHD1L1, ENAH, ATF3, GAS7, LIMK1, MPZ, C3* and *SLC26A2,* related to ion transport, glucose and pyruvate metabolic process and glycosylation, were identified as target genes of this DE miRNA. Supporting our findings, these genes were previously identified as DE in RNaseq study performed using liver and muscle tissues of this same set of samples. This study provides a better understanding of the role of miRNAs in biological mechanisms related to feed efficiency in Nellore beef cattle.

Key Words: *Bos indicus*, residual feed intake, gene regulation

0341 miRNAs related to fatty acids composition in Nellore cattle. P. S. N. Oliveira*[1], A. S. M. Cesar[2], G. B. Oliveira[2], P. C. Tizioto[1], M. D. Poleti[2], W. J. S. Diniz[3], A. O. D. Lima[3], J. M. Reecy[4], L. L. Coutinho[2], and L. C. A. Regitano[5], *[1]Embrapa Southeast Livestock, São Carlos, Brazil, [2]Animal Biotechnology Laboratory-ESALQ, University of São Paulo, Piracicaba, Brazil, [3]Federal University of São Carlos, Brazil, [4]Iowa State University, Ames, [5]Embrapa Southeast Livestock, São Carlos, Brazil.*

Fatty acid (FAs) content is an important trait that can influence the sensorial and nutritional value of meat and play a significant role in biological processes such as adipogenesis. In beef cattle, adipogenesis as well as several other biological processes have been reported that could be regulated by miRNAs. The goal of this study was identify differentially expressed (DE) miRNAs and biological processes associated with FA content between the groups Nellore steers that showed extreme genomic breeding values (GEBV) for oleic acid (OA) and conjugated linoleic acid cis9 trans11 (CLAc9t11). In this study, small RNA libraries from Longissimus dorsi (LD) muscle tissue from a group of 28 (top 14 animals with highest GEBV distribution (H) and bottom 14 with lowest GEBV distribution (L) for OA and CLAc9t11 content) were sequenced on a MiSeq using the Miseq Reagent Kit V3 150 cycles. After quality control, the miRDeep2 software was used to identify and quantify novel and known miRNAs using *Bos taurus* UMD3.1 as reference genome. Differentially expressed (FDR = 10%) miRNAs were identified by DESeq2 R package and potential regulatory target transcripts were predicted by TargetScan software. The bta-miR-126–5p (padj = 0.0987) and bta-miR-2419–5p (padj = 0.0041) were DE for OA and CLA, respectively. The genes *CDS2, FAR2, DIP2B, NAB1, EPT1, UBE2E3*, *PRKAG2* and *CAV3* were identified as target genes of these DE miRNAs, which were identified as DE in a previously RNaseq study. These genes are related to some biological process for fatty acids composition; like phospholipid and lipid metabolism, skeletal system development, proteolysis and insulin signaling pathway. This study helps to better understand of the biological mechanisms that control intramuscular fat deposition and composition, and could positively benefit beef production by supplying the product that the consumer wants.

Key Words: *Bos indicus*, adipogenesis, gene regulation

0342 Expression levels of the bovine SCD gene are significantly associated with fatty acid composition of cattle. H. Chung*, *National Institute of Animal Science, Wanju, Korea (The Republic of).*

The experiment shows that a long-term administration of low and high-energy diets may not functionally either increase or decrease SFA and UFA. The interesting finding was that variation for proportions of all FAC in the low-energy diet group were higher than that of the high-energy diet group except Linoleic acid (18:2n6) and PUFA. According to the variance analysis, the proportions of FAC in the low group tended to have an approximate normal distribution while the high group showed a skewed pattern. Expression analysis of stearoyl-CoA desaturase (SCD) revealed at least twofold high expression levels in the high-diet group, and especially, the SCD4 and SCD6 segments detected more than 10 folds high expressions, whereas none of the SCD segments had high expression values in the low-diet group. The results indicate that long-term feeding with high energy levels of diets lead high expression levels of the SCD gene. However, excessive proportions of nutritional materials limited metabolic availabilities or restricted functional systems for the ruminal bio hydrogenation between FA. Therefore, the present results deliver a critical issue to the public that manipulations of FAC with high nutritional levels in diets may be oriented toward increases of expression levels of SCD, but not activities of other genes that functional elongate and desaturase FA.

Key Words: expression, SCD, FAC

0343 Profiling microRNA expression in longissimus dorsi muscle of F2 pigs from the Michigan State University Duroc x Pietrain resource population. K. R. Perry*[1], J. P. Steibel[1,2], D. Velez-Irizarry[1], S. A. Funkhouser[3], N. E. Raney[1], R. O. Bates[1], and C. W. Ernst[1], *[1]Department of Animal Science, Michigan State University, East Lansing, [2]Department of Fisheries and Wildlife, Michigan State University, East Lansing, [3]Genetics Program, Michigan State University, East Lansing.*

MicroRNAs (miRNAs) are a class of small, non-coding RNAs shown to regulate gene expression post-transcriptionally through complementary binding with an approximately 7 nt "seed" sequence in the 3'UTR of target mRNAs. MiRNAs have been shown to regulate numerous complex biological processes across tissue types, including fetal and postnatal skeletal muscle in pigs. While miRNAs have been characterized for these developmental stages, a more comprehensive understanding of the effects of miRNA regulation in market-age pigs is needed. The objective of this study was to profile the expression of miRNAs in the Longissimus dorsi (LD) muscle of 174 F2 pigs (~5.5 mo of age) from the MSU Duroc x Pietrain Resource Population. Total RNA was extracted from LD samples using the QIAGEN miRNeasy Mini Kit, and library preparation for sequencing was conducted utilizing the Bioo Scientific NEXTflex Small RNA Sequencing Kit (v2) with one cDNA library prepared per sample. The 174 libraries were multiplexed and sequenced on an Illumina HiSeq 2500 platform in 1x50 bp format. Raw sequence reads (fastq format) were trimmed for adaptor sequences, size- and quality-filtered, and PCR duplicates were removed. After processing, 232,826,977

total reads (mean 1338,086 reads per library) were aligned to the *Sus scrofa* reference genome (10.2.79) using miRDeep2. In total, 74.8% of reads were successfully mapped to the reference genome (median = 76.4% of reads per library). The miRDeep2 software package was then utilized to quantify annotated *Sus scrofa* mature miRNAs from miRBase (Release 21). The mature miRNA expression profiles were then filtered for abundance across samples; miRNAs expressing less than 1 read count per million (cpm) in less than 44 samples were removed from the analysis. The remaining 295 profiles were normalized relative to quantified library size (cpm) utilizing the *cpm* function of the *edgeR* package of R. Among the expressed miRNAs ssc-miR-1, ssc-miR-133a-3p, ssc-miR-378, ssc-miR-206, and ssc-miR-10b were the most abundant, all of which have previously been shown to be expressed in pig skeletal muscle. The expression of these five miRNAs represented 47.85% of the total read cpm in the dataset. Further characterization of miRNA expression profiles in adult pig skeletal muscle tissue will help to elucidate the role of miRNA regulation on production efficiency-related phenotypes including skeletal muscle accretion and meat quality.

Key Words: microRNA, skeletal muscle, pig

0344 Scan for allele frequency differences from pooled samples in lines of pigs selected for components of litter size. B. A. Freking*, J. W. Keele, and G. A. Rohrer, *USDA-ARS, U.S. Meat Animal Research Center, Clay Center, NE.*

Direct single trait selection within two seasonal replicates for 11 generations resulted in a 1.6 pig advantage for uterine capacity (UC) and a 3.0 advantage for ovulation rate (OR) compared with an unselected control (CO) population. Our objective was to gain insight and identify genetic loci impacted by quantitative selection for these component traits. We utilized historical DNA samples from all three lines obtained five and six generations after selection had ceased. A total of 402 gilts contributed to pooled samples; 8 unique pools per line with an average of 16.6 gilts per pool with paternal-half-sibs kept in the same pool. These 24 DNA pools were applied to Neogen GGP Porcine HD BeadChips. Bead-level normalized X and Y values were analyzed rather than allele calls. Analyses to compare the populations were conducted on individual SNP frequency estimates using REML and also using a sliding 25-SNP window with Wright's fixation index (F_{ST}). Pedigree relationships of all gilts back to the common base population 18 generations prior were utilized to compare to the genomic relationships. The overall relationship between pedigree and genomic information was highly predictive (r^2 = 97.5%); however, OR and UC selected lines differed from CO line with above average genomic relationships observed for the same degree of pedigree relationship. This would be consistent with the idea that selection increased the average within line relationships beyond what was accounted for by drift. Sixteen SNPs had allele frequency differences that exceeded a modest false discovery rate ($P < 0.05$) with none exceeding a genome-wide level of significance. However, three SNP were closely linked on SSC 13 near 203 Mb, while two SNP each were identified on SSC 5 at 63–65 Mb and on SSC 14 at 22–24 Mb offering additional support to those locations. F_{ST}values marked similar chromosomal regions but, again, did not by themselves identify regions that exceeded genome-wide significance. In conclusion, the pooling strategy reduced the cost to initially scan the genome but estimates of allele frequency differences needed to be extreme to exceed differences expected from modeling genetic drift in these populations. Additional samples need to be added to supplement this initial scan.

Key Words: pigs, selection, pooling

0345 Construction and functional analysis of expression vector and miRNA interference vectors of Gsdma of Tibetan sheep. C. Li[1], L. Ren[1], Y. Wang[1], J. Zhong[2], L. Huang[1], Y. Lin[1], X. Zi[1], and Y. Zheng[*1], [1]*Southwest University for Nationalities, Chengdu, China,* [2]*Auburn University, Auburn, AL.*

Gsdm(*gsdermin*) is a newly reported gene family. The human *Gsdma* and mouse *Gsdma3* were demonstrated to regulate the formation and development of hair follicle through signaling pathways such as Wnt and TNF-α. However the functions of *Gsdm* family members from other animal species are poorly studied. The objective of this study was to explore possible functions of *Gsdma* of Tibetan sheep (*Ovis aries*) at cellular level. RNA were extracted from skin tissues of Tibetan sheep (n = 5), and the cDNA sequence of *Gsdma* was cloned by PCR. Tissue expression profile analysis and sequence alignments showed that Tibetan sheep *Gsdma* is skin-specific and shows 99.9% coding sequence similarity to that of predicted sheep *Gsdma* (XM_004012853.1). The deduced protein sequences of Tibetan sheep and human *Gsdma* have high similarity (approximately 90%). An eukaryotic expression vector (pCDsRed2-KG) containing skin-specific KAP6.1 promoter and four interference vectors (pcDNA6.2-GW/EmGFP-miR 1 to 4) for Tibetan sheep *Gsdma* were constructed. The pCDsRed2-KG vector was transfected into human hair inner root sheath cells in vitro, and the positive transfected cells were sorted by flow cytometry. Quantitative real time PCR using *GAPDH* and β-actin as reference genes proved that the expression vector was highly expressed in human hair inner root sheath cells after transfection. In addition, two of the four interference vectors exhibited significant silencing effect on pCDsRed2-KG expression (interference efficiency > 50%). Further analysis showed that the significantly increased *Gsdma* mRNA level was correlated with elevated caspase-3 mRNA level ($P < 0.05$) in the transfected human hair inner root sheath cells. However, the β-catenin showed no significant changes at both mRNA and protein levels. Since caspase-3 is involved in apoptotic pathway, our data suggest that

Gsdma gene may play an important role in regulating hair follicle development through this signaling mechanism.

Key Words: *Gsdma* gene, Tibetan sheep, hair follicle

0346 Genetic characteristics of semi-domesticated reindeer populations from different regions of Russia based on SNP analysis. V. R. Kharzinova*[1], A. V. Dotsev[1], I. M. Okhlopkov[2], K. A. Layshev[3], V. I. Fedorov[4], L. D. Shimit[5], G. Brem[1,6], K. Wimmers[7], H. Reyer[7], and N. A. Zinovieva[8], *[1]L. K. Ernst Institute of Animal Husbandry, Moscow, Russian Federation, [2]Science Institute of Biological Problems Cryolithozone, Yakutsk, Russian Federation, [3]North-West Center of Interdisciplinary Researches of Food Maintenance Problems, Federal Agency of Scientific Organizations, St. Petersburg, Russian Federation, [4]Federal Government Budget Scientific Institutions Yakut Scientific Research Institute of the Agriculture Federal Agency Scientific Institutions, Yakutsk, Russian Federation, [5]Tuva State University, Tyva Republic, Russian Federation, [6]Institute of Animal Breeding and Genetics, VMU, Vienna, Austria, [7]Genome Biology, Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany, [8]L. K. Ernst Institute of Animal Husbandry, Moscow, Russian Federation.*

Semi-domesticated reindeer are herded on the entire territory of Russian Far North and are represented by several populations which vary in exterior and morphological features. In the present work we considered the following populations: Nenets-NEN (the largest, with 800,000 individuals), Evenk-EVN (100.000 individuals) and Todzha-TOD (the smallest with around 1000 individuals). Genetic characteristics and structure of Russian reindeer populations are insufficiently studied and research in this field is undoubtedly necessary.

Our study aimed at evaluating genetic diversity and structure of NEN (n = 11), EVN (n = 29) and TOD (n = 11). Wild reindeer from Yakutia region (n = 14) were used as outgroup for cluster analysis. DNA was extracted from tissue samples using the Nexttec column (Nexttec Biotechnology GmbH, Germany) according to the manufacturer's recommendations and genotyped using the Bovine SNP50 v2 BeadChip. After quality control (MAF = 0.01) 544 polymorphic SNPs were selected for further analysis. Statistical analysis was performed with PLINK 1.07, Arlequin 3.5.2.2, HP-Rare 1.1, GENETIX 4.05 and STRUCTURE 2.3.4 software.

Greater values of unbiased expected heterozygosity were observed for NEN (0.214 ± 0.008) and EVN (0.211 ± 0.008) populations, while for TOD this was only 0.195 ± 0.008. Inbreeding coefficient (F_{is}) showed heterozygote deficiency in the TOD population (0.049) while NEN and EVN were in H-W equilibrium (0.003 and −0,004, respectively). Allelic richness was significantly higher for EVN (1.74 ± 0.02) and NEN (1.70 ± 0.02) in comparison with TOD (1.65 ± 0.02). AMOVA revealed that most of the variation was within populations (91.8%) and less (8.2%) among populations. The genetic differentiation (pairwise F_{ST}) among populations ranged from 0.05 between EVN and NEN to 0.11 between TOD and NEN. F_{ST}value between EVN and TOD was 0.10 ($p < 0.01$).

Since wild populations coexist with semi-domesticated populations and gene exchange may occur between them, the SNP profiles of wild reindeers were included in dataset for cluster analysis. At k = 4 all animals belonging to the EVN and NEN were distinctly differentiated, while admixture of wild reindeer was observed in three samples belonging to the TOD population.

The genome scan approach in reindeer used in our study revealed that every population was characterized by unique gene pool. Subsequent studies in this field will provide further information for investigating population structure along with a better understanding of biological features of reindeer. The study was supported by the Russian Science Foundation within Project no. 14–36–00039

Key Words: semi-domesticated reindeer, SNPs, genetic diversity, population structure

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0347 Candidate gene and marker for equine metabolic syndrome. S. Lewis*, H. Holl, M. T. Long, M. Mallicote, and S. Brooks*, University of Florida, Gainesville.*

Equine obesity gives rise to life-threatening secondary chronic conditions, similar to those in humans, livestock and other companion animal species, leading to loss of use or euthanasia. Elevated circulating insulin levels often characterize the primary disease associated with equine obesity, Equine Metabolic Syndrome (EMS). Due to clinical similarities with other conditions like Pituitary Pars Intermedia Dysfunction (PPID, formerly Equine Cushing's Disease) and hypothyroidism, conclusive diagnosis of EMS often proves challenging. Aside from changes in diet and exercise, few targeted treatments are available for EMS, emphasizing the need for genetic testing to identify at-risk individuals and implement preventative measures. A previous genome-wide association study, using horses with EMS and/or PPID and exhibiting severe laminitis, revealed statistically significant markers for the condition near a single candidate gene, *FAM174A*. A single study describing the function of this gene suggests it may play a role in cholesterol homeostasis. Sequencing of the *FAM174A* gene in EMS affected Arabian horses identified at least five polymorphic haplotypes. In this study, additional samples from a larger population of horses, consisting of 56 individuals, diagnosed with EMS disease were genotyped by Sanger sequencing for polymorphisms in the *FAM174A* gene and the results assessed for association with indicators of the EMS condition. Additionally, we genotyped the most significant intergenic marker

SNP from the previous GWAS, BIEC2–263524, by High Resolution Melt (HRM). An allele in a 3' untranslated region (UTR) of *FAM174A* correlated with both elevated insulin values ($p = 0.0082$) and BCS > 6.5 ($p = 0.0116$). The BIEC2–263524 marker SNP displayed similar associations to elevated insulin values ($p = 0.0060$) and BCS > 6.5 ($p = 0.0049$). The risk allele at both BIEC-263524 and the *FAM174A* 3'UTR correlated at a 95% frequency, indicating strong LD across this haplotype. Confirmation of the association between these markers and the EMS condition will enable genetic tests for the horse as a helpful tool in diagnosing and preventing EMS. In addition to improving our understanding of the etiology of this troubling condition in the horse, the *FAM174A* locus may prove an interesting candidate gene for human obesity.

Key Words: equine, obesity, metabolic

0348 The polymorphisms of Toll-like receptor 4 gene influences milk production traits in Chinese Holstein cows. X. Zhu, M. Wang, S. Xing, Z. Yang, and Y. Mao*, *College of Animal Science and Technology, Yangzhou, China.*

Toll-like receptor 4 (*TLR4*) is an important member of the Toll-like receptor gene family that is widely found in various organisms. *TLR4* can identify molecular patterns from various pathogenic microorganisms, and induce natural immunity and acquired immunity. Two single nucleotide polymorphisms (SNPs) of *TLR4* (c.-226 G > C and c.9788 C > T) were genotyped using Sequenom MassARRAY (Sequenom Inc., San Diego, CA) for Chinese Holstein cows ($n = 866$), and the EBV for each individual cow of milk production traits and somatic cell score (SCS) were analyzed by the multiple-traits multiple-lactation random regression test-day model, and then the associations between SNPs or haplotype and the EBV of milk production traits and SCS were analyzed by PLINK software. The c.-226 G > C and c.9788 C > T showed low linkage disequilibrium ($r^2 = 0.192$). There was no association between these two SNPs and SCS, but significant effects were found for SNP c.-226 G > C on fat content ($P < 0.025$), and SNP c.9788 C > T and haplotype CT on fat content and total solids ($P < 0.005$). The software MatInspector revealed that c.-226 G > C was located within several potential transcription factor binding sites, including transcription factor AP-2, and may alter gene expression, but further investigation will be required to elucidate the biological and practical relevance of these SNPs.

Key Words: milk production traits, SNP, Toll-like receptor 4

Table 0348.

Table Effects of SNPs of TLR4 genes on SCS and milk production traits

SNPs	Genotypes	DHI Records number	TDMY(kg)	FC(%)	Pers.	PC(%)	LC(%)	TS(%)	SCS	MUN
TLR4- -226	GG	4229	2.87±4.65	-12.63±4.23^{A}	0.36±0.13	-1.62±0.70	0.32±0.159	-8.34±4.71	-0.02±0.07	-0.85±0.39
	CG	10147	0.15±3.59	-0.14±3.422^{b}	0.47±0.12	-0.95±0.60	0.10±0.14	1.92±3.73	0.02±0.06	-0.15±0.28
	CC	6123	-3.96±6.30	2.914±5.89^{b}	0.14±0.14	0.04±0.99	-0.04±0.24	0.76±6.23	-0.01±0.01	0.27±0.49
	P value	20499	0.1804	0.0085*	0.2124	0.0836	0.08505	0.0875	0.44395	0.02607*
	a		3.416	-7.7735*	0.1095	-0.827	0.181	-4.549	-0.006	-0.5585
	d		0.691	4.7245	0.2185	-0.162	-0.047	5.702	0.022	0.1455
	a		3.4851	-7.3011*	0.1314	-0.8432	0.1763	-3.9788	-0.0038	-0.54395
TLR4-9788	CC	15414	0.48±3.05	-6.12±2.79^{Aa}	0.32±0.08	-1.25±0.47	0.18±0.11	-5.64±3.08^{Aa}	0.02±0.05	-0.39±0.24
	CT	4643	0.65±5.27	1.154±5.12^{B}	0.59±0.18	-0.48±0.88	0.12±0.12	7.57±5.37^{b}	-0.04±0.09	-0.13±0.42
	TT	442	-15.82±13.25	44.78±17.54^{Bb}	-0.11±0.37	3.87±3.47	-1.01±0.63	47.27±15.01^{Bb}	-0.03±0.31	2.05±1.41
	P value	20499	0.27345	0.0025**	0.2037	0.04228	0.1051	0.00054**	0.2322	0.0779
	a		8.1510	-25.4525**	0.2150	-2.5615	0.5945	-26.4515**	0.0265	-1.2185
	d		8.3200	-18.1755	0.4840	-1.7885	0.5335	-13.2405	-0.0365	-0.9585
	a		14.1414	-38.5389**	0.5635	-3.8492	0.9786	-35.9847**	0.00022	-1.90862

*significant association after Bonferroni correction for multiple testing at the significance level of 0.025; **significant association after Bonferroni correction for multiple testing at the significance level of 0.005. A,B within the same column with different superscripts indicate $P < 0.01$; a,b indicate $P < 0.05$.

TDMY: test-day milk yield; FC: fat content; PC: protein content; Pers.: Persistency; SCS: somatic cell score; LC: lactose content; TS: total solid; MUN: milk urea nitrogen.

0349 A polymorphism within the *PAPPA2* gene is associated with postpartum fertility traits in Holstein dairy cattle located in southern Sonora Mexico. P. Luna-Nevarez*[1], J. C. Leyva-Corona[1], M. A. Sanchez-Castro[1], R. Zamorano-Algandar[1], J. F. Medrano[2], G. Rincon[3], R. M. Enns[4], S. E. Speidel[4], and M. G. Thomas[4], *[1]Instituto Tecnologico de Sonora, Ciudad Obregon Sonora, Mexico, [2]University of California, Davis, [3]Zoetis Inc., Kalamazoo, MI, [4]Department of Animal Sciences, Colorado State University, Fort Collins.*

Postpartum fertility in Holstein cattle is challenging for dairy production systems in southern Sonora Mexico as lactating cows need to get pregnant early in spring to avoid the negative impacts of summer heat stress. The GH-IGF1 signaling

pathway is known as important mediator of physiological mechanisms that regulate fertility in dairy cattle. The PAPPA2 gene is one component of this pathway, which codes for a protease responsible to increase IGF1 bioavailability for reproduction. The objective was to study the associative relationship between a SNP polymorphism in the *PAPPA2* gene (rs109952914-A/T within intron 10) with fertility traits such as first-service pregnancy (FSP), services per conception (SPC), and days open (DO) in postpartum Holstein cows. This SNP had a minor allele frequency of 18% and did not deviate from Hardy-Weinberg equilibrium (X^2 = 1.00, P > 0.42) in 676 Holstein cows. Reproductive records were collected from these cows that were located in three dairy herds in southern Sonora. A blood sample from each cow was spotted on FTA cards and used to genotype a 179 tag SNP panel within 45 genes in the GH-IGF1 pathway. The associative analyses among SNP genotypes and reproductive phenotypes were performed using a mixed effects model for categorical traits (i.e., FSP) and continuous traits (i.e., SPC and DO). The model included phenotype as the response variable, genotype and herd as fixed terms, sire as a random term, and days in milk as a covariate. Frequencies of FSP among genotypes AA, AT, and TT were 38.8 ± 2.6, 54.1 ± 1.9, and 66.7 ± 1.8%, respectively. Least square means among genotypes AA, AT, and TT were 2.3 ± 0.12, 2.0 ± 0.08, and 1.9 ± 0.06 services for SPC, and 159.8 ± 6.4, 153.9 ± 5.9, and 131.2 ± 3.9 d for DO, respectively. The most favorable allele from the SNP was the T allele (P < 0.001) as it increased FSP (12.6 ± 1.3%), and reduced SPC (−0.16 ± 0.05) and DO (−19.5 ± 5.6 d). In conclusion, a SNP within the *PAPPA2* gene appears to be a predictor of postpartum fertility, as it was positively associated to FSP, SPC and DO in postpartum dairy cows. These results provide evidence to propose the *PAPPA2* gene as candidate gene associated with fertility traits in postpartum Holstein cows and that it could be useful in DNA-based genetic selection tools.

Key Words: fertility, Holstein, *PAPPA2*, polymorphism.

0350 Using LD structure of several populations to optimize an SNP panel for conservation and selection. C. Díaz*[1], L. Varona[2], M. J. Carabaño[1], E. Nicolazzi[3], M. Bichard[4], J. Baro[5], A. Molina[6], J. Piedrafita[7], A. Rossoni[8], H. Schwarzenbacher[9], F. Seyfried[10], T. R. Solberg[11], D. Vicario[12], J. Altarriba[2], and K. J. Abraham[13], *[1]INIA, Madrid, Spain, [2]Universidad de Zaragoza, Spain, [3]Fondazione Parco Tecnologico Padano, Lodi, Italy, [4]English Guernsey Cattle Society, Launceston, UK, [5]Universidad de Valladolid, Palencia, Spain, [6]Universidad de Córdoba, Spain, [7]Universitat Autònoma de Barcelona, Bellaterra (Barcelona), Spain, [8]ANARB, Italian Brown Cattle Breeders' Association, Bussolengo (VR), Italy, [9]ZuchtData EDV-Dienstleistungen GmbH, Vienna, Austria, [10]Qualitas AG, Zug, Switzerland, [11]Geno Breeding and A.I. Association, Hamar, Norway, [12]National Simmental Cattle Breeders Association, ANAPRI, Udine, Italy, [13]Estacio-Uniseb, Ribeirão Preto, Brazil.*

The success of conservation of genetic variability and/or prediction of breeding values by genomic selection is based on the existence of LD between SNP markers and the QTVs. The existing LD is the result of several driving forces acting in each population along their history. Commercial SNP panels have been designed based on the genomic information of a reduced number of breeds. Within the Gen2Farm project framework, communalities and singularities of LD of 12 breeds from 8 countries were used to improve the design of existing SNP panels to fulfill the conservations and/or breeding needs in a breed and/or multibreed context. We analyzed the genomic information provided by the Illumina's BovineHD Beadchip of a total of 1534 individuals from: Asturiana de los Valles (AST, N = 75), Avileña-Negra Ibérica (ANI, N = 72), Brown Swiss (BS, N = 418), Bruna del Pirineus (BP, N = 75), Fleckvieh (Fl,N = 317), Guersey (GUE, N = 28), Morucha (Mo, N = 75), Norwegian Red (NR, N = 100), Pirenaica (Pi, N = 72), Retinta (Re, N = 72), Rubia Gallega (RG, N = 72) and Simmental (Si, N = 158). After editing, 604,551 phased SNP markers per animal were available for the analysis. LD matrices were obtained for each breed-chromosome (348 in total). TagSNPs defined in terms of independency and representativeness, were obtained by a graphical clustering algorithm. After setting aside singletons in each chromosome-breed, a minimum set of TagSNPs along the genome was obtained by maximizing the distance between TagSNPs and minimizing the distance between TagSNPs (centers of clusters) and markers of the same LD block. This was so provided some threshold values obtained from the empirical distribution of the LD values. Communalities and connectivity as a measure of the ratio of the number of tight links present to the maximum number possible were calculated. Connectivity varied between 0.00018 and 0.0013 for the first chromosome in

AST and the chromosome 21 in RE, respectively. All breeds shared a total of 17,720 TagSNPs, with values ranging from 421 TagSNPs in chromosome 25 to 1130 in chromosome 19. Moreover, there was also a high number of private TagSNPs present only in one breed, ranging from 1225 in chromosome 21 to 5827 in chromosome 1. Finally singletons were incorporated to the set of identified TagSNPs. Singletons represented more than 50% of TagSNPs in most cases. However, as the LD between singletons and QTVs is unknown, the maintenance of singletons in the SNP array may be considered as a choice to prevent loosing information.

Key Words: linkage disequilibrium, tags, selection, multibreed

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0351 Meiotic recombination differences in ruminant livestock species. K. M. Davenport* and B. M. Murdoch, *University of Idaho, Moscow.*

Homologous recombination or crossovers (CO) ensures proper chromosome segregation while contributing to genetic variation. It is clear from previous studies that at least one CO per chromosome arm is necessary to avoid mis-segregation. Furthermore, it has been well documented that the locations of CO are not random, with some genomic regions exhibiting preferences, called hotspots. Global meiotic recombination rates determined from offspring studies underestimates the total number of meiotic recombination events due to independent assortment. Despite the importance of meiotic recombination in the production of viable gametes and toward predicting or estimating genetic breeding values, we know very little about meiotic recombination rates in livestock species. In this study we have used a cytological approach to quantify the number of recombination events in male sheep and cattle. Characterizing recombination events using a cytological approach allows us to accurately identify all recombination events during meiosis without the need for a large number of offspring and independent of an accurate reference genome that does not exist. Testicular tissue samples were taken from mature rams and bulls, and spermatocytes were spread and fixed on slides. Immunofluorescent staining was used to identify the synaptonemal complexes (SYCP3) and CO events (MLH1) of pachytene stage prophase cells. The total number of CO per meiocyte was quantified for different livestock species. Interestingly, the average number of CO per meiocyte in sheep is approximately 20% higher than in cattle despite having a similar number of chromosome arms and genome size. More specifically, sheep have on average a greater number of recombination events per chromosome arm (~ 2.8 CO per arm) in comparison to cattle (~ 1.7 CO per arm). This research provides important information regarding differences in recombination rates in sheep and cattle spermatocytes, and has a direct impact on the genetic predictions in these species. Moreover, this research contributes valuable information toward a greater understanding of the factors that control meiotic recombination in different species to enhance reproduction, improve accuracy of genetic prediction, and advance selection strategies that support the sustainability of the livestock industry.

Key Words: meiosis, recombination, selection

0352 Genetics of heat stress in purebred and crossbred pigs from different states using BLUP or ssGBLUP. B. D. Fragomeni*[1], D. Lourenco[1], S. Tsuruta[1], K. A. Gray[2], Y. Huang[2], and I. Misztal[1], *[1]University of Georgia, Athens, [2]Smithfield Premium Genetics, Rose Hill.*

The objective of this study was to evaluate potential of regular and genomic selection to mitigate impacts of heat stress in swine populations. Phenotypes of body weight were available for purebred Duroc nucleus animals from farms in North Carolina (n = 151,336) and Texas (n = 55,897); and for commercial crossbred animals (Duroc x Landrace-Large White), hot carcass weight was available from North Carolina (n = 141,756) and Missouri (n = 86,435). Pedigree file combined the two populations and included 553,442 animals. Genotypic information was available for 8232 Duroc animals, for 60k SNP. Analyses were done with an animal model as either single- or two-trait model using phenotypes measured in different states as separate traits. Additionally, reaction norm models were fitted for one or two traits using heat load index as covariable. Heat load was calculated as temperature humidity index above 70 degrees (equivalent to 21°C and 100% relative humidity) and was averaged over 30 d before data collection. Variance components were estimated by AIREML and (genomic) estimated breeding values ((G)EBV) by BLUP or single-step GBLUP (ssGBLUP). Validation was assessed for 146 genotyped sires with progeny in last generation. Accuracy was calculated as correlation of (G)EBV from reduced data (all animals, except the last generation) and (G)EBV with complete data. Heritabilities for purebred animals were similar across states (varying from 0.23 to 0.26), and reaction norm models did not show evidence of heat stress effect. Genetic correlations between states and heat loads were always high (> 0.91). For crossbred animals, no difference in heritabilities were found in single- or two-trait analysis (from 0.17 to 0.18), and genetic correlations between states were moderate (0.43). In the reaction norm for crossbreds, heritabilities ranged from 0.15 to 0.30 and genetic correlation between heat loads were as low as 0.36. Accuracies with genomic information by ssGBLUP were on average 25% higher than by BLUP. Accuracies were higher in two-trait reaction norm models and at extreme heat load values. Impacts of seasonality are evident only for crossbred animals. Genomic information can help mitigating heat stress in swine by identifying superior sires more resistance to heat stress.

Key Words: genotype-by-environment interaction, heat stress, single-step GBLUP

0353 Genetic evaluation for heat tolerance in growing Angus cattle. H. L. Bradford[*1], B. D. Fragomeni[2], D. Lourenco[2], and I. Misztal[2], *[1]University of Georgia, Athens, [2]University of Georgia, Athens.*

The purpose was to investigate the existence of heat stress on preweaning growth in Angus cattle and to develop a genetic evaluation to improve heat tolerance. The American Angus Association provided weight data, and records from the southern United States (n = 82,669) were used because of the hot, humid summer months. Heat stress was measured using heat load, defined as the average degrees of temperature-humidity index greater than 24°C for 30 d before the weigh date. Forty-five percent of cattle experienced heat loads greater than 0. Heat load was used in a reaction norm to assess phenotypic plasticity, and the results were compared with a univariate analysis. For both models, random effects included direct genetic, maternal genetic, maternal permanent environment, and residual; and fixed effects included a linear age covariate, age of dam class, sex, herd, and year. Moderate differences in heat load resulted in strong direct genetic correlations (r > 0.80), but large heat load differences had weaker direct genetic correlations. The same pattern occurred for Spearman rank correlations for proven bulls (n = 1048) with r = 0.30 between no heat load and extreme heat load. Selection decisions should differ depending on heat load, and producers could benefit from environment-specific selection tools. As heat load increased, the maternal genetic effect remained consistent even though heat stress decreased milk production in dairy cows. To compensate for the expected reduction in dam milk production during heat stress, calves may have consumed creep feed or other forages to maintain growth. In addition to comparing results, accuracy was assessed by the ability to predict phenotypes for young animals. Predictivity did not improve when using the reaction norm (r = 0.31) instead of the univariate model (r = 0.30). Thus, the univariate analysis performed as well as the reaction norm and sufficiently evaluated genetic differences in growth despite heat stress. Additional research is needed on methods for assessing heat tolerance in national cattle evaluations. Researchers implemented heat load successfully in species raised in confinement including dairy and swine, but heat load was confounded with contemporary group, calving season, seasonal fluctuations in forage quality and quantity, and fescue toxicity for beef cattle. A more robust measure of heat load would aid in understanding the effect of heat stress on preweaning growth and creating selection tools for improving beef cattle heat tolerance.

Key Words: beef cattle, heat stress, weaning weight

0354 Angus cattle at high elevation: Comparison of models to estimate breeding values of yearling pulmonary arterial pressure. X. Zeng[*1], T. N. Holt[2], S. E. Speidel[1], R. M. Enns[1], and M. G. Thomas[1], *[1]Department of Animal Sciences, Colorado State University, Fort Collins, [2]College of Veterinary Medicine and Biomedical Sciences, Colorado State University, Fort Collins.*

As an indicator of pulmonary hypertension, pulmonary arterial pressure (PAP) is widely used in the selection of cattle to reduce the incidence of high altitude disease (HAD). In initial analyses of yearling PAP data, a violation of normal distribution of residuals (i.e., skewed right tail) was observed. To remedy, alterative expressions of yearling PAP were investigated in this study with a goal of determining the effect of alternative expressions on genetic evaluation outcomes. Yearling PAP records (42.46 ± 0.58mmHg) were collected from 5296 Angus cattle from 280 sires from Colorado State University Beef Improvement Center (2150m elevation). The alternative phenotypes included power-transformed (PT) PAP records, an ordinal three-category phenotype (CAT3), an ordinal two-category phenotype (CAT2) and the non-transformed PAP observations (RAW). The CAT3 observations were defined as low risk (PAP < 41mmHg), moderate risk (41mmHg ≤ PAP ≤ 49mmHg) and high risk (PAP > 49mmHg) for HAD. The CAT2 observations were constructed by combining low and moderate risk categories of CAT3. Univariate linear and threshold animal models were applied in analyses of RAW and PT; CAT3 and CAT2, respectively. The fixed effects for PAP phenotypes included sex, age of dam, date and age (covariate) of PAP measurement. All fixed effects were significantly (P < *0.05*) associated with each PAP phenotype. The estimated heritabilities were 0.24, 0.24, 0.26, and 0.31 for RAW, PT, CAT3 and CAT2, respectively. Sire EBV accuracies from univariate models of RAW, PT, CAT3 and CAT2 ranged from 0.03 to 0.67, 0.03 to 0.68, 0.01 to 0.65 and 0.01 to 0.58 with means of 0.31, 0.31, 0.28 and 0.21, respectively (pooled sd = 0.13). The Rank correlations between EBV from RAW and PT, CAT3 or CAT2 were 0.92, 0.84 and 0.77, respectively. The lowest Rank correlation (0.69) was identified between PT and CAT2, while Rank correlation of 0.91 was obtained between PT and CAT3. All phenotypes resulted in decreasing genetic trends. Results suggested similar heritability, accuracy and rank of animals based on EBV from RAW and PT, yet losses in EBV accuracy and some re-ranking of sires was observed in ordinal categorical phenotypes compared with continuous PAP scores. In conclusion, violation of normality had limited influences on the genetic evaluation of yearling PAP measurements. Ordinal categorical phenotypes can be alternative dependent variables in studying susceptibility of HAD, however, they would cause some re-ranking of sires relative

to non-transformed PAP scores.

Key Words: cattle, pulmonary arterial pressure, genetic evaluation

0355 The effect of heterosis on pulmonary arterial pressure on beef cattle. M. M. Culbertson[*1], M. G. Thomas[2], L. L. Leachman[3], R. M. Enns[2], and S. E. Speidel[2], *[1]Colorado State University, Department of Animal Sciences, Fort Collins, [2]Department of Animal Sciences, Colorado State University, Fort Collins, [3]Leachman Cattle of Colorado, Fort Collins.*

Pulmonary hypertension can develop due to hypoxia-induced pulmonary vascular remodeling leading to right ventricular hypertrophy and edema, a condition known as brisket or high altitude disease (HAD). Pulmonary arterial pressure (PAP) is used at high altitude regions (> 1500 m) as an indicator of an animal's susceptibility to pulmonary hypertension and HAD. Cattle located at altitudes greater than 1500 m with PAP measurements between 31 and 43 mm Hg are considered to have a low risk of developing HAD at most elevations. To date, there has been no reported research for the effects of heterosis on PAP and therefore, the objective of this study were to examine the effect of heterosis on PAP measurements. Classically, heterosis is most beneficial for survival and fertility related traits; therefore, we hypothesized that increased heterozygosity would decrease an animal's PAP phenotype. Data collected from 2009 to 2015, was obtained from a multibreed seedstock database with an average PAP measurement of 44.56 ± 11.58, and a minimum and maximum of 32 and 149 mm Hg. Data included PAP records (n = 2001), PAP testing date, yearling management code, date of birth, sex and breed. A mixed animal model was used to estimate the effect of heterosis on PAP with the model containing degree of outcross and PAP age as covariates; and contemporary group (i.e., combination of PAP date and yearling management code) and sex as categorical fixed effects. Animal was included as a random effect. A 3-generational pedigree consisting of 9353 animals was used to estimate genetic parameters for PAP (h^2 = 0.29 ± 0.07). Breed effects were included as covariates of breed percentages for Angus, Red Angus, Charolais, South Devon, Gelbvieh, Simmental and "Other" breeds. The effect of breed on PAP had a range of 8.75 mm Hg. The estimated regression coefficient for PAP on heterosis was −0.02 ± 1.31 mm Hg/percent outcross ($P < 0.155$). These results indicate that heterozygosity has no effect on PAP measurements, although other multibreed populations should be examined. As a result we would reject our hypothesis that an increase in heterosis would decrease PAP.

Key Words: pulmonary arterial pressure, heterosis, regression

0356 Genetic and phenotypic analysis of Israeli Holstein milk, fat, and protein production as determined by the Afilab real-time milk analyzer. J. I. Weller[*1] and E. Ezra[2], *[1]ARO, The Volcani Center, Bet Dagan, Israel, [2]Israel Cattle Breeders Association, Caesaria, Israel.*

Given the day-to-day variation in milk components, especially fat, the standard DHIA procedure of measuring milk components in just 1 milking per month, may not be very representative of total production. The combination of much more frequently, but less accurately analyzed milk components, may be more representative of a cow's longer-term milk composition. The AfiLab system (Afimilk, Kibbutz Afikim, Israel) is a real-time individual cow milk analyzer that uses near-infrared spectroscopy for on-line milk analysis. AfiLab records for milk production and fat and protein concentration collected from January 2014 through January 2016 from 47 large Kibbutz (communal) herds distributed throughout Israel with a total of 37,486 Israeli Holstein cows were compared with the same statistics derived from monthly test day records derived by Bentley and Foss milk analyzers at the central laboratory of the Israel Cattle Breeders Association (ICBA). The SD for first and second parity daily records scored by the ICBA and AfiLab system were very similar for all traits, except for fat percentage. The SD for complete lactation production were slightly lower for the AfiLab results for all traits, except protein production. The lactation means for all traits were quite similar by the two methods in both parities, except for fat production, which was higher for the ICBA records. This corresponds to the fat lactation curves, which show that the ICBA results were higher with low DIM, but nearly equal to the AfiLab results after 125 DIM. AfiLab overestimated protein percentage before 150 DIM, and underestimated protein percentage in the second half of the lactation. First parity heritabilities (see table) were higher for AfiLab lactations for all traits, except for protein percentage. For AfiLab records, coefficients of determination to predict future lactation production from truncated lactations were greatest and root mean squared errors were smallest if the mean production from the last 2 wk before the truncation date were used to estimate future production. AfiLab first parity partial lactations with < 150 DIM predicted future lactation more accurately than the corresponding ICBA partial lactations. With only 30 DIM, genetic correlations between predicated and actual lactations ranged from 0.73 to 0.79 for the 3 traits. Further study is required to compare results of individual cows on multiple lactations, and to determine the optimum interval between calibrations for AfiLab meters.

Key Words: dairy cattle breeding, genetic evaluation, milk analysis

Table 0356.

Heritabilites (in **bold type**), genetic (above the diagonal) and environmental (below the diagonal) correlations among 7,866 first parity 305 d milk, fat and protein production records and fat and protein percentage computed from the ICBA and AfiLab records.

		Milk		Fat		Protein		% fat		% protein	
Trait	Method	ICBA	AfiLab	ICBA	AfiLab	ICBA	AfiLab	ICBA	AfiLab	ICBA	AfiLab
Milk	ICBA	**0.334**	0.996	0.267	0.529	0.848	0.902	-0.707	-0.519	-0.640	-0.420
	AfiLab	0.963	**0.351**	0.258	0.515	0.847	0.911	-0.709	-0.534	-0.633	-0.407
Fat	ICBA	0.548	0.509	**0.229**	0.590	0.333	0.263	0.492	0.312	-0.023	-0.046
	AfiLab	0.682	0.712	0.703	**0.309**	0.632	0.444	-0.042	0.449	-0.070	-0.263
Protein	ICBA	0.909	0.863	0.639	0.731	**0.271**	0.858	-0.526	-0.267	-0.137	-0.154
	AfiLab	0.894	0.932	0.535	0.668	0.869	**0.321**	-0.621	-0.510	-0.441	0.004
% fat	ICBA	-0.479	-0.481	0.464	0.015	-0.288	-0.384	**0.479**	0.698	0.556	0.345
	AfiLab	-0.367	-0.375	0.256	0.378	-0.171	-0.344	0.661	**0.565**	0.585	0.171
% protein	ICBA	-0.506	-0.515	0.010	-0.120	-0.106	-0.343	0.552	0.526	**0.545**	0.564
	AfiLab	-0.294	-0.299	0.006	-0.200	-0.057	0.066	0.319	0.133	0.524	**0.460**

0357 ADSA®-EAAP speaker exchange presentation: Genetic analysis of multivariate indices of detailed fatty acid profile determined by gas chromatography in bovine milk.

N. P. P. Macciotta*[1], M. Mele[2], A. Cecchinato[3], G. Conte[4], S. Schiavon[5], and G. Bittante[6], *[1]Dipartimento di Agraria, University of Sassari, Italy, [2]University of Pisa, Italy, [3]University of Padova, Legnaro PD, Italy, [4]Department of Agriculture, Food and Environment, Universitã di Pisa, Italy, [5]Department of Agronomy, Food, Natural resources, Animals and Environment (DAFNAE), University of Padova, Italy, [6]Department of Agronomy, Food, Natural Resources, Animals and Environment (DAFNAE), University of Padova, Italy.*

The genetic improvement of fatty acid (FA) composition is a crucial point for enhancing milk dietary and nutritive properties. However the development of an appropriate breeding goal for this trait is hampered by the large number of FA and the complex correlation pattern among them. Multivariate factor analysis (MFA) is able to derive synthetic variables that can describe efficiently a multivariate system with a complex covariance structure. This study was aimed at: (1) elucidating the structure of relationships between milk yield, composition and detailed FA composition by using the MFA, and (2) estimating genetic parameters for the new-derived synthetic variables. Individual milk samples were collected from 1158 Brown Swisscows and gas chromatography was used to obtain detailed milk FA compositions. MFA was performed on 53 variables (i.e., 47FA and 6 milk production and composition traits). A total of 12 factors were extracted, able to explain about the 75% of the total variance. Factor scores were then used as new phenotypes for estimating (co)variance components using a Bayesian linear animal model via Gibbs Sampling. The model accounted for the effect of days in milk, parity, herd and animal additive genetic effect. Factor scores exhibited a clear structure in term of relationship with the original variables and they were classified, from a biological point of view, as: 'de novo FA,' 'milk yield-branched FA,' 'biohydrogenation,' 'long chain FA,' 'short chain FA,' 'milk-fat-protein,' 'odd FA,' 'conjugated linoleic acid,' 'linoleic,' 'udder health,' and 'vaccelenic,' respectively. Marginal posterior means (SD) of heritabilitiesfor the aforementioned factor scores ranged from 0.048(0.02) for 'vaccelenic' to 0.310(0.09) for 'desaturation.' Moderate heritability estimates were observed for 'milk yield-branched FA' (0.214 ± 0.07), 'linoleic' (0.201 ± 0.08), 'biohydrogenation' (0.193 ± 0.08), and 'short chain FA' (0.157 ± 0.07), respectively. Results highlight the existence of important and exploitable genetic variation in these derived phenotypes. In particular factors strongly associated with variables related to mammary neo-synthesis and desaturation, may offer interesting perspectives for improving

milkfat nutritional properties by selective breeding.

Key Words: fatty acid profile, multivariate factor analysis, heritability

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0358 Effectiveness of genomic prediction of boar taint components in Pietrain sired breeding populations. C. Große-Brinkhaus[*1], E. Heuß[1], J. Trautmann[2], D. Mörlein[2,3], K. Schellander[1], C. Looft[1], J. Dodenhoff[4], K. U. Götz[4], and E. Tholen[1], *[1]Institute of Animal Science, University of Bonn, Germany, [2]Department of Animal Science, University of Göttingen, Germany, [3]Isi GmbH & Co. KG, Rosdorf, Germany, [4]Bavarian State Research Centre for Agriculture, Institute of Animal Breeding, Poing, Germany.*

Systematic concern for animal welfare with regard to piglet castration without anesthesia is one challenge in European pig production. For instance, in 2013 the German Federal Council passed the law that non-anesthetized surgical castration will be prohibited by 2019. One alternative is the fattening of entire boars which is controversially discussed, because the risk of tainted meat has to be minimized. One possibility is to include selection for a low incidence of boar taint in breeding programs.

In this study, beside androstenone (And) and skatole (Ska), boar taint perception was recorded by a 10-member trained sensory panel (SENS) established by Mörlein and colleagues. Compiling data from four research projects, in total 4,000 records for And and Ska, and 1,016 records for SENS were available.

Genetic marker effects of 45,645 SNPs on And, Ska and SENS scores were estimated for 1,240 crossbred boars and 976 purebred Pietrain boars. These crosses and purebred boars reflect the heterogeneous population-structure of the Pietrain breed in Germany. Genomic BLUP was used to estimate genomic breeding values for animals in calibration and validation sets. Reliability of genomic prediction was assessed as correlation between genomic breeding value and conventional breeding values. Several scenarios were investigated to evaluate the effectiveness of genomic prediction.

Heritabilities for And, Ska and SENS were 0.64, 0.48 and 0.36, respectively. In a first scenario genomic prediction was evaluated using a five-fold cross validation within all crossbred animals and showed reliabilities ranging from 0.33 to 0.49. Based on a forward prediction, using crossbred boars as calibration set and Pietrain boars as validation set, reliabilities between 0.15 and 0.50 for all boar taint traits were observed.

Our analysis showed that genomic selection against boar taint is promising. It was possible to reach adequately high reliabilities, even in small populations.

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Key Words: swine, boar taint, genomic selection

0359 Understanding the genetic archticture of Hays Converter Cattle. M. K. Abo-Ismail[*1,2], R. Khorshidi[1], E. C. Akanno[1], J. Crowley[1,3], S. P. Miller[4,5,6], A. Fleming[7], J. Basarab[1,8], C. Li[1,9], P. Stothard[1], and G. Plastow[1], *[1]Livestock Gentec, Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Canada, [2]Animal and Poultry Production, Damanhour University, Egypt, [3]Canadian Beef Breeds Council, Calgary, AB, [4]AgResearch Limited, Mosgiel, New Zealand, [5]Centre for Genetic Improvement of Livestock, University of Guelph, ON, Canada, [6]University of Queensland, Centre for Animal Science, QAAFI, St. Lucia, Australia, [7]Centre for Genetic Improvement of Livestock, Department of Animal Biosciences, University of Guelph, ON, Canada, [8]Lacombe Research Centre, Alberta Agriculture and Forestry, Lacombe, Canada, [9]Lacombe Research and Development Centre, Agriculture and Agri-Food Canada, Edmonton, AB, Canada.*

The Hays Converter (HC) was the first Canadian breed to be recognized in terms of the Canadian Livestock Pedigree Act and combines the genetics of the Hereford, Holstein and Brown Swiss breeds. Although, the improvement program has continued there is now a risk to its sustainability. The objective of this study is to utilize genomic tools to assess genetic diversity and inbreeding within the HC population. Historical samples for 265, 238, and 208 animals born between 1973 and 2015 have been genotyped for 19K (19,792 SNPs,), 6K (6829 SNPs) and Illumina BovineSNP50 (50K, 49,100 SNPs), respectively. A total of 49,100 SNPs across 29 autosomes that passed all quality control criteria were considered for imputation of the target populations with 19k (7496 SNPs) and with 6k (6253 SNPs) using FImpute. The actual and imputed genotypes were filtered for 702 animals and 41,734 SNPs across 29 autosomes passed quality control. Using only actual 50K genotypes of 208 animals, the genetic structure of the HC population was assessed in conjunction with individuals genotyped for Illumina BovineSNP50 from Angus (AN, $n = 486$), Hereford (HE, $n = 591$) and Holstein (HO, $n = 32$) breeds using principal component analysis (PCA). The genomic inbreeding coefficients for individuals within HC were estimated using pedigree information and 4 genomic methods. The genetic distances between animals within each population were calculated based on their genomic profile using Prevosti Distance. Although, the PCA indicated that the HC breed is genetically divergent from Holstein, Hereford and Angus, it was more closely related to Holstein cattle than the other breeds. Genomic inbreeding coefficients using imputed or actual genotypes indicated that the HC is inbred over years,

particularly from 1993 till 2005. Thus, this indicates a smaller effective population size for the HC population at that time. The result from genetic distance and phylogeny of the HC population indicated existence of sub populations within the HC. In conclusion, the study showed an increase of inbreeding within HC breeds so that managing inbreeding and maximizing diversity is required to avoid inbreeding depression. The observed diversity will influence HC design for future mate allocation using genomic information.

Key Words: genetic structure, Inbreeding, Illumina BovineSNP50 chip, Hays Converter beef cattle

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0360 Genetic parameters and trends for length of productive life and lifetime production efficiency traits in Thai Landrace and Yorkshire sows.

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Data from a commercial swine population in Northern Thailand were used to estimate genetic parameters and trends for length of productive life (LPL), lifetime number of piglets born alive per year (LBAY), lifetime number of piglets weaned per year (LPWY), lifetime litter birth weight per year (LBWY), and lifetime litter weaning weight per year (LWWY). Phenotypic records were from 2259 Landrace and 826 Yorkshire sows that had their first farrowing between 1989 and 2013. An average information restricted maximum likelihood procedure was used to estimate variance and covariance components, heritabilities and correlations. The 5-trait animal model included first farrowing year-season, breed group, and age at first farrowing as fixed effects, and sow and residual as random effects. Heritability estimates were 0.17 ± 0.04 for LPL, 0.07 ± 0.03 for LBAY, 0.13 ± 0.03 for LPWY, 0.04 ± 0.02 for LBWY and 0.13 ± 0.03 for LWWY. Genetic correlations between LPL and all lifetime production efficiency traits (LBAY, LPWY, LBWY and LWWY) were all positive ranging from 0.66 ± 0.14 (LPL-LBAY) to 0.95 ± 0.02 (LPL-LBWY). Rank correlations between EBV for LPL and lifetime production efficiency traits were, on the average, higher for boars than for sows in the top 5% (0.51 vs. 0.19), 25% (0.68 vs. 0.42) and 50% (0.86 vs. 0.58). Sire genetic trends were negative for LPL (−2.41 ± 0.59 d/yr; $P < 0.001$) and LWWY (−0.14 ± 0.06 kg/yr; $P < 0.04$) and near zero for LBAY, LPWY, and LBWY. Conversely, dam genetic trends were positive for LPL (1.10 ± 0.39 d/yr; $P < 0.01$), LPWY (0.12 ± 0.01 piglets/yr; $P < 0.0001$), and LWWY (0.26 ± 0.04 kg/yr; $P < 0.0001$) and near zero for LBAY and LBWY. Sow genetic trends were near zero for all traits. Improvement for LPL and lifetime production efficiency traits in this commercial swine population will require these traits to be included in the selection indexes used to identify replacement boars and gilts.

Key Words: swine, length of productive life, lifetime production efficiency

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0361 Estimation of genetic parameters on carcass traits and body type measurements in Hanwoo.

Y. S. Choi*[1], S. W. Kim[1], K. S. Kim[1], D. J. Yu[1], M. J. Ku[1], G. H. Lee[1], S. G. Park[1], and J. W. Lee[2], *[1]Livestock Research Institute, Jeollanamdo Agricultural Research & Extension Service (JARES), Jeollanamdo, Korea (The Republic of), [2]Chonnam National University, Gwangju, Korea (The Republic of).*

The objective of this study is to estimate genetic parameters on carcass traits and body type measurements in Hanwoo cows (Korean native cattle). The data for this study were obtained from local rearing farms in Jeonnam province, South Korea from 2003 to 2014. Two hundred seventy-seven head of reproductive cattle were measured for withers height, rump height, body length, chest depth, chest width, rump length, pelvic width, rump width, hipbone width, chest girth, and shank girth. Of the 277 head of cattle, 151 were randomly selected for investigation of carcass traits. Birth year, birth location, and sex were considered as fixed factors.

Genetic correlation coefficients of live weight with chest depth, chest width, rump width, and chest girth were 0.67, 1.00, 0.97, and 0.99, respectively. Genetic correlation coefficients of rump length with withers height, rump height, chest width, and pelvic width were 0.85, 0.92, 0.85, and 0.98, respectively.

Positive selection for chest girth, chest width, chest depth, and rump width resulted in increased live weight. Correlation coefficients of rump length with withers height and rump height were highly positive, which suggests that rump length and rump width are informative indicators for selection of body type measurements.

Heritabilities of body type measurement and carcass traits ranged from 0.19 to 0.83. Estimates of heritability on marbling score, body length, and rump height were 0.18, 0.19, and 0.24, respectively. Estimates of heritability on eye muscle area, shank girth, and withers height were 0.30, 0.36, and 0.48, respectively. Heritabilities of carcass weight, chest width, live weight, hipbone width, rump length, and chest depth were 0.51, 0.67, 0.68, 0.71, 0.76, and 0.77, respectively.

The genetic correlation between carcass weight and chest depth was a negative value of −0.98. The genetic correlation between carcass weight and chest width was 0.68. Genetic correlation coefficients of eye muscle area with rump length, chest depth, hipbone width, and shank girth were 0.67, 0.84, 0.66, and 0.94, respectively. Genetic correlation coefficients of marbling score with withers height, rump length, and hipbone width were −0.54, −0.74, and −0.83, respectively.

Improvement in both quality and quantity traits of Hanwoo cows is difficult due to the negative correlation between the two traits. To develop an optimal breeding scheme for Hanwoo cows, rearing farms need to establish breeding goals for Hanwoo cows individually and obtain informative data, including

pedigree information and reproductive records, from each cow.

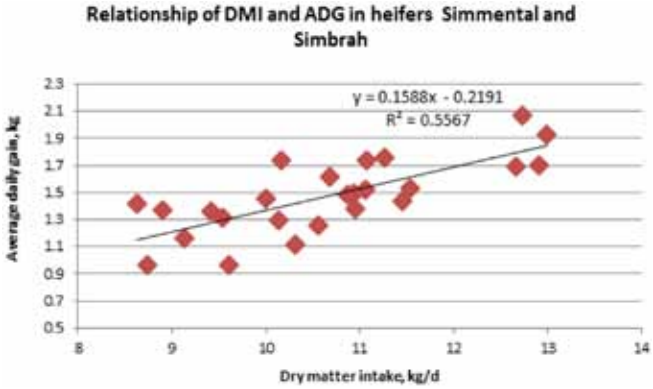
Key Words: Korean native cattle, genetic parameters, body measurement, genetic correlation

0362 Residual feed intake (RFI) for genetic selection of Simmental and Simbrah cattle. N. Manzanares-Miranda*[1], J. R. Kawas[2], H. Villalon-Mendoza[2], and G. Moreno-Degollado[2], *[1]Universidad Autonoma de Nuevo Leon, Posgrado Conjunto de las Facultades de Agronomia y Medicina Veterinaria y Zootecnia, San Nicolas de los Garza, Mexico, [2]Universidad Autonoma de Nuevo Leon, San Nicolas de los Garza, Mexico.*

Since two-thirds of the cost of cattle production is directly related to feed costs, strategies that improve the efficiency of feed utilization will increase the economic viability of livestock operations. An alternative measurement for feed efficiency is the residual feed intake (RFI). The objective of this study was to determine the possibility of using RFI as an indicator for genetic selection of males and females of Simmental and Simbrah cattle breeds. Thirty-one Simmental and 26 Simbrah, males (32) and females (25), were randomly assigned to a 2 × 2 factorial design (breeds and gender). Variables measured were dry matter intake (DMI), average daily gain (ADG) and RFI. There was no correlation between RFI, DMI and ADG. Individuals with negative RFI were detected in the test group among both breeds. ADG was greater ($P < 0.05$) for males (1.81 kg/d) than females (1.47 kg/d). A significant association ($P < 0.05$) between the different variables studied. No statistical differences in RFI were observed for breed ($p = 0.44$) or gender ($p = 0.52$). It was not possible to use RFI as an indicator for genetic selection for Simmental and Simbrah cattle.

Key Words: Simmental, Simbrah, residual feed intake

Table 0362.



0363 Multivariate analysis of reproductive and productive traits in Sindhi breed females (*Bos indicus*). R. R. C. Mello[1], L. D. P. Sinedino*[2], S. L. G. Sousa[1], and M. R. B. Mello[1], *[1]Federal Rural University of Rio de Janeiro, Seropedica, Brazil, [2]University of Florida, Gainesville.*

The aim of this study was to investigate the possibility to generate different productive groups in Sindhi breed through multivariate techniques, to give directions to genetic improvement programs in this breed. For this goal, performance data provided by the Brazilian Association of Zebu Breeders related to 560 Sindhi breed females from 28 different herds in Brazil, born in the period from 1987 to 2011, were used. The traits age at first calving, calving interval, reproductive efficiency, total milk yield and lactation period were analyzed, being submitted to the principal components and cluster analysis, with the GENES® statistical program. By the principal components analysis, these five components were estimated, and the first three explained 90.79% of the data's total variation. The traits considered most relevant to the discrimination of the data set, in decreasing order of importance, were: calving interval, lactation period, age at first calving, total milk yield, and reproductive efficiency. By cluster analysis, 12 different groups were generated from the pool of Sindhi herds analyzed, with a great homogeneity among females for the traits evaluated, and only few females generating separate groups. Four hundred twenty-nine females were clustered in one group, representing 76.60% of the genotypes. This indicates that, although there are genotypes with large genetic diversity, more than two thirds of the animals are similar to the traits evaluated, showing a high degree of relationship between them. The traits for total milk yield showed 71.92% of the total variation, and age at first calving contributed with 23.06% of the variation, being the two most important traits for the variability of the data. Thus, there is evidence of divergence between the groups regarding total milk yield, indicating that this trait stands out in the differentiation of groups, and these groups could be benchmarks for the use of genetic improvement programs whose focus is the increase in milk yield. In conclusion, the multivariate procedures were effective to summarize the evaluated information and to discriminate the most important traits, providing better identification of the most appropriate females to certain herds or milk production systems. The analysis of the relative contribution was effective in identifying total milk yield and age at first calving as the most relevant traits for the differentiation of groups, and they can be useful targets for genetic improvement programs that focus on milk yield and reproductive precocity.

Key Words: cluster analysis, reproductive efficiency, milk yield

0364 Repeatability of egg weight in Japanese quail. O. T. Abanikannda, O. N. Ottun*, and A. O. Leigh, *Lagos State University, Ojo-Lagos, Nigeria.*

Knowledge of genetic parameters is useful in designing efficient breeding systems, and accurate estimates of genetic parameters are essential for construction of applied breeding. Repeatability, the ability of individual animal to repeat its performance and maintain its ranking in a population in successive records is of immense benefit in predicting the expected rate of annual genetic gain in the trait. The objective of the study was to evaluate and assess changes in measurements of eggs by quail hens over a period of time and estimate its repeatability. The study was conducted at the Poultry Breeding Research Laboratory of the Lagos State University, Ojo-Lagos, lying at 06.48N and 003.20E in the humid tropics of Nigeria. The hens studied were brooded and raised from hatch to 6 wk before being separated and raised in individual compartments for ease of egg collection, identification and measurements. In all, 70 hens were studied over a period of 34 d, with each hen laying between 17 and 33 eggs during the study period. The eggs were picked as soon as it was laid and properly tagged to reflect the hen's identification and day of lay. Measurements taken include, hen weight (HenWt), feed consumed (FeedCon), egg weight (EggWt), egg length (EggLt) and egg width (EggWd). The statistical model describing each of the three (egg weight, egg length and egg width) variables studied is given as $Y_{ijklm} = D_i + H_j + C_k + F_l + e_{ijklm}$, where day of lay (D) and Hen (H) are fixed factors and HenWt (C) and FeedCon (F) are covariates to adjust for differences among hens, and it accounted for 62.67%, 49.40% and 71.94% of the total variation, respectively. With the exception of feed consumed which was not significant ($P > 0.05$) on any of the three responses and day of lay which was not significant ($P > 0.05$) on egg weight, all other factors/covariates were highly ($P < 0.01$) significant. Repeatability estimates for the three variables studied were estimated using the one way ANOVA of Hen effect on each of the three variables by $r = [(MS_b – MS_w)/n_0]/\{MS_w + [(MSb\text{-}MS_w)/n_0]\}$ and repeatability values obtained were 0.56, 0.15 and 0.12 respectively for egg weight, egg length and egg width. The repeatability estimate for egg weight, the most desirable trait in successful poultry business is moderate (0.56) and can be employed early in lay to select hens with potentials for bigger eggs.

Key Words: repeatability estimates, quail, Nigeria

365 Genetic parameters of cyclicity and other fertility indicators in dairy cattle. D. Gonzalez-Pena[*1], H. Jeong[2], P. J. Pinedo[3], J. E. P. Santos[4], G. M. Schuenemann[5], G. J. M. Rosa[6], R. O. Gilbert[7], R. C. Bicalho[7], R. Chebel[4], K. N. Galvão[8], C. M. Seabury[9], W. W. Thatcher[10], and S. L. Rodriguez Zas[2], *[1]Zoetis, Kalamazoo, MI, [2]University of Illinois, Urbana-Champaign, [3]Colorado State University, Fort Collins, [4]University of Florida, Gainesville, [5]Department of Veterinary Preventive Medicine, The Ohio State University, Columbus, [6]University of Wisconsin, Madison, [7]Cornell University, Ithaca, NY, [8]Department of Large Animal Clinical Sciences, University of Florida, Gainesville, [9]Texas A&M University, College Station, [10]Department of Animal Sciences, University of Florida, Gainesville.*

Resumption of ovarian cyclicity after calving is crucial to achieving reproductive efficiency in cattle. Early onset of ovulation after calving can decrease veterinary costs and calving interval while augmenting the length of lactation, total milk yield, and genetic improvement of the herd. Four fertility indicators are frequently used: probability of cycling at 45 d post-calving (Pr_Cyc), probability of disease diagnosis at 45 d post-calving (Pr_Sck), probability of pregnancy after 2 AIs (Pr_Prg), and days open (DO). The goal of this study was to identify significant covariables that affect these fertility indicators and to estimate their genetic parameters in dairy cattle. Measurements from approximately 5000 cows from 4 U.S. states (CA, FL, MN, TX) across two calving years were analyzed and relevant covariables were identified by stepwise selection. The three indicator probabilities were described using a logistic model including the explanatory variables: dystocia, retained placenta, stillbirth, body condition score at 7 d and 35 d post-calving (BCS7 and BCS35, respectively), score of vaginal mucous (0 = no mucus to 5 = brownish fetid discharge) at 7 d, 12 d, and 35 d post-calving, and blood β-hydroxybutyrate (BHBA), an indicator of subclinical ketosis. A univariate sire model including the effects of contemporary group and lactation number was used to estimate the genetic parameters of four fertility indicators: Pr_Cyc, Pr_Sck, Pr_Prg, and DO. The percentage of cows cycling, diagnosed with a disease, and pregnant after 2 AIs were 75.5%, 16.6%, and 62.5%, respectively. The marginal probabilities of the significant covariables indicated that Pr_Cyc was 4.8%, 1.5%, and 1.2% lower per unit increase in BHBA, and mucus score at 7 d and 35 d post-calving, respectively. Also, Pr_Cyc was 7.0% higher per unit increase in BCS35. Similarly, the Pr_Prg was 3.2% and 3.0% lower per unit increase in BHBA and mucus score at 35 d post-calving, respectively. The Pr_Sck increased 33.8% per unit increase in BHBA and 2.3% with stillbirth. The heritability estimates for Pr_Cyc, Pr_Sck, Pr_Prg, and DO were 0.12, 0.03, 0.07, and 0.06, respectively. Our findings

corroborate that early resumption of cyclicity postpartum is an important indicator of cow reproduction performance and has substantial genetic variability that can be exploited in selection practices. Improved accuracy of pregnancy predictions is maybe one of the potential benefits of including this indicator in fertility indices. These findings contribute to a long-term multistate project database (USDA-NIFA-AFRI-003542) for direct measures of fertility.

Key Words: reproduction, cattle, pregnancy

0366 Genetic parameters of early lactation diseases in dairy cattle. D. Gonzalez-Pena[*1], T. M. Goncalves[2], P. J. Pinedo[3], J. E. P. Santos[4], G. M. Schuenemann[5], G. J. M. Rosa[6], R. O. Gilbert[7], R. C. Bicalho[7], R. Chebel[4], K. N. Galvão[8], C. M. Seabury[9], W. W. Thatcher[10], and S. L. Rodriguez Zas[2], *[1]Zoetis, Kalamazoo, MI, [2]University of Illinois, Champaign-Urbana, [3]Colorado State University, Fort Collins, [4]University of Florida, Gainesville, [5]Department of Veterinary Preventive Medicine, The Ohio State University, Columbus, [6]University of Wisconsin, Madison, [7]Cornell University, Ithaca, NY, [8]Department of Large Animal Clinical Sciences, University of Florida, Gainesville, [9]Texas A&M University, College Station, [10]Department of Animal Sciences, University of Florida, Gainesville.*

Early lactation diseases impact herd profitability, compromise animal welfare, increase antibiotic use, and affect consumer preferences. Therefore, genetic improvement of disease resistance is becoming an increasingly important goal in dairy cattle breeding. The objectives of this study were to estimate the genetic parameters of major diseases and to identify variables that affect the incidence of these diseases. The probabilities of a cow to develop metritis (Pr_Met), clinical endometritis (Pr_End), ketosis (Pr_Sck), and clinical mastitis (Pr_Mas) were evaluated. Disease records from approximately 5000 cows across U.S. regions (West, Midwest, South, and Southwest) and two calving years were analyzed. Univariate logistic sire models including the effects of contemporary group and lactation number and additional covariates were used to estimate genetic parameters. Additional explanatory variables included: dystocia, retained placenta, stillbirth, body condition score at 7 d and 35 d post-calving (BCS7 and BCS35, respectively), vaginal mucous score at 7 d, 12 d, and 35 d post-calving (on scale of 0 = no mucus to 5 = brownish fetid discharge), and blood β-hydroxybutyrate (BHBA) as indicator of subclinical ketosis. Stepwise selection enabled the identification of the explanatory variables significantly associated with the probability of each disease. The percentage of cows with metritis, endometritis, ketosis, and mastitis were 28.8%, 22.4%, 16.6%, and 7.6%, respectively. Among the significant explanatory variables, Pr_Met increased 5.1% per unit increase in BHBA. Also, Pr_Met increased 35.9% and 7.6% in cows diagnosed with retained placenta and dystocia, respectively. On the other hand, Pr_Met decreased 6% per unit increase of BCS7. The heritability estimates (and standard errors) for Pr_Met, Pr_End, Pr_Sck, and Pr_Mas were 0.06 (0.01), 0.07 (0.02), 0.03 (0.02), and 0.02 (0.007), respectively. The association between explanatory variables and early postpartum disease probabilities and low heritability estimates identified in this study confirm that reliable prediction of disease incidence in dairy herds requires comprehensive accounting for health and management information. These findings contribute to a long-term multistate project database (USDA-NIFA-AFRI-003542) for direct measures of fertility.

Key Words: resistance, genetic parameters, indicators

0367 Genetic evaluation of mastitis, metritis, and ketosis in Holstein cattle using producer recorded data. G. C. Márquez*, Y. Zare, K. L. Stephan, and K. Olson, *ABS Global, DeForest, WI.*

The objective of this study was to develop a genetic evaluation of mastitis (MAST), metritis (MET), and ketosis (KET) from producer recorded data. The period from calving to 60 d postpartum is one of the most challenging times in a cow's lactation when up to 75% of diseases occur. Dairy producers routinely collect health data for management purposes, and these data are also valuable for genetic evaluation. Limited genetic evaluation of these traits exists. Data from on farm management systems was mined by finding keywords that would indicate that a cow had a case of one of the diseases. Only cases within the first 60 d of a cow's first lactation were used. A total of 3264,415, 2822,312, and 2035,174 observations from first lactation Holsteins coming from 776, 593, and 421 farms were used in the evaluations of MAST, MET, and KET, respectively. ASReml was used to fit a linear sire model with an eight-generation pedigree. For each trait a mean as well as herd-year-season of calving and age at first calving were fitted as fixed effects. The random genetic effect of sire was used for all traits. The mean first lactation disease incidence was 16%, 10%, and 3% for MAST, MET, and KET, respectively. The heritability of MAST, MET, and KET was 2%, 4%, and 3%, respectively. There was genetic variation between the best 10% and the worst 10% of sires by EBV. On average the disease incidences of the bottom 10% of sires was higher than the incidences of the top 10% of sires by 5%, 8%, 4% for MAST, MET, and KET, respectively. MAST, MET, and KET have a large economic impact on dairies, and selecting sires whose daughters have lower disease incidence is a cost effective way to make cumulative and permanent change in the population. Given the low heritability of these traits and the wide array of economically relevant traits in dairy, these should be incorporated into a selection index to achieve healthier transition cows.

Key Words: dairy cattle, genetic evaluation, transition period

0368 Genetic evaluation of dairy cow livability.

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Predicted transmitting abilities (PTA) for cow livability (LIV) were developed to measure a cow's ability to stay alive while on the farm, whereas PTA for productive life (PL) measures a cow's ability to avoid dying on the farm or being culled. About 20% of dairy cows died instead of being sold over the last decade, averaging 7% per lactation. LIV has been recorded since 1970. Records for 69,710,392 lactations of 25,514,760 cows were evaluated with an all-breed animal model, using edits similar to a 2008 study. The scale reports cow livability instead of mortality so that positive PTAs are favorable (0 = died; 100 = lived for each lactation) and reports PTA on lifetime instead of per lactation basis to express LIV differences as a percentage of all cows exiting the herd. The model used individual lactation records for culling as a correlated trait to increase reliability of LIV. Heritability was 1.3% on the observed scale for LIV per lactation vs. 3.0% for overall culling per lactation. The SD of true transmitting ability for LIV was 0.82% per lactation or 2.3% per lifetime using an average of 2.8 lactations per cow. For recent bulls with > 80% reliability, PTA LIV were correlated favorably to PTA for PL (0.70), daughter pregnancy rate (0.45), and somatic cell score (−0.25); correlations with PTA for yield traits were low. The 0.70 correlation with PL was sufficiently below 1 to add value from selecting for both LIV and PL in an index. Genomic PTA (GPTA) for young bulls computed from 4-yr truncated LIV data had squared correlations with future data about twice as high as parent averages (PA) for LIV. Genomic reliability was 56% compared with 30% for PA, but lower than 70% for GPTA PL. Economic values for LIV and PL were estimated assuming $1,200 less income for cows that die than for those sold for beef. Relative emphasis on LIV was 7% of total emphasis, but relative emphasis on PL declined to 14% from 19% currently used in net merit. Thus, total emphasis on PL and LIV could increase to 21% using 2 correlated traits instead of 19% with just 1 trait. The United States in 1994 was the first country to evaluate longevity, and can also become the first country to evaluate cow mortality or livability as a specific economic trait.

Key Words: mortality, productive life, economic value

0369 Genetic associations between milk production and growth traits in Guzerat breed.

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In Brazil, the Guzerat breed is used for beef, milk production or as dual purpose breed. Progeny tests of dairy bulls are available for the breed (Programa Nacional de Melhoramento Genético do Guzerá para Leite–National Breeding Program of Dairy Guzerat Cattle), in addition to genetic evaluations of growth traits performed by the Brazilian Association of Zebu Breeders (Associação Brasileira de Criadores de Zebu-ABCZ). For this reason, beef bulls are used in dual purpose herds. To identify differences in the growth and milk production patterns of bulls of this breed, two-trait analyses were performed between cumulative milk production at 305 d (P305) and weight at 120 d (W120), weaning weight (WW), yearling weight (YW), post-weaning weight (PWW), and weight at 24 mo of age (W24). The data files contained 97,394, 65,181, 50,443, 40,425, and 31,279 records, respectively, obtained from the database maintained by ABCZ. The model used included the fixed effects of contemporary group and age of cow at calving (linear and quadratic covariate), and direct additive genetic, permanent environmental (maternal for weights; direct for milk) and residual effects as random effects. The variance components were estimated by the restricted maximum likelihood method using the WOMBAT program. The heritabilities estimated in the two-trait analyses were 0.24 (0.003), 0.14 (0.009), 0.16 (0.0012), 0.18 (0.0014), 0.21 (0.0017) and 0.22 (0.020) for P305, W120, WW, YW, PWW and W24, respectively. The genetic correlations between weights at different ages and P305 were positive but low, ranging from 0.27 (0.111) to 0.38 (0.099), indicating a low association between the breeding values of the traits. Selection for P305 resulted in a low correlated response to increase weights at the ages studied. Based on the breeding values estimated, bulls with a high milk production potential and bulls with a high beef production potential were identified by cluster analysis. The separation of bulls for each selection objective will potentiate the result of genetic selection of the breed.

Key Words: production traits, selection criteria, dual purpose, genetic parameters, Zebu

0370 Production, reproduction, and health of Holstein, Jersey, and crossbred cattle in a seasonal calving pasture-based dairy.
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Crossbreeding of dairy cattle has received increasing interest among researchers and farmers over the past several years. In a seasonal calving herd, crossbreeding could improve reproductive performance to ensure that more cows become pregnant during the relatively short breeding season. In the current study, we examined data from 14 yr of Holstein–Jersey crossbreeding in a seasonal calving, pasture-based dairy herd in Goldsboro, NC. Approximately 125 calves were produced each year, maintaining populations of pure Holsteins (HH, n = 286), pure Jerseys (JJ, n = 335), reciprocal F1 crosses (HJ, n = 182; JH, n = 233); F1 crosses were backcrossed to either H or J sires on alternate years, and crosses that were > 50% of one breed were always mated to the other breed (HX, n = 571; JX, n = 501). HJ, HX, JH, and HH cows had greater milk, fat, and protein yields per lactation than JX and JJ cows ($P <$ 0.05), whereas JJ and JX cows had greater fat and protein percentage in their milk than HH and HX cows. Milk production and fat percentage for the various breed crosses were 8042 ± 121 kg and 4.15 ± 0.06% for HH, 7828 ± 86 kg and 4.70 ± 0.04% for HX, 8063 ± 144 kg and 4.77 ± 0.07% for HJ, 7439 ± 124 kg and 4.85 ± 0.06% for JH, 6776 ± 94 kg and 4.91 ± 0.04% for JX, and 6180 ± 108 kg and 4.64 ± 0.05% for JJ. Crossbreds had some reproduction advantages, including younger age at first service, age at conception, fewer days to first service, and a greater percentage of cows pregnant during the breeding season. Holstein heifers were less likely than other breed groups to survive to 26 mo of age, but those that survived had reproductive success similar to Jerseys and crosses for subsequent lactations. HH were significantly more likely than JJ to have mastitis (16.4 ± 3.0% vs. 9.3 ± 1.9%, $P < 0.05$). Incidences of retained placenta, metritis, cystic ovaries, udder edema, lameness, milk fever, and the need for hormonal intervention for reproduction were no different among breed groups. Within a seasonal calving pasture-based system, Holstein-Jersey crossbred cattle have some production and reproduction advantages over their purebred contemporaries.

Key Words: dairy crossbreeding, pasture system, lifetime performance

0371 Between and within-lactation repeatabilities for hoof lesions in Canadian Holsteins.
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This study aimed to estimate genetic parameters and between and within-lactation repeatabilities for hoof lesions, considering the hoof lesions as binary traits or as categorical traits, using a severity score. Hoof lesions were recorded by 23 hoof trimmers during the routine trimming activity in 365 herds located in Alberta, British Columbia, and Ontario from 2009 to 2012. The hoof trimmers were trained to use a rugged touchscreen computerized lesion recording system. The lesions included in the analysis were: digital dermatitis, interdigital dermatitis, interdigital hyperplasia, sole hemorrhage, sole ulcer, toe ulcer, and white line lesion. Hoof lesions were coded as binary traits (0; 1), where 1 was assigned to the presence of a lesion in any claw or leg or as categorical traits, using a severity score from 0 to 3, where 0 was assigned to the absence of a lesion, 1 to less severe lesions, 2 to moderately severe lesions, and 3 to more severe lesions. The edited dataset contained 107,933 observations from 53,654 animals. The final pedigree file contained 196,899 animals and included 7 past generations. Hoof lesions were analyzed with univariate animal models using the average information-restricted maximum likelihood procedure in the DMU package. Two different permanent environmental effects were included to separate between-lactation permanent environmental effects from within-lactation permanent environmental effects when multiple lactations per cow occurred. For most lesions, affected cows showed higher proportion of moderate severe cases. Sole hemorrhage and white line diseases had very similar proportion of less severe and moderate severe cases (45.8% and 41.1%; 43.4% and 40.7%, respectively). Most of the cows affected by interdigital dermatitis showed less severe lesions (75.6%), and only 1.2% of affected cows showed more severe cases of interdigital dermatitis. Heritabilities ranged from 0.005 (for toe ulcer) to 0.07 (for digital dermatitis). Heritabilities estimated considering the presence or absence of the lesion, or using a severity scale, were very similar. Repeatabilities were low to moderate, both between and within-lactation. However, they were 3- to 90-fold larger than the heritabilities. The most repeatable lesion was toe ulcer, which showed a within-lactation repeatability coefficient of 0.45, and a between-lactation repeatability coefficient of 0.36. Sole hemorrhage showed the lowest coefficients (0.10, for both within and between-lactation repeatabilities). Results suggested that all the repeated observations might be valuable

for increasing accuracy of estimated breeding values.

Key Words: hoof lesions, repeatability, severity

0372 Sexed-semen usage for Holstein AI in the United States. J. L. Hutchison*[1] and D. M. Bickhart[2], *[1]Animal Genomics and Improvement Laboratory, USDA-ARS, Beltsville, MD, [2]Animal Genomics and Improvement Laboratory, USDA-ARS, Beltsville, MD.*

The dairy industry has used sexed-semen to increase the number of heifer calves born on the farm for over a decade. While the efficacy of sexed-semen has been determined experimentally, we sought to tabulate statistics on the generalized use of the technology in the U.S. dairy herd and determine its effectiveness in the field. Sexed-semen breeding status was determined by a National Association of Animal Breeders' 500-series marketing code or by individual breeding information in a cow or heifer reproduction record from a dairy records processing center. Only breedings from 2007 through 2015 with confirmed outcomes (pregnant or not pregnant) were included: 5,963,876 heifer breedings (1,323,721 to sexed semen) and 42,232,502 cow breedings (253,586 to sexed semen). Sexed-semen breedings resulted in 87 and 89% female offspring, for cows and heifers, respectively. This was a notable improvement over conventional Artificial Insemination (AI), which results in 48% female births, on average. Usage of sexed-semen in heifers has increased from 9% in 2007 to 31% in 2015. Furthermore, mean conception rates for heifer sexed-semen breedings has recently increased due to improved technology (42% in 2007 compared with 49% in 2015). Comparable conception rates for heifer conventional breedings were 56, and 59% for 2007, and 2015, respectively. Smaller increases were seen in sexed-semen breedings to cows where 0.2% of all breedings used sexed semen in 2007, and 1% in 2015. Conception rates for sexed-semen breedings to cows were 26% in 2007, and 30% in 2015 compared with 30, and 32% for conventional breedings during the same years, respectively. Usage of sexed-semen for both heifers and cows has increased, with a bigger increase seen in heifers. Mean conception rates for sexed-semen breedings have also increased for both heifers and cows.

Key Words: sexed semen, conception rate, breeding

0373 Effect of semen type (cooled-fresh vs. frozen-thawed) on fertility of lactating dairy cows. A. H. Souza*[1], H. J. Bessoff[2], and E. Danzeisen[3], *[1]Ceva Animal Health, Libourne, France, [2]Dairy Management Solutions, Tulare, CA, [3]Global AG Alliance, Tulare, CA.*

The objective of this retrospective data analysis was to compare pregnancy per AI (P/AI) in dairy cows inseminated with cooled-fresh semen or frozen-thawed semen. Lactating Holstein cows from 11 confined dairies in CA were detected in estrus or synchronized with a Ovsynch-like timed AI protocol and received an AI with a single dose of either fresh (15 to 40 x 10^6 sptz/straw) or frozen semen (15 x 10^6 sptz/straw) once/day in the mornings. Both types of semen from multiple service-sires were used within all herds throughout a period of 10 mo (Jan 2015 to October 2015). Transcervical AI procedure was performed regularly with deposition of semen in the body of the uterus with the assistance of an AI applicator. Fresh semen was delivered to all farms on a daily basis and kept at 2° to 7°C until AI, which was performed within 24 h after fresh semen delivery to the farm. Pregnancy diagnosis was performed at 30 to 40 d post AI across all participating herds. The final database comprised 37,281 breeding records with confirmed AI outcomes (Fresh = 18,042 and Frozen 19,239). Statistical analysis was performed with the proc GLIMMIX of SAS (version 9.3), considering main effects and meaningful one-way interactions with service-sire and cow included in the model as random effects. At 30–40 d after AI, P/AI was greater for cows bred with fresh semen compared with frozen-thawed semen [Fresh = 36.6% (6603/18,042) vs. Frozen = 30.8% (5926/19,239); $P = 0.02$]. In addition, the amount of sperm cells in the fresh semen straw did not influence P/AI ($P > 0.10$). Interestingly, there were no significant interactions ($P > 0.10$) between type of semen (fresh vs. frozen) and month-of-AI, herd, cow parity, days in milk at AI, or even AI breeding-code (natural estrus vs. synchronization programs), suggesting that positive effects of fresh semen in relation to frozen semen was independent from the above mentioned variables. We conclude that the use of cooled-fresh semen improved P/AI in lactating dairy cows compared with the standard AI utilizing frozen-thawed semen.

Key Words: fresh semen, dairy cow, fertility

0374 Subclinical ketosis in the oocyte donors of Holstein × Gir cows. R. C. de Souza*[1], R. C. Souza[1], B. C. M. V. Reginaldo[1], G. C. M. V. da Silva[1], C. A. G. Pellegrino[2], M. I. V. Melo[1], J. P. Lustosa[1], and A. B. D. Pereira[3], *[1]Pontificia Universidade Catolica de Minas Gerais, Betim, Brazil, [2]Faculdade Alis de Bom Despacho, Brazil, [3]University of New Hampshire, Durham.*

In Brazil, the prevalence of subclinical ketosis in F1 *Holstein* × *Gir* oocyte donors has never been assessed in published literature. The aim of this study was to evaluate the prevalence of subclinical ketosis (SK) in F1 Holstein × Gir embryo donors and the effects of this syndrome on reproductive and economic efficiency. Data was collected from several farms in Minas Gerais, Brazil, from May to August 2015. Twenty-eight lactating F1 Holstein × Gir cows were used as oocyte donors. The dosage of ketone bodies was performed using the handset Ketovet (Ketovet Brazil, TaiDoc technology, Taiwan). Cows with blood β-hydroxybutyrate (BHBA) above 1.2 mmol/dL in

the blood were considered as with SK. Donor cows were aspirated for follicules, which were then taken to the laboratory and classified into viable, non-viable and irregular, according to the methodology recommended by the International Embryo Transfer Society (IETS, 2010). Economic analysis was performed considering the following: average price of one follicular aspiration ($75.00), in vitro production of one embryo ($17.75) and cost of each embryo transfer ($12.75). The experiment was analyzed as a complete randomized block design, and means were compared by the Tukey test with significance declared as $P < 0.05$. Results show that each cow produced an average of 20 oocytes, with only 6 oocytes converted into embryos with a final ratio of 3.5: 1 (oocytes:embryos). Two embryos were required to result in 1 pregnancy. Of the 28 donors evaluated, 17 were healthy and 11 had SK, resulting in a disease prevalence of 39.3%. Specifically, the prevalence of SK was higher in primiparous cows (71.4%) compared with multiparous cows (28.6%, $P < 0.05$). Cows with SK produced less total oocytes (11.5 vs. 26.1; $P = 0.014$); less non-viable oocytes (2.09 vs. 10.65; $P = 0.004$), less viable oocytes (6.45 vs. 15.41; $P = 0.005$) and fewer embryos (1.82 vs. 5.41; $P = 0.038$) when compared with healthy cows. The total cost of pregnancy in cows with SK was $142.41, whereas, for healthy cows, was $87.25. In summary, oocyte donors with SK were less efficient as embryo donors. High prevalence of SK observed in this study had a negative effect in the economic efficiency of embryo transfer, causing this technology to be 60% more costly when compared with the same technology used in healthy cows.

Key Words: subclinical ketosis, economic efficiency, embryo transfer

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0375 Clinical signs associated with bovine respiratory disease diagnosis and high heritability in beef and dairy cattle.

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Bovine respiratory disease (BRD) is an infectious multifactorial disease in cattle. To facilitate industry selection of cattle that are less susceptible to BRD, a uniform diagnosis of the disease that maximizes heritability (h^2) estimates, and is easy to measure is needed. Therefore, the objective of this study was to evaluate the effect of different clinical signs used to diagnose BRD on heritability estimates of BRD in dairy and beef cattle. This study was conducted on two pre-weaned dairy calf populations (California-CA, $n = 2000$; New Mexico-NM, $n = 798$) and two beef feedlot populations (Colorado-CO, $n = 1000$; Washington-WA, $n = 1000$). Cattle within each population were initially diagnosed with BRD using the McGuirk scoring system, which evaluates five clinical signs (CS): cough, temperature, nasal discharge and either eye discharge or ear droop (McGuirk, 2008). Heritability was calculated using EMMAX in each population for 15 different CS combinations, including the original combination used by the McGuirk scoring system. The CS that explained the most h^2 varied by population. In dairy cattle, the h^2 in the different CS combinations ranged from 0.12–0.24 for CA and 0.07–0.2 for NM and in beef cattle ranged from 0.04–0.24 in CO to 0.2–0.25 in WA. Identification of cattle using cough alone as the CS resulted in the highest h^2 estimates in CA ($h^2 = 0.23$) and CO ($h^2 = 0.22$), whereas eye or ear CS resulted in the highest h^2 estimates in NM ($h^2 = 0.17$) and WA ($h^2 = 0.19$). Two CS explained the most h^2 (mean $h^2 = 0.17$) across all populations: temperature, cough and nasal and the McGuirk scoring system. In each population, the CS explaining the least h^2 also differed (CA = nasal, NM = cough, CO = temperature, WA = nasal) although collectively, the nasal CS was ranked lowest (mean $h^2 = 0.14$). Multiple factors (age, pathogens and location) contributed to the differences in importance of CS between the different populations. These results determined that diagnosing BRD based on temperature, cough and nasal CS would facilitate a uniform diagnosis of BRD that could be used for development of breeding values to select beef and dairy cattle that are less susceptible to BRD. This project was supported by Agriculture and Food Research Initiative Competitive Grant no. 2011–68004–30367 from the USDA National Institute of Food and Agriculture.

Key Words: BRD, cattle, heritability

0376 Estimating enteric methane and carbon dioxide emission from lactating dairy cows using GreenFeed system.

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Enteric methane (CH_4) and carbon dioxide (CO_2) emissions from lactating dairy cows vary over time depending on various factors that include feed intake, feeding strategy, diet composition, and the time of day. GreenFeed system (C-Lock Inc., Rapid City, SD) is an on-farm "bait station" that captures the breath of cattle when they visit and quantitatively analyzes

the emitted gasses for CH_4 and CO_2 flux. The objective of this study was to determine the correlation between measurements of CH_4 and CO_2 at 2 selected time points of the day vs. 8 equally spaced time points over the 24 h in the diurnal cycle. A GreenFeed system was placed at the University of Alberta-Dairy Research and Technology Center in an open area and cows were moved from their stalls to the unit during measurement time. Individual average daily CH_4 and CO_2 emissions were estimated from lactating dairy cows (N = 29) varying from 32–76 average days in milk (DIM). Individual daily CH_4 and CO_2 emissions were estimated 2 times a day (09:00–12:00; 18:00–20:30 h) for 14 consecutive days and then emissions were measured on the same cows at 8 equally spaced time points (0200, 0500, 0800, 1100, 1400, 1700, 2000, and 2300 h) in the diurnal cycle within 2–3 d. The two time points during the day included the higher and the lower peaks in the diurnal pattern of CH_4 and CO_2 emissions. The number of visits during the 2 times a day and over 24 h measurement ranged from 11–31 and 2–8, respectively. Daily individual CH_4 and CO_2 emissions were estimated by averaging visit fluxes and extrapolating over a day. The result showed a strong correlation of dry matter intake (r = 0.73; P < 0.001), CH_4 g/d (r = 0.74; P < 0.001) and CO_2 g/d (r = 0.72; P < 0.001) production between 2 times vs. 8 time-point measurements. The Pearson correlation coefficient for CH_4 yield (g/kg of DMI) also showed moderate correlation (r = 0.41; P < 0.05) between the two measurements. Taken together, daily CH_4 and CO_2 emissions can be estimated with lower frequency of sampling per day as long as the minimum and maximum emission points in the diurnal cycle are included with an adequate number of visits.

Key Words: methane, carbon dioxide, GreenFeed

0377 Evaluation of factors affecting NaCl content the evolution in ewes milk and of its effect on technological properties.

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The work was aimed at investigating factors affecting variation of NaCl content in sheep milk and at evaluating its relationships with (MCP) and cheese yield. A total of 2778 individual milk samples were collected from 607 Sarda dairy ewes farmed in 34 flocks. MCP (rennet coagulation time = RCT, curd firming time = k20, curd firmness = a30) were measured by Formagraph. Individual laboratory cheese yield (ILCY) were determined by micro-manufacturing experiments. NaCl content (mg NaCl/100 mL milk) was measured by MilkoScanTM. NaCl content was analyzed with a mixed linear model that included the fixed effects of parity, season of lambing, birth type, altitude, and the random effects of flock-test-date and of the animal. Moreover effects of NaCl on MCP were investigated with a similar model, that included also the fixed effect of NaCl class. Four classes were considered according to the 25th, 50th, 75th and 100th percentiles of the NaCl distribution: A = 57–113.3, B = 113.4–132.9, C = 133–157.8 and D = 157.9–259.6. The average content of NaCl was 137.55 ± 34.44 mg/100 mL, ranging from 57.60 to 259.60. NaCl content increased with days in milk, and it was lowest in secondiparous ewes compared with older parities. The season of lambing influenced NaCl concentration, which was higher in milk of ewes lambing in late winter and early spring (from February to April) compared with ewes lambed in early winter (October and November), with values for December and January being intermediate. Birth type at lambing and altitude of location of flocks did show significant effects on NaCl content. MCP were affected by NaCl concentration. In particular, RCT and k20 tended to increase moving from A to D NaCl classes, whereas a30 exhibited the opposite pattern. ILCY showed the highest value for in the class of the highest content of NaCl. Results of the present study highlight the influence of factors related to the physiological status of the animal on the NaCl variation. The results on milk coagulation properties found in this work seems to suggest a relationship between NaCl and cheese making attitude of sheep milk.

Key Words: NaCl, milk coagulation properties, sheep milk

0378 A survey on breeding strategies and selection objectives for increased feed efficiency and decreased methane emission.

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The combined effects of world population growth, rising incomes and dietary changes have resulted in an increasing

international demand for dairy and meat products. However, livestock can have negative impacts on the environment and the greater awareness of climate change has placed pressure on the dairy industry to reduce its environmental impact. Enteric methane from cattle has been recognized as one of the major contributor to greenhouse gas emissions. In addition, methane resulting from digestive processes in ruminants represents important dietary energy losses. Therefore, reducing methane emissions (ME) will not only improve the environmental impact of livestock but also increase cows feed efficiency (FE). Collecting phenotypes for FE and ME is difficult and expensive. The increased use of genomic data in dairy cattle breeding programs has provided an opportunity to investigate the selection of more complex traits requiring fewer phenotypic observations. However, a sizeable genotyped and phenotyped reference population is required to accurately predict genomic breeding values. Combining international data sets will help to achieve the overall goal of producing genomic predictions for FE and ME to be used for breeding application in the dairy cattle industry. However, this could be quite challenging, as different traits that describe FA and Me have been proposed, and different methods are used for measuring the same trait. The International Committee for Animal Recording (ICAR) recently approved the creation of a Feed & Gas working group. This group aims to provide an overview of the current data available, to facilitate the standardization of recording dry matter intake and methane output in cattle around the world, and to enhance international collaboration by providing technical and methodological tools for data sharing and merging. A survey to collect information about current and future measurements of FA and ME has been developed. The survey will be sent to research centers and to industry organizations in member countries of ICAR and it contains some specific questions regarding the breeding strategies for these two novel traits. Results of the survey will allow assessment of a better understanding of the breeding strategies planned in different country once routine genomic evaluations will be available for the two novel traits.

Key Words: feed efficiency, methane emission, survey

0379 Genetic analysis of superovulation and embryo transfer traits in Holstein cattle. K. L. Parker Gaddis*[1], S. Dikmen[2], J. B. Cole[3], and P. J. Hansen[1], *[1]Department of Animal Sciences, University of Florida, Gainesville, [2]Uludag University, Faculty of Veterinary Medicine, Department of Animal Science, Bursa, Turkey, [3]Animal Genomics and Improvement Laboratory, USDA-ARS, Beltsville, MD.*

The objectives of this study were to estimate variance components and investigate genomic regions of interest associated with superovulation and embryo transfer in dairy cattle. Superovulation and embryo transfer are methods commonly used by dairy producers to increase the rate of genetic gain achievable from superior females. A limiting factor of these reproductive technologies remains the variability of animal response to treatment. If some of this variability is attributable to genetics, selection for traits related to superovulation and embryo transfer may allow for further improvement. Data were collected from a Holstein dairy operation in Florida from 2008 through 2015, including 926 superovulation records (total number of structures recovered, total number of good embryos), 628 in vitro fertilization records (number of ooctyes recovered, number of cleaved embryos, number of high- and low-quality embryos, number of transferred embryos), and 12,399 embryo transfer records (pregnancy success). Two transformations of count data were compared: Anscombe and logarithmic. Univariate repeatability animal models were fitted for each trait of interest, with the exception of pregnancy success, for which a threshold liability model was used. For traits where a significant genetic component was estimated (total structures collected and number of good embryos), single-step genomic BLUP analyses were conducted using AIREMLF90 (version 1.116). PostGSf90 (version 1.35) was used to calculate SNP effects and 10-SNP window variances. The two transformation methods produced very similar results. Significant genetic components were estimated for total number of structures recovered and number of good embryos in the superovulation dataset, with heritabilities of 0.31 ± 0.07 and 0.21 ± 0.06, respectively. Genetic components estimated from the in vitro fertilization dataset were not significantly different from zero. Heritability of recipient pregnancy success after embryo transfer was estimated to be 0.024 (SD = 0.01). The region explaining the largest proportion of variance for total structures collected in the superovulation data was located on chromosome 8, at 55,663,248 basepairs with additional peaks located on chromosomes 5, 13, 14, and 21. Similar regions were identified for total number of good embryos, with the largest proportion of variance explained by a region on chromosome 14 at 26,713,734 basepairs. Results indicate that these traits have a genetic component. Significant genomic regions can be further investigated for genes putatively associated with these traits.

Key Words: embryo transfer, genetic analysis, superovulation

0380 Genetic correlations of hoof lesions and trimming status with feet and leg conformation traits in Canadian Holsteins.

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The objectives of this study were to estimate genetic correlations between hoof lesions and feet and legs conformation traits and to evaluate the association between those latter traits and the pre-selection process that leads a cow to be presented or not to the hoof trimmer. Hoof lesions were recorded by 23 hoof trimmers in 365 Canadian herds from 2009 to 2012. Hoof lesions included in the analysis were digital dermatitis, interdigital dermatitis, interdigital hyperplasia, sole hemorrhage, sole ulcer, toe ulcer, and white line lesion. Hoof lesions recorded during the first parity and hoof lesions recorded in second or later parities were considered as different traits. Conformation traits considered were bone quality (BQ), foot angle (FA), heel depth, rear leg side view, rear leg rear view (RLRV), locomotion (LOC) and the overall score for feet and legs (FL). In total, 37,158 cows that had a trim record in first and/or later parities also had conformation traits records. A second series of analyses considered all cows that were in a given herd during the trimming period, including cows that did not have any hoof data during the lactation. An additional trait, the trimming status, was defined as follows; a value of 1 was assigned to cows that had been visited at least once by the trimmer during the lactation, and a value of 0 to cows that did not have a hoof trim recorded during the lactation but were in the herd during the trimming session. Approximately 30% of cows were not presented to the trimmers during the lactation. Digital dermatitis, interdigital dermatitis and interdigital hyperplasia detected in first and later parities were negatively correlated to RLRV, FL, and LOC, with genetic correlations ranging from -0.24 ± 0.11 to -0.62 ± 0.15. With the exception of white line lesions, all of the horn lesions recorded in parities ≥ 2 showed moderate positive correlations with FA (from 0.29 ± 0.12 to 0.55 ± 0.20). White line lesions detected in parity 1 showed moderate genetic correlation with RLRV (0.65 ± 0.19), FL (0.53 ± 0.18), and LOC (0.44 ± 0.21), and those detected in parities ≥ 2 were correlated to BQ (-0.27 ± 0.10) and LOC (0.37 ± 0.16). The trimming status had moderate negative correlations with LOC and FL, suggesting that the pre-selection process for which cows are presented to the hoof trimmer is not random, but rather is associated with mobility and the conformation of the cow.

Key Words: hoof lesions, conformation traits, trimming status

0381 Genetic parameters for number of embryos produced by superovulated donors as heifers or cows using an in vivo or in vitro technique.

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Genetic gain in a population can be improved by using multiple ovulation and embryo transfer (MOET) in elite females. Multiple embryos can be produced using two different techniques, either using superovulation and producing the embryos in vivo or using ovum pickup (OPU) and in vitro production (IVP) of the embryos. Moreover, embryos can be produced by donor cows or virgin heifers as young as 7 mo of age. The objectives of this study were to assess the genetic parameters for the number of embryos produced by Holstein donors superovulated either in vivo or in vitro and for the number of embryos produced by donors either as a cow or a heifer at embryo recovery. Data was provided by Holstein Canada and contained the number of viable embryos from every successful flushing performed across Canada. After editing, 137,446 records of superovulation performed on 54,463 donors between 1992 and 2014 provided information about the type of technique used, and 130,252 records from 51,323 donors provided information about the status of the donor (heifer or cow) at embryo recovery. Bivariate repeatability animal model analyses were performed. Heritability estimates for the donor were between 0.135 (0.007) and 0.155 (0.038), whereas estimates for the service sire were close to zero (from 0.004 ± 0.002 to 0.019 ± 0.010), indicating that the number of embryos produced is influenced by the genetic potential of the donor and not by the service sire. Moreover, moderate repeatability estimates indicated that the number of embryos produced should be somewhat consistent within a donor. Genetic correlations found for the number of embryos produced using either type of technique was strong (0.834 ± 0.094) for the donor, but not significant for the service sire (-0.202 ± 0.234). For the number of embryos produced by either a heifer or a cow, the genetic correlations were 0.702 (0.058) for the donor and 0.699 (0.206) for the service sire. Overall, our results suggest that the number of embryos produced by a superovulated donor should be similar regardless of the technique (in vivo or in vitro) used or the status (heifer or cow) of a donor at embryo recovery. On the other hand, using the same service sire will not increase similarity between the two techniques, but could influence the number of embryos produced by a donor as a heifer or as a cow in a similar way.

Key Words: superovulation, Holstein, genetic parameter

0382 Estimation of genetic progress and profitability of dairy herds using varying proportions of in-vitro produced sexed embryos. K. Kaniyamattam[1], J. Block[2], P. J. Hansen[1], and A. De Vries[*1], [1]*Department of Animal Sciences, University of Florida, Gainesville,* [2]*OvaTech LLC, Gainesville, FL.*

The objective of the study was to estimate the genetic and economic performance of a dairy herd in which varying proportions of animals were impregnated with in-vitro produced sexed embryos (IVP-ET) obtained from the genetically best heifers. A daily dynamic stochastic model that includes the 12 genetic traits in the lifetime Net Merit index (NM$) was used. Phenotypic performance depended on genetic values. A herd of 1000 milking dairy cows, heifers and embryos were simulated over time. Genetic progress came from selecting superior donors and external sires. Eleven scenarios were evaluated, from 0% IVP-ET conceptions to 100% IVP-ET conceptions, with increments of 10% points. Each scenario was run 20 times. Animals with the greatest Estimated Breeding Value (EBV) for NM$ were selected as donors. Recipients were selected from heifers first, and from cows with the greatest EBV for fertility traits second. Sexed semen was used on the genetically better heifers for 2 inseminations. All other non-recipients were inseminated with conventional semen. To maintain a 33% annual cow cull rate, surplus heifer calves were sold based on the lowest EBV of NM$ and received a premium price based on their EBV of NM$. Results were measured by the true breeding values (TBV) of NM$ of all cows and profit per cow per year in yr 15 after the start of the IVP-ET program, and cumulative profit in the 15 yr after the start of the program. The mean ± SE of TBV of NM$ of all cows was $608 ± 7 greater for 100% IVP-ET compared with 0% IVP-ET in yr 15. The maximum increase in profit per cow per year (and optimum IVP-ET program) in yr 15 when embryo costs were $120 and $160 was $125 (100% IVP-ET) and $75 (42% IVP-ET), respectively, compared with a 0% IVP-ET program. Because return on investment in an IVP-ET program is not immediate, the 15-yr cumulative discounted profits per cow in comparison with the 0% IVP-ET program at embryo costs of $80, $120, and $160 were obtained at 72% IVP-ET, 21% IVP-ET, and 0% IVP-ET, respectively. The optimal proportions of IVP-ET depended greatly on the costs of embryos and the sale price of surplus calves. In conclusion, the use of IVP-ET at current prices was profitable but the optimal amount of IVP-ET was sensitive to realistic variations in prices of embryos and surplus heifer calves.

Key Words: in-vitro production, embryo, profit

0383 Single-step genomic prediction accuracies for lactation and reproduction traits in Yorkshire sows. D. M. Thekkoot[*1], R. A. Kemp[2], N. J. Boddicker[2], and G. Plastow[3], [1]*Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Canada,* [2]*Genesus Inc., Lethbridge, AB, Canada,* [3]*Livestock Gentec, Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Canada.*

Most economically important traits associated with lactation and reproduction in pigs are either less heritable, sex-limited, expressed later in life, or difficult to measure on a routine basis. Genomic predictions using single-step BLUP (SSBLUP) methodologies, which utilizes information on phenotypes, pedigree and markers from genotyped and non-genotyped animals simultaneously, is an alternative to phenotype and pedigree based (BLUP) methods. The objective of this study was to estimate and compare prediction accuracies for lactation and reproduction traits using SSBLUP and BLUP methods. Data from 2481 litters from 1431 Yorkshire sows farrowed between August 2011 and August 2015 were used in this study. Of these 1161 sows were genotyped using Illumina's Porcine SNP60 Bead Chip. The sows were weighed and scanned for back fat and loin depth before farrowing and at weaning. Piglets were weighed at birth, weaning and death. Feed consumption of each sow during lactation was measured using the Gestal feed recording system. Reproductive traits studied were total number born, number born dead, number alive at 24 h and number weaned. Lactation traits analyzed were average daily feed intake of sow during lactation, sow body weight, back fat and loin depth at farrowing, body weight, back fat and loin depth loss during lactation, and litter weight gain from birth to weaning. The training data included sows born before April 1, 2013, and validation data included sows (n = 242) born on or after April first 2013. BLUP breeding values for animals in the validation data were computed using all information from the test data plus pedigree information for animals in the validation data. Both SSBLUP and BLUP evaluations were computed using MiX99 software. Accuracies for animals in the validation data were estimated as the correlation between their estimated breeding values and phenotypes, corrected for fixed effects, divided by the square root of heritability of the trait. For all traits studied, prediction accuracies using SSBLUP were higher (0.23 to 0.84) than those from BLUP (0.18 to 0.72). On average the SSBLUP accuracies were 39% and 33% higher, respectively for reproductive and lactation traits. The results indicate that the SSBLUP methodology produces more accurate estimated breeding values for lactation and reproduction traits in pigs.

Key Words: single-step genomic prediction, pig, reproduction, lactation

0384 WS Influence of first calving date on stayability in *Bos indicus* crossbred cows. B. N. Engle*, C. A. Gill, J. O. Sanders, D. G. Riley, J. E. Sawyer, and A. D. Herring, *Department of Animal Science, Texas A&M University, College Station.*

Longevity is one of the most important, complex, and difficult to improve traits sought by cow-calf producers. Consequently, a measurement or tool that could be utilized early in a cow's life to predict her future reproductive performance would be advantageous to producers and researchers alike. In this study, we sought to determine the effect of first calving season period on stayability in Nellore-crossbred females through 5 yr, 6 yr, and 7 yr of age. Stayability through each age was scored as a binary trait, with 1 indicating the cow remained in the herd and 0 indicating she was culled, given either a perfect calving or weaning record. Each female was assigned a value of 1, 2, 3, or 4 corresponding to the respective 21-d period of her first calving season (for first, second, or third 21-d period, or > 63 d, respectively). Cow stayability models were evaluated through mixed model procedures (PROC MIXED in SAS). Of the cows with perfect calving records, more ($P < 0.05$) females that calved in the first 21-d period remained in the herd than those that calved in the second 21-d period through 5 yr (66.9% vs. 53.6%), 6 yr (60.0% vs. 45.9%), and 7 yr of age (56.7% vs. 39.3%). They also differed ($P < 0.005$) from females whose first calf was born 63 d or later into the calving season through ages 5 (66.9% vs. 36.0%), 6 (60.0% vs. 29.5%), and 7 (56.7% vs. 27.2%). Of the cows with a perfect weaning record, more ($P < 0.05$) of the females that calved in the first 21-d period of the calving season remained in the herd through 5 yr (56.1% vs. 31.0%) and 6 yr of age (48.3% vs. 26.0%) than heifers whose calf was born at the end of the calving season. These results document that regardless of the culling criteria, *Bos indicus* crossbred heifers that calve early in their first calving season are more likely to maintain a perfect calving or weaning record later in life than females that calve late in the first calving season. Consequently, there is potential that the heifer's first calving season period may be used as valuation or culling criteria when selecting for stayability and longevity, or when merchandizing beef replacements.

Key Words: beef cows, calving season, stayability

0385 Use of a threshold animal model to estimate calving ease and stillbirth (co)variance components for U.S. Holsteins. J. B. Cole*[1], D. J. Null[1], and S. Tsuruta[2], [1]*Animal Genomics and Improvement Laboratory, USDA-ARS, Beltsville, MD,* [2]*University of Georgia, Athens.*

(Co)variance components for calving ease and stillbirth in U.S. Holsteins were estimated using a single-trait threshold animal model and two different sets of data edits. Six sets of approximately 250,000 records each were created by randomly selecting herd codes without replacement from the data used for the December 2015 national evaluations, and from a second extract using more stringent edits than the official run. The stricter edits required that records have a valid dam ID in addition to a known sire, cows have corresponding lactation records, and animals have a breed composition of at least 93.75% of the breed of evaluation. Calving ease was recorded on a five-point scale ranging from no assistance needed (most common) to extreme difficulty (least common). Stillbirth was coded as a binomial trait indicating whether or not the calf was alive 48 h postpartum. Gibbs sampling was used to estimate (co)variance components from each sample; 100,000 samples were drawn, the first 10,000 rounds were discarded as burn-in, and every fifth sample was retained. The model included fixed parity (1 through 5) and sex-of-calf effects, and random herd-year-season, animal (direct), maternal, maternal permanent environment, and residual error effects. (Co)variance components and heritabilities were averaged over the six replicates of each scenario for each trait and are shown (with standard errors). Direct animal effects in the animal model are comparable to sire calving ease and sire stillbirth in the sire-maternal grandsire (S-MGS) model, and heritabilities were similar for the S-MGS and animal models. Maternal heritabilties were slightly lower in the animal model. Heritability estimates were very similar between scenarios within traits, although maternal heritabilities were slightly higher using the new edits. These differences may be due in part to larger estimates of direct-maternal covariances than reported in previous studies, as well as stricter requirements for known parent IDs in the new edits. The implementation of an animal model for calving traits will provide direct estimates of genetic merit for all animals, not only males, and the adoption of stricter

Table 0385.

	Calving Ease		Stillbirth	
Component of variance	Official	New edits	Official	New edits
Herd-year-season	0.6312 (0.07)	0.7294 (0.14)	0.1064 (0.007)	0.0873 (0.005)
Direct genetic	0.2679 (0.02)	0.3233 (0.07)	0.0546 (0.002)	0.0370 (0.004)
Maternal genetic	0.0997 (0.02)	0.1118 (0.02)	0.0467 (0.002)	0.0572 (0.006)
Direct-maternal covariance	0.0387 (0.02)	0.0489 (0.04)	0.0083 (0.002)	0.0164 (0.002)
Maternal permanent environment	0.1604 (0.02)	0.2364 (0.06)	0.0731 (0.003)	0.0373 (0.007)
Residual	1.8558 (0.21)	2.0667 (0.32)	1.0000 (0.000)	1.0000 (0.000)
Direct heritability	0.09 (0.01)	0.09 (0.02)	0.03 (0.002)	0.03 (0.003)
Maternal heritability	0.03 (0.01)	0.04 (0.01)	0.04 (0.001)	0.05 (0.005)

edits will improve data quality without having large effects on the (co)variances used in the evaluation. It also is anticipated that such a change will increase correlations of U.S. evaluations with other Interbull participants for calving traits.

Key Words: animal model, calving traits, (co)variance components

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0386 Genetic parameters for production traits and heifer pregnancy in Red Angus cattle.

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Heifer pregnancy (HPG) is a prediction of the probability that a female will conceive during her first breeding season, typically at a year of age. An inherent issue in the genetic prediction of HPG is that phenotypes can only be collected on females, which limits the amount of information available. To overcome this, inclusion of correlated traits that can be recorded on both sexes, or fertility traits recorded on males could be used to improve accuracy of HPG predictions. Therefore, the objective of this study was to estimate genetic parameters for HPG, 205-d weight (WW), 160-d post weaning gain (PWG), 365-d weight (YW), and scrotal circumference (SC). The project included records on 142,146 animals from the Red Angus Association of America. (Co)Variance parameters were estimated using multiple, two trait animal models and a REML procedure. Heritability and genetic correlations between HPG and production traits were then calculated. Contemporary group was included as a fixed effect for all analyses, additionally, sex and age of dam were included for BW, WW, PWG, and YW analyses, and the linear effect of age was fit for HPG. The random effect of animal was used to estimate additive genetic effects for all analyses, the random effect of dam was fit for the WW and YW analyses to estimate maternal effects, and a random, maternal permanent environment effect was included for WW. Heritability estimates were 0.58 ± 0.01, 0.27 ± 0.01, 0.22 ± 0.01, 0.29 ± 0.01, 0.45 ± 0.02, and 0.12 for BW, WW, PWG, YW, SC, and HPG (averaged across all analyses on the underlying scale), respectively. Genetic correlations between HPG and BW (−0.06 ± 0.05), SC (−0.08 ± 0.09), WW maternal (−0.02 ± 0.09), PWG (0.06 ± 0.07), YW maternal (0.00 ± 0.11), had confidence intervals that included or were near zero, suggesting minimal genetic relationship between the traits. Correlations were highest between HPG and WW direct (0.29 ± 0.08) and YW direct (0.21 ± 0.07). These results suggest that Red Angus females with high genetic potential for weight at 205 d and 365 d have an increased probability of becoming pregnant during their first breeding season. Additionally, the traits WW or YW could be used to help improve accuracy of HPG genetic predictions.

Key Words: beef cattle, genetic correlation, growth, heifer pregnancy

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0387 Daily rumination time in Italian Holstein cows: Heritability and correlation with milk production.

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The aim of the study was to investigate the genetic variation of daily rumination time (min) and its correlation with test-day milk production (kg). Data for the analysis consisted of 91,589 records for rumination time and milk yield from 398 cows (age: 43.21 ± 16.11 mo), collected from September 2014 to October 2015 in two Italian Holstein herds (TAD and MIL). There were 493 calvings, and data distribution across parities was 46.4%, 26.7% and 26.7% for first, second and later parities, respectively. DIM classes were defined as one class for every 30 d, resulting in 11 classes, and there were a total of 378 herd-test-day contemporary groups. The average rumination time was 513.51 ± 115.84 min, and the average milk yield was 33.59 ± 9.18 kg.

Pedigree information was available for 11,634 animals. A Repeatability Animal Model was fitted using the AIREMLF90 software. Herd, yr/mo of calving, and DIM classes within parity were treated as fixed effects, while herd-test-day, permanent environmental, and the additive genetic cow effects were treated as random. Rumination time was longer in pluriparous than in primiparous cows and showed a decreasing trend across DIM. On average, at the beginning of the lactation, pluriparous cows ruminated 75 min longer than primiparous. As expected, pluriparous cows had a higher production levels across DIM than primiparous, with a peak around DIM class 2 and 3 (i.e., 60–90 d). The herd with the highest daily rumination time had the lowest milk production yield: the fixed effects solutions were 569.5 min and 25.8 kg (Herd TAD; rumination time and milk yield, respectively) and 446.4 min and 31.9 kg (Herd MIL; rumination time and milk yield, respectively). The heritabilities for test-day milk yield and daily rumination time were 0.13 (SE = 0.06) and 0.32 (SE = 0.09), respectively. Although the negative phenotypic correlation observed, genetic correlation between the two traits was 0.38 (SE = 0.47); this high standard error is possibly the consequence of the dataset dimension. So far, rumination time has been used as a key monitor of dairy cow health at farm level. Investigating its genetics aspect and the relationship with other important yields and health traits may turn this management tool in a new informative selection criterion for

the dairy cattle breeding strategies.

Key Words: rumination time, milk production, genetic variation

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0388 Relationship between linear type and fertility traits in Nguni cows. T. J. Zindove*[1], K. A. Nephawe[2], S. P. Ndou[3], and M. Chimonyo[1], *[1]University of KwaZulu-Natal, Pietermaritzburg, South Africa, [2]Tshwane University of Technology, Pretoria, South Africa, [3]University of Manitoba, Winnipeg, Canada.*

The objective of the study was to assess the dimensionality of seven linear traits (body condition score, body stature, body length, heart girth, navel height, body depth and flank circumference) in Nguni cows using factor analysis and indicate the relationship between the extracted latent variables and calving interval and age at first calving. The traits were measured between December 2012 and November 2013 on 1559 Nguni cows kept under thornveld, succulent karoo, grassland and bushveld vegetation types. Low partial correlations (−0.04 to 0.51), high Kaiser statistic for sampling adequacy (MSA) scores and significance of the Bartlett sphericity test ($p < 0.01$) showed that there were significant phenotypic correlations between the linear traits and the data were suitable for factor analysis. Two factors had eigenvalues greater than 1. Factor 1 included body condition score, body depth, flank circumference and heart girth and represented body capacity of cows. Factor 2 included body length, body stature and navel height and represented frame size of cows. Calving interval and age at first calving decreased linearly with increase of factor 1. There was a quadratic increase in age at first calving as factor 2 increased ($P < 0.05$). It was concluded that the linear type traits under study can be grouped into two distinct factors, one linked to body capacity and the other to the frame size of the cows. Small-framed cows with large body capacities have shorter CI and AFC.

Key Words: Nguni cows, body depth, calving interval, flank circumference, heart girth

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0389 Estimation of genetic parameters for birth to weaning traits in meat goats. K. M. Andries*, F. Bebe, A. McKay, A. Bodrick, and A. Hartell, *Kentucky State University, Frankfort.*

Meat goat production in American grew repeatability in the early 2000s and has started to slow in growth over the past several years. Different reasons have been given for this decline, including limited improvement in animal performance and production. There has been a limited amount of research into the genetic parameters for goat growth and repeatability of dam production. A project was conducted at Kentucky State University to evaluate heritability and genetic correlations of birth and weaning weights in meat goat kids and to evaluate the heritability and repeatability of number of kids born and weaned by meat goat does in a multi-breed herd of meat goat. Records of birth to weaning performance and dam reproduction were collected between 2005 and 2015 in the meat goat research herd at Kentucky State University. The data set included 886 kidding records. The data included birth type, number reared, birth and weaning weights and daily gain between birth and weaning. The data was analyzed using ASReml with maternal effects in an animal model. The results of this study found that direct heritability of birth weight was 0.27% ± 0.081 and maternal heritability of 0.14 ± 0.035. For weaning weight heritability estimates were 0.33 ± 0.078 and 0.25 ± 0.042 for direct and maternal, respectively. Genetic correlation between these two traits was 0.39 ± 0.102 and the maternal correlation was 0.56 ± 0.074. Reproduction is one of the most economically important traits in livestock production. Number of kids born and weaned is critical for success of the meat goat industry. We used a repeated measures model in ASReml on the dam performance data set that contained 886 kidding records. We found that the heritability for number of kids born was 0.07 ± 0.068 with a repeatability of 0.14 ± 0.044 and for number of kids weaned was 0.18 ± 0.092 and 0.25 ± 0.046 for heritability and repeatability, respectively. Based on this research birth and weaning weights in meat goats are highly heritable and maternal effects on weaning weight are high. While heritability of number of kids born was low, the repeatability was significantly and number of kids weaned had a moderate heritability. Repeatability of both traits was lower than expected.

Key Words: meat goat, heritability, repeatability

0390 Economic selection index coefficients for terminal traits in Beefmaster cattle. K. P. Ochsner*[1], R. M. Lewis[1], M. D. MacNeil[2], and M. L. Spangler[3], *[1]University of Nebraska, Lincoln, [2]Delta G, Miles City, MT, [3]University of Nebraska, Lincoln.*

In the design of an economic selection index, the relative importance of traits in the breeding goal is reflected by their economic weighting in the index. The objective of this study was to develop an economic selection index for Beefmaster cattle for a terminal production system where bulls will be mated to mature cows with all resulting progeny harvested. Selection criteria were chosen from expected progeny differences (EPD) currently reported by Beefmaster Breeders United (BBU), and included yearling weight (YW), ultrasound rib-eye area (UREA), ultrasound rib fat (UFAT), and ultrasound intramuscular fat percentage (UIMF). Goal traits, which directly influence profitability in a terminal system, included hot carcass weight (HCW), marbling score (MS), rib-eye area (REA), 12th–rib fat (FAT), and feed intake (FI). Phenotypic and genetic parameter values among the selection criteria and goal traits were obtained from literature. National averages of feed prices, veterinary costs, and carcass premiums/discounts from 2010 to 2014 were used to establish income and expenses associated with a terminal system. Economic values

were determined from a simulation of 100,000 animals using SAS 9.4. Values were obtained by approximating the partial derivatives of the profit function by perturbing traits one at a time, by one unit, while holding the other traits constant at their respective means. In the simulation, the means (SD) for HCW, MS, REA, FAT and FI were based on literature values, and were 320 (38.8) kg, 5.4 (0.9) marbling score units, 76.5 (9.3) cm^2, 1.2 (0.32) cm, and 8.59 (1.09) kg, respectively. Relative economic values for HCW, MS, REA, FAT and FI were found to be 91.29, 17.01, 8.38, −7.07, and −29.66, respectively. By using phenotypic (co)variances among the selection criteria in the derivation, index coefficients may be applied to phenotypic measures. Index coefficients for phenotypic measures of YW, UREA, UFAT and UIMF were 0.74, 0.08, −31.04, and 13.32, respectively. By using genetic (co)variances among the selection criteria in the derivation, index coefficients may be applied directly to EPD. Index coefficients for EPD of YW, UREA, UFAT and UIMF were 1.72, 0.81, −36.60, and 12.37, respectively. The application of this index would aide Beefmaster breeders in their sire selection decisions, facilitating genetic improvement for a terminal breeding objective.

Key Words: beef cattle, economic weight, selection index

0391 Genomic regions associated with residual feed intake of divergently selected lines of Yorkshire pigs when fed a low-energy, high-fiber diet.

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Feed intake and efficiency remain key targets for improvement in the pork industry, as feed is the number one source of production costs. To better understand feed efficiency, divergent selection for residual feed intake (RFI) was performed in purebred Yorkshire pigs for 10 generations at Iowa State University. Phenotypes for RFI (n = 2623) and component traits were recorded across generations and lines (High RFI and Low RFI). A corn and soybean-meal based diet that was higher in energy and lower in fiber content (HELF) was fed during selection. To explore the effect of diet on RFI, a lower-energy, higher-fiber (LEHF) diet was fed to a subset of pigs from generations 8, 9, and 10 (n = 314). The LEHF diet had 18% less net energy and 175% more neutral detergent fiber, yet lysine to metabolizable energy ratios were similar between diets. Pigs were genotyped using the Illumina Porcine SNP60 BeadChip. (Serão et al., 2016) reported genomic regions on *Sus scrofa*chromosome (SSC) 2 and 6 associated with RFI of pigs fed the HELF diet (n = 1692). The objective of this study was to identify genomic regions associated with RFI when pigs were fed a LEHF diet. Using bivariate models for RFI between diets, heritability of RFI was estimated to be 0.24 ± 0.05 for the HELF diet and 0.35 ± 0.17 for the LEHF diet, while the genetic correlation of RFI between diets was 0.82 ± 0.28. Pigs (n = 310) fed the LEHF diet with phenotypes and genotypes for 46,467 SNP, after quality control, were used for a genome wide associate study. GenSel4 was used to fit BayesB and C models with $\pi = 0.9933$. Results from BayesC found no significant genomic associations for RFI. BayesB identified associations for RFI on SSC 6 and 14 that each explained ~0.75% of the genetic variance and on SSC 1, 5, and 16 that each explained ~0.50% of the genetic variance. None of these regions overlapped with those reported by Serão et al. (2016). In conclusion, RFI is a polygenic trait with many QTL across the genome with small effects and those effects may depend on the diet fed. This work was supported by AFRI-NIFA Grant no. 2011–68004–30336.

Key Words: genomic regions, RFI, swine

0392 Genetic architecture of feed efficiency in mid-lactation Holstein dairy cows.

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The objective of this study was to explore the genetic architecture and biological basis of feed efficiency in lactating Holstein cows. In total, 4918 cows with actual or imputed genotypes for 60,671 SNP had individual feed intake, milk yield, milk composition, and body weight records. Cows were from research herds located in the United States, Canada, the Netherlands, and Scotland. Feed efficiency defined as residual feed intake (RFI) was calculated as the residual of the regression of DMI on milk energy (MilkE), metabolic body weight (MBW), and body weight change along with systematic effects of parity class by days in milk fitted as a fifth order Legendre polynomial (fixed), diet within experiment within location (random) and test week (random). Adjusted phenotypes for DMI, MilkE, and MBW were calculated as the sum of the animal and residual components from the regression of each trait on the same systematic effects used for RFI. Animal

relationships were represented with a genomic relationship matrix. Genome-wide association studies were performed for RFI, DMI, MilkE, and MBW using the Bayes B method in GenSel version 4.4 with 1% of SNP assumed to have a non-zero effect. One megabase windows with the greatest percent of the total genetic variation explained by the markers (TGVM) were identified, and within windows explaining more than 0.5% of the TGVM, the SNP with the highest posterior probability of a non-zero effect was tested for significant additive and dominance effects. Marker-based heritabilities were estimated for RFI (0.10), DMI (0.25), MilkE (0.20), and MBW (0.44). Tentative results for RFI identified regions explaining the greatest percent of the TGVM on chromosomes X, 9, and 14, and all tested SNP had significant additive effects ($p < 0.05$). Four of the 10 regions with the greatest effect on DMI also were included in the 10 regions with greatest effects on RFI, but not in the top 10 regions for MilkE or MBW, suggesting a genetic basis for intake that is unrelated to energy consumption required for milk production or maintenance. Candidate genes found within windows explaining the greatest percent of the TGVM for RFI include solute carrier family 25 member 14 and leptin. In conclusion, feed efficiency is a polygenic trait exhibiting genetic variation distinct from that underlying maintenance requirements and milk energy output.

Key Words: residual feed intake, genome-wide association study, feed efficiency

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0393 Analysis of genetic residual feed intake in Danish Holstein cows by covariance functions using random regression models. C. Pfeiffer*, B. Li, P. Lovendahl, and J. Lassen, *Department of Molecular Biology and Genetics, AU Foulum/ Aarhus University, Tjele, Denmark.*

Feed efficiency is of major concern due to economic reasons and environmental impacts but also because of limited feed resources. So far, feed efficiency cannot be defined unambiguously. One trait to select for can be residual feed intake (RFI), which is primarily determined by dry-matter intake (DMI), production traits and body weight. The aim of this study was to derive variance-covariance components of RFI over the first 44 lactation wk in primiparous Danish Holstein cows by a covariance function from a tri-variate random regression analysis to describe genetic and permanent environmental effects of average DMI, average metabolic body weight (mBW) and average kg milk (Mkg) over the whole lactation. Commonly, RFI is derived from phenotypic regression and subsequently genetically analyzed. In total, 22,375 records of 648 primiparous Holstein cows from the Danish Cattle Research Centre were used. Phenotypic information was collected between 2003 and 2015 over the entire standard-lactations. The random regressions were fitted using DMU 6.5.2. The pedigree was traced back as far as possible resulting in 16,339 animals. After estimating variance-covariance components of DMI, mBW and Mkg, the covariance function was applied to directly derive RFI due to the assumption that RFI is defined as a depended genetic variance of DMI, body weight and milk yield. The approach gave reliable results for RFI. Heritabilities for RFI ranged from 0.05 to 0.15. The highest heritability for RFI was observed in the first wk of lactation, the lowest in lactation wk 22. Heritabilities for the traits DMI, mBW and Mkg ranged from 0.30 to 0.46, 0.53 to 0.61 and 0.25 to 0.55, respectively. The genetic variance of RFI was on average 9.5% (ranging from 4.3% in lactation wk 23 to 28.7% in lactation wk 1) of the genetic variance of DMI. Heritabilities of RFI, DMI, mBW and Mkg were in accordance with previous studies. The genetic variance of RFI in DMI has to be considered as low to moderate. Results imply that a genetic improvement of DMI, independent of production, is limited, except for the first 4 wk of lactation where the genetic variance of RFI was > 20% of the genetic variance of DMI.

Key Words: dairy cow, random regression model and residual feed intake

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0394 Greenhouse gas emission related traits differ in RFI divergent lactating dairy cows. D. Hailemariam*[1], G. Manafiazar[1], J. Basarab[1,2], F. Miglior[3,4], G. Plastow[1], Z. Wang[1], *[1]Livestock Gentec, Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Canada, [2]Lacombe Research Centre, Alberta Agriculture and Forestry, Lacombe, AB, Canada, [3]Canadian Dairy Network, Guelph, ON, Canada, [4]Centre for Genetic Improvement of Livestock, Department of Animal Biosciences, University of Guelph, ON, Canada.*

In dairy cattle, the magnitude of dry matter intake (DMI), methane (CH_4) and carbon dioxide (CO_2) reduction in feed efficient (-RFI) lactating cows is not well documented. The objective of this study was to quantify the comparative advantage of -RFI lactating dairy cows managed in an intensive tie-stall system with regard to DMI, CH_4 and CO_2 emission. RFI was predicted for 43 lactating dairy cows with components of metabolic body weight (MBW), empty body weight change (EBWC), and milk production energy requirements (MPER) over 255 d in milk (DIM) using a random regression technique, and correspondingly, DMI, CH_4, CO_2 and other traits were measured. CH_4 and CO_2 emissions were measured from lactating dairy cows using a GreenFeed system (C-Lock Inc., Rapid City, SD). The measurement was performed in three batches (15 cows in each) twice a day (0900–1200; 1800–2030 h) for 14 consecutive test days. Before each test period cows were allowed to visit the unit twice a day (4–7 d) for adaptation purpose. The RFI prediction revealed 19 cows with–RFI (efficient) and 24 cows with +RFI (inefficient). The mean dry matter intake (DMI), CH_4 production (g/day), CH_4

yield (g/kg of DMI), CH_4 g/kg of milk, milk yield (kg/d) and CO_2 g/d were calculated for both-RFI (N = 19) and +RFI (N = 24) groups. Data was analyzed using t test for each trait and the result indicated that -RFI cows have significantly (P < 0.05) decreased DMI (20 ± 3 vs. 23 ± 3), CH_4 g/d (334 ± 71 vs. 392 ± 70), and CO_2 g/d (12,070 ± 1348 vs. 12,895 ± 1704) and CH_4 g/kg of milk (9 ± 2 vs. 10 ± 2) compared with their +RFI counterparts. As expected, body weight, milk yield and CH_4 (g/kg DMI), were not statistically significant (P > 0.05), between -RFI and +RFI groups. Taken together, feed efficient lactating dairy cows compared with the inefficient cows consumed less feed, emitted less daily CH_4 (g/d), CH_4 (g/kg of milk) and CO_2 (g/d) by 13.0, 14.8, 10, and 6.4% respectively, without differing in milk production.

Key Words: RFI, methane, carbon dioxide

0395 Genetic relationship between methane emissions and conformation traits in Danish Holstein cattle. L. Zetouni[*1], M. Kargo[1,2], J. Lassen[1], *[1]Aarhus University, Tjele, Denmark, [2]SEGES, Aarhus N, Denmark.*

Conformation traits have been widely explored in dairy cattle evaluation, being a part of the total merit index for Holstein cows in different countries. They have been used as a way to access the cow's condition in general, based on its body features. Lots of studies have analyzed the relationship between conformation traits and other traits of interest in dairy cattle, such as fertility, longevity and feed efficiency, but little is known about how methane emissions correlate with conformation traits. Therefore, our goal was to evaluate the genetic correlations between methane and six conformation traits in Holstein cows: height (H), body depth (BD), chest width (CW), dairy character (DC) and body condition score (BCS). Data was collected on 1114 Holstein cows from 11 commercial herds in Denmark. Methane emission was measured during milking in milking robots, and then quantified using information on milk production, weight and days carried calf to predict carbon dioxide production and multiplied by the ratio between methane and carbon dioxide. Bivariate linear models were used in the analysis to estimate the correlations between methane and each one of the traits analyzed. Heritabilities estimates were moderate, ranking around 0.3 for methane and between 0.11 (for CW) and 0.5 (for H) for the other traits. The estimated genetic correlations were mainly positive, implying that the bigger the cow, the more methane it produces. Our results could be partially explained by the fact that, in general, broader, deeper cows eat more, and it is a known fact methane production is associated with higher feed intake in ruminants. Due to high standard errors of the estimates further analyses are being conducted to more deeply evaluate and understand how conformation traits relate to methane emissions.

Key Words: methane, conformation traits, genetic correlations

0396 Genetic variation of predicted milk fatty acids groups in Canadian Holsteins. S. G. Narayana[*1], F. S. Schenkel[1], A. Fleming[1], A. Koeck[1], F. Malchiodi[1], J. Jamrozik[1,2], M. Sargolzaei[1,3], M. Corredig[4,5], B. Mallard[1,6], A. Ali[7], and F. Miglior[1,2], *[1]Centre for Genetic Improvement of Livestock, Department of Animal Biosciences, University of Guelph, ON, Canada, [2]Canadian Dairy Network, Guelph, ON, Canada, [3]Semex Alliance, Guelph, ON, Canada, [4]University of Guelph, ON, Canada, [5]Gay Lea Foods, Guelph, ON, Canada, [6]Department of Pathobiology, OVC, University of Guelph, ON, Canada, [7]Department of Mathematics and Statistics, University of Guelph, ON, Canada.*

The objective of this study was to investigate genetic variability of mid infrared predicted fatty acids groups in Canadian Holstein cows. Milk samples were collected by CanWest DHI (Guelph, ON, Canada) and Valacta (Ste.-Anne-de-Bellevue, QC, Canada) during routine milk recordings. Milk samples were analyzed using MilkoScan FT6000 spectrometers (Foss, Hillerød, Denmark). Milk mid infra-red spectra generated from January 2013 to July 2015 were standardized and then predicted for five groups of fatty acids: short-chain (C_4–C_{10}), medium-chain (C_{12}–C_{16}), long-chain (C_{17}–C_{22}), saturated (no double bond), and unsaturated (one or more double bonds) fatty acids. The predicted fatty acid values were log transformed to improve normality. The data set included 49,127 test-day records from 10,029 first lactation Holstein cows in

Table 0395.

Table 1. Heritabilities and correlations between methane and conformation traits

		Methane			
	h^2	r_g	SE	r_e	SE
BCS	0.4	-0.009	0.2	-0.14	0.08
BD	0.14	0.45	0.24	-0.12	0.07
CW	0.11	0.3	0.3	-0.13	0.06
H	0.5	-0.12	0.2	0.0963	0.0931
DC	0.12	0.12	0.2	0.05	0.07
Methane	0.3	-	-	-	-

BCS = body condition score; BD = body depth; CW = chest width; H = height; DC = dairy character
r_g = genetic correlations; r_e = residual correlations

810 herds. The total number of animals in the pedigree was 76,074. The random regression animal test-day model included: days in milk, herd test day, and season-age of calving (polynomial regression) as fixed effects, and herd-year of calving, animal and permanent environment effects as random polynomial regressions, and random residual effect. The significance of fixed effects and the best degree of the fixed Legendre polynomial regressions for season-age effect (third degree) were determined using AI-REML. Bayesian methods with Gibbs sampling were then used for fitting models with different degree of random regressions, assuming the best degree for fixed regressions, and the same increasing degree for all random effects (from intercept only to 4thdegree). Fourth degree random regressions yielded the best fitting based on the Deviance Information Criterion (DIC). No polynomials with degree higher than 4 were fit due to low number of cows with more than 5 fatty acid measurements and the cubic shape of the phenotypic distribution of the fatty acid groups. The estimate of average daily heritability over the lactation for medium-chain fatty acid (0.37) was higher than for short-chain (0.30) and long-chain (0.24). The average daily heritability for saturated fatty acid (0.38) was larger than for unsaturated fatty acid group (0.23). These results provide evidence for the existence of genetic variation in fatty acids groups, and thus indicate possibility of altering milk fatty acid composition through genetic selection.

Key Words: milk fatty acids, mid-infrared, random regression model

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0397 Genetic correlations between predicted milk fatty acids and milk production traits in Canadian Holsteins.

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The fatty acid profile of milk is of importance due to its implications on human health and nutrition, and technological attributes. Any consideration of selection for fatty acids requires knowledge of their genetic relationship with other milk production traits. The objective of this study was to investigate the genetic correlations between mid-infrared predicted milk fatty acids and recorded production traits and somatic cell score (SCS) in Canadian Holsteins. Test-day records for milk yield, fat and protein percentage, fat:protein ratio, and SCS, along with predicted quantities of short (4 to 10 carbon length), medium (12 to 16 carbon length), and long-chain (17 to 22 carbon length) fatty acid groups were analyzed. First lactation Holstein cows between the ages of 19 and 43 mo with at least 3 test-day fatty acid records were considered in the analysis. A total of 109,249 records from 29,542 Holstein cows and 2198 herds acquired between January 2013 and April 2015 were used. Genetic analysis was performed using bivariate sire random regression models fitted using the Average Information-Restricted Maximum Likelihood (AI-REML) procedure in the DMU package with Legendre polynomials used to describe the regression curves. Daily genetic correlations were averaged across the lactation. Strong genetic correlations of 0.90, 0.96, and 0.88 were found between fat percentage and short, medium, and long-chain fatty acids, respectively. Ranges of genetic correlations for fatty acid groups and milk yield (−0.48 to −0.50), protein percentage (0.69 to 0.80), and fat protein ratio (0.51 to 0.63) were similar to those found between the production traits and milk fat percentage. Weak, negative genetic correlations were observed between SCS and short and medium-chain fatty acids (−0.14 for both), while a weak, positive correlation was found between SCS and long-chain fatty acids (0.17). Milk fatty acids had moderate to strong genetic correlations with production traits, but weak genetic correlation with SCS. However, disentangling the high correlation of fatty acids with fat percentage may be challenging for selection purposes.

Key Words: fatty acid, milk production, genetic correlation

0398 Genetic associations between milk β-hydroxybutyrate and fatty acids in early first lactation of Canadian Holsteins.

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Hyperketonemia (or ketosis) is one of the most frequent diseases in dairy cattle. As clinical ketosis is not widely recorded, the level of milk β-hydroxybutyrate is used as its indicator. Milk fatty acid profile is considered to be related to the energy balance of cows in early lactation. The objective of this study was, therefore, to investigate the genetic associations between milk β-hydroxybutyrate and milk fatty acids in early first lactation of Canadian Holstein cows. Test-day data were available on milk β-hydroxybutyrate and five fatty acid groups: short-chain (C_4–C_{10}), medium-chain (C_{12}–C_{16}), long-chain (C_{17}–C_{22}),

saturated (no double bond) and unsaturated (one or more double bonds). Only the first cow's test-day record between 5 and 40 DIM was considered for all traits, because most of the metabolic changes occur over this time period. The data set consisted of 23,345 cow records from 1541 sires and 2510 herds. Data were analyzed with a 6-variate linear sire model using the Average Information-Restricted Maximum Likelihood (AI-REML) procedure in the DMU package. Heritability of 0.13 was found for milk β-hydroxybutyrate. Heritability estimates for fatty acids ranged from 0.10 to 0.29. Genetic correlations between milk β-hydroxybutyrate and short chain, medium chain and saturated fatty acids were low and not significantly different from zero. Genetic correlations between milk β-hydroxybutyrate and long chain and unsaturated fatty acids were 0.51 and 0.48, respectively. These results confirm the known relationship between milk β-hydroxybutyrate and energy balance status in early lactation, explained by the release of long chain fatty acids from the mobilization of body fat reserves.

Key Words: milk β-hydroxybutyrate, fatty acid, genetic correlation

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0399 Relevance of mid-infrared spectroscopy predictions of milk fine composition and technological properties for selective breeding.

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To evaluate the potential use of novel milk infrared predictions as indicator traits in selective breeding, genetic variation in 92 traits, describing the fine composition and technological properties of milk, and their predictions was assessed in the Italian Simmental (IS) population. The genetic relationship between measured traits (MT) and infrared predictions (IP) was investigated. Fatty acid and protein composition, lactoferrin and mineral contents were available for 1040, 3337, 558, and 689 individual milk samples, respectively. Measures of pH and milk coagulation properties were available for 3438, and 3266 samples, respectively. Curd yield and curd composition were obtained by laboratory micro-cheese making techniques for 1177 samples. Infrared calibration models were developed for all traits and IP were obtained for 143,198 spectra of 17,619 IS cows. (Co)variance components for MT and IP were estimated in a set of bivariate analyses, each including one MT and its IP. There was a positive relationship between the R^2 in cross-validation (R^2_{CV}) of calibration models and the decrease in both the phenotypic variance ($r = 0.78$; $P < 0.01$) and the additive genetic variance ($r = 0.61$; $P < 0.01$) of IP compared with the estimates for MT. For the 92 traits, the average decrease in total variance of IP compared with the variance of MT was approximately 35%. The decrease in genetic variance was on average 64%. As a consequence, 88 traits exhibited lower h^2 estimates for IP than for MT. The R^2_{CV} exhibited a positive relationship ($r = 0.57$; $P < 0.01$) with the estimated genetic correlation (r_a) between MT and IP. For calibration models having $R^2_{CV} > 0.75$, r_a between IP and MT was greater than 0.9. The variability in the estimated r_a values increased when R^2_{CV} decreased and, for calibration models having moderate predictive ability, estimates of r_a ranged from 0.2 to 1.

Calibration equations showing high predictive accuracy would lead to a faster genetic progress compared with calibration models having moderate or low prediction accuracy. Nevertheless, the estimated r_a between IP and MT was generally very high, even when calibration models had moderate R^2_{CV}. Hence, even calibrations showing low predictive accuracy may be successfully used in selective breeding, particularly when multiple predictions per animal are available from the routine application of calibration models.

Key Words: infrared spectroscopy, animal breeding, fine milk composition

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0400 Markers associated with metabolome, and microbiome measures in a grain and sugar challenge in dairy heifers.

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The aim of this preliminary study was to identify associations between the bovine genome, metabolome, and microbiome in cattle subjected to a grain and sugar challenge. The objective was to identify markers for ruminal acidosis. Genome wide association was performed on Holstein heifers ($n = 34$ samples with quality DNA out of 40) that were allocated to 5 feed additive groups. Heifers were fed twice daily a 62% forage:38% concentrate total mixed ration at 1.25% of bodyweight (BW) dry matter (DM)/d for a 20-d adaptation period with their additive(s). Fructose (0.1% of BW/d) was added to the ration for the last 10 d of adaptation. On d-21 heifers were challenged with a ration consisting of 1% of BW DM wheat and 0.2% of BW fructose plus their additive(s). Stomach tube rumen samples were collected weekly and at 5 time points over 3.6 h after consumption of the challenge ration on d-21 and analyzed for pH, and ammonia, D- and L-lactate, and volatile fatty acids (VFA) concentrations and relative abundance of total bacteria and archaea using an Illumina MiSeq platform. All rumen fermentation measures were normalized and combined to produce an eigenvector to indicate the risk of ruminal acidosis. Bovine DNA was sequenced using the Geneseek® Genomic Profiler Bovine 150K Illumina SNPchip. Genome wide association was completed using an additive model and linear regression with PCA population stratification and a Bonferroni correction for multiple comparisons. There were few genome associations found with rumen pH,

acetate, propionate, total VFA, or ammonia concentration or the relative abundance of the Firmicutes and Bacteroidetes phyla ($P < 0.5$). A number of associations occurred for D-lactate, L-lactate, and total lactate concentration and the acidosis eigenvectors at all time points before d 21 ($P < 0.05$). Ten associations were found at one time-point only for butyrate and valerate concentrations ($P < 0.05$). A number of associations were found with the Actinobacteria, Chloroflexi, Euryarchaeota, Fibrobacteres, Proteobacteria, and Tenericutes phyla at one or more time points ($P < 0.05$). Gene-wide associations with the metabolome and microbiome were present despite the small population size and suggest the presence of markers for ruminal acidosis. Qualitative trait loci and candidate gene analysis is being conducted.

Key Words: genome wide association, lactic acid, ruminal acidosis

BREEDING AND GENETICS SYMPOSIUM: RESILIENCE OF LIVESTOCK TO CHANGING ENVIRONMENTS

0401 Production, biological, and genetic responses to heat stress in ruminants and pigs.

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Heat stress (HS) compromised efficient animal production and reduced livestock output during the summer was traditionally thought to result from decreased nutrient intake. Our data from ruminants and monogastrics challenge this dogma and indicate that heat-stressed animals utilize homeorhetic strategies to modify metabolic and fuel selection priorities independently of feed intake. Systemic shifts in bioenergetics are characterized by increased basal and stimulated circulating insulin. Hepatocytes and myocytes also show clear differences in glucose production and metabolic flexibility, respectively, during HS. Intriguingly, HS animals do not mobilize adipose tissue despite being in both a negative energy balance and catabolic state. The origin of the aforementioned metabolic changes may lay at the gastrointestinal tract. For a variety of reasons, HS compromises intestinal integrity. Increased permeability to luminal contents results in local and systemic inflammatory responses. Consequently, heat-stressed animals are simultaneously confronted with life-threatening hyperthermia and endotoxemia. Determining how these systems are homeostatically and homeorhetically coordinated to prioritize acclimation and survival vs. agriculturally productive purposes would presumably reveal mechanisms amenable to manipulation. Interestingly, thermoregulatory and production responses to HS are only marginally related. In other words, increases in body temperature indices poorly predict the decrease in both milk yield and growth. Further, HS-induced decreased feed intake is also an inaccurate predictor of milk yield or growth during HS. This suggests that traits associated with production and thermoregulation during HS may be governed by separate genomic loci and potentially interdependent biological mechanisms. Thus, selecting animals with a "tolerant" phenotype based solely or separately on thermoregulatory capacity or production may not ultimately increase HS resilience. Therefore, the variation of multiple phenotypes and genotypes needs to be accounted for to generate a more comprehensive heat tolerant animal. In summary, HS is one of the primary hurdles to efficient animal production. Defining the physiological mechanisms through which HS and other environmental factors influence complex, multifactorial traits, is critical for developing approaches to ameliorate current production issues and is a prerequisite for generating future strategies (genetic, managerial, nutritional, and pharmaceutical) to maximize livestock efficiency.

Key Words: heat stress, genetics, insulin, tolerance

0402 Breeding for resilience to heat stress effects: A comparison across dairy ruminant species.

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Dairy animals are more susceptible to heat stress (HS), because milk production results in a large metabolic heat strain. As a consequence, selection for increased milk production will tend to decrease animals' tolerance to increasing heat loads. A comprehensive approach to characterize HS effects on dairy production and to develop breeding tools to select for heat tolerance (HT) was followed by making use of available milk recording information, climatological data and genomic information on three dairy ruminant populations, Holstein cattle and local breeds Manchega sheep and Florida goats raised in the warm southern regions of Spain. Heat stress thresholds were around 55/63 (15/18) and 63/65 (19/20) for average daily values of THI (°C temperature) for fat/protein yields in Holstein and Manchega, respectively. For goats, HS thresholds could not be clearly identified. Sufficient genetic variability was observed in productive response to heat to consider this trait for selection in the three populations. Genetic antagonism between milk production and HT (ability to maintain milk production under high heat loads) was found for the three populations but stronger for cattle and goats. Several selection criteria including eigen-components of the response variability (looking for tolerance criteria independent of production level) were compared and slopes of the genetic response curves in the HS region were recommended. Estimated genetic correlations between production