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SYMPOSIA AND ORAL SESSIONS

Late-Breaking Original Research

LB1 Performance of Illumina and Affymetrix bovine high-density genotyping platforms in Holsteins and Jerseys. G. Rincon¹, K. Weber¹, A. Van Eenennaam¹, B. L. Golden², and J. F. Medrano^{*1}, ¹*Department of Animal Science, University of California Davis, Davis,* ²*Dairy Science Department, California Polytechnic State University, San Luis Obispo.*

Two high-density single nucleotide polymorphism (SNP) genotyping arrays have recently become available for bovine genomic analyses, the Illumina High-Density Bovine BeadChip Array (777,962 SNP) and the Affymetrix Axiom Genome-Wide BOS 1 Array (648,855 SNP). These products each have unique design and chemistry attributes, and the extent of marker overlap and their potential utility for QTL fine mapping, detection of copy number variation, and multi-breed genomic selection are of significant interest to the cattle community. This study compares the performance of these 2 arrays using DNA samples from 16 dairy cattle (10 Holstein, 6 Jersey). Data were analyzed with SVS7 software (Golden Helix) filtering to remove SNP having a call rate less than 90% and linkage disequilibrium (LD) pruning was used to remove linked SNP ($r^2 \geq 0.9$). Maximum, average, and median gaps were calculated for each analysis based on genomic position of SNP on the bovine UMD3.1 genome assembly. The Illumina and Affymetrix arrays include 49,345 and 47,741 SNP from the widely used Bovine Illumina SNP50, respectively. All samples were successfully genotyped ($\geq 98\%$ SNP genotyped) with both platforms. Average number of genotyped SNP in the Illumina platform was 775,681 and 637,249 for the Affymetrix platform. Only 96,640 SNP were shared between the 2 platforms, and the average SNP concordance at these loci was 99.9%. Despite fewer total SNP on the Affymetrix array, 19% more SNP remained (480,196) after LD pruning resulting in a smaller average gap size of 5,159 bp relative to the Illumina array where 388,263 SNP remained resulting in a 6,881 bp average gap size. However, only 224,115 Illumina and 241,038 Affymetrix SNP remained following removal of SNP with a minor allele frequency (MAF) of zero in these Holstein and Jersey samples, resulting in an average gap size of 11,887 bp and 11,018 bp, respectively. Combining the 354,348 informative ($r^2 \geq 0.9$), polymorphic (MAF ≥ 0), unique SNP data from both platforms reduced the average gap size to 7,560 bp. This marker density of informative SNP has been projected to be sufficient to obtain consistent marker effects across breeds.

Key Words: SNP, genomics, cattle

LB2 Independent assessment of commercial DNA tests for beef cattle production traits. K. L. Weber* and A. L. Van Eenennaam, *Department of Animal Science, University of California, Davis.*

Two commercial companies offer DNA tests to improve the accuracy of selection in Angus cattle. The American Angus Association (AAA) national cattle evaluation incorporates DNA test information using genetic correlations estimated from the genetic relationship between DNA test results and phenotypic data in their database. The genetic

correlation between the target trait and test results is expected to decrease as the relationship between the training and evaluation populations becomes more distant. The objective of this study was to estimate the genetic correlation between DNA test results and target traits in typical commercial ranch bulls (born 2003–2007) sourced from the Angus seedstock sector. Molecular breeding values (MBV) from Igenity (Duluth, GA) and HD 50K molecular value predictions (MVP) from Pfizer Animal Genetics (Kalamazoo, MI) were obtained for 29 registered Angus bulls that had sired 1852 progeny with commercial cows on 3 northern California ranches. Each bull had at least 20 progeny weaning weight records or 10 carcass records. Traits evaluated were weaning weight (WW; $n = 1734$), ADG ($n = 341$) from feedlot entry to estimated feedlot final weight (derived from HCW/0.63), HCW ($n = 455$), ribeye area (RE; $n = 455$), and marbling score (MS; $n = 455$). DNA test results were correlated with the target trait using a bivariate animal model with the DNA test treated as a second trait. REML estimates of the genetic correlation \pm SE estimated in this data set (and those estimated by AAA where available) for Igenity MBV were WW 0.12 ± 0.22 (0.45), ADG -0.01 ± 0.42 , HCW 0.33 ± 0.27 (0.54), RE 0.35 ± 0.24 (0.58), and MS 0.61 ± 0.19 (0.65). For Pfizer MVP, genetic correlations were WW 0.51 ± 0.17 (0.52), ADG 0.10 ± 0.39 , HCW 0.08 ± 0.28 (0.48), RE 0.57 ± 0.21 (0.60), and MS 0.71 ± 0.17 (0.57). Genetic correlation estimates were generally positive and somewhat lower than the AAA value, although estimates had large SE. Incorporating the DNA test information as a correlated trait to improve the low accuracy AAA EPD associated with yearling bulls did not consistently improve rank order correlation with commercial ranch estimated breeding values based on observed progeny performance.

Key Words: genomic selection, beef, accuracy

LB3 Multivariate factor analysis of genomic correlation matrices in three US dairy cattle breeds. N. P. P. Macciotta*¹ and J. B. Cole², ¹*Dipartimento di Scienze Zootecniche, Università di Sassari, Sassari, Italy,* ²*Animal Improvement Programs Laboratory, Agricultural Research Service, USDA, Beltsville, MD.*

High-density marker maps allows the prediction of genomic values both genome-wide (GW) and for each chromosome (CHR). The comparison of correlations between traits on the GW and CHR levels may be of great help for understanding the genetic architecture of single or groups of traits. Multivariate factor analysis (MFA) models the (co) variance of a multivariate system by extracting latent variables able to reconstruct the common (co)variance structure. In this work, GW and CHR (*Bos taurus* autosomes (BTA) 6, 14, and 18) correlation matrices for 3 US dairy cattle breeds were analyzed with MFA. Data refer to 2,038 Brown Swiss (BS), 63,615 Holstein (HO) and 8,084 Jersey (JE) cattle, respectively. A total of 23 productive and functional traits were considered. About 80% of the (co)variance was explained by 6 or 7 latent factors. The comparison of correlations between the factors and the traits highlighted some similarities between breeds at the GW level. Latent factors associated ($r > 0.60$) with milk yield

traits, milk composition, udder morphology, strength, and functional traits (productive life, SCS, daughter pregnancy rate) were extracted. Some differences were observed at CHR level. On BTA6 BS showed an overlapping of yield and composition with a single factor, whereas they tend to remain distinct in HO and JE. However, in HO and JE there are 2 latent factors associated with functional traits on BTA6, which harbors genes affecting milk production and reproduction. The analysis of BTA14 highlighted in the JE a factor associated with both milk yield and composition traits, except for protein percentage, and differences between GW and CHR was noted, which is consistent with the presence of genes known to affect selected traits (DGAT1). Results for GW and CHR were similar for BTA18, which is known to harbor a QTL affecting calving traits and conformation in Holsteins. Multivariate factor analysis is capable of identifying differences in genetic correlations among traits across the genome and on individual chromosomes, and may be a useful tool to identify regions of the genome affecting multiple traits for further study.

Key Words: genomic selection, chromosome, factor analysis

LB4 Transcriptional profiling during pig fetal skeletal muscle development using direct high-throughput sequencing and cross-platform comparison with gene expression microarrays. C. W. Ernst^{*1}, J. P. Steibel¹, B. P. Soller^{1,2}, G. M. Strasburg¹, S. E. F. Guimarães², and N. E. Raney¹, ¹Michigan State University, East Lansing, ²Federal University of Viçosa, Viçosa, MG, Brazil.

§§Skeletal muscle fiber formation is under genetic control, but little is known about the specific genes involved or how their expression patterns are coordinated. The aim of this study was to identify differentially expressed genes in *longissimus dorsi* muscle of Yorkshire × Landrace pigs at 40 and 70 d of gestation (encompassing the transition from primary to secondary fibers). Total RNA was pooled from 3 fetuses from gilts at each gestational age (n = 3). Transcriptional profiling was performed by direct sequencing (RNaseq) with an Illumina GAIIx revealing 6,299 differentially expressed tags (FDR <0.10). The same samples were previously evaluated using the Pig-oligoarray microarray comprised of 20,400 70-mers, and qPCR was completed for a subset of genes. To perform a cross-platform comparison between RNaseq and microarray analyses, microarray results were expressed as log-fold change (FC) with associated p-value and q-value (FDR), and comparisons filtered with FDR <0.10 (n = 1,218). Microarray oligonucleotides were matched to RNaseq tags based on HGNC annotation resulting in 1,410 matching pairs of oligonucleotides and sequenced transcripts (with multiple transcripts mapping to the same oligonucleotide). Correlation of log-FC between the technologies was 0.72. Expression patterns obtained with RNaseq for 11 genes assayed by qPCR (annotated in Build 9) were validated. These included 4 non-differentially expressed genes (FDR >0.10 in both assays; CTNNA1, HPRT1, STAT1, TIMP3), 6 genes more highly expressed at 70 d (FDR <0.10; CA3, DLK1, FBXO32, MYOZ1, NRAP, USP13), and 1 gene more highly expressed at 40 d (FDR <0.10; TNC). Relative FC from RNaseq and qPCR for all genes agreed in both direction and magnitude. As expected, RNaseq identified additional differentially expressed transcripts over the microarray results. However, this analysis demonstrated that the microarray results were repeatable, and results of both technologies were comparable to qPCR. Thus, both microarrays and RNaseq are reliable and RNaseq may complement and extend microarray studies.

Key Words: RNaseq, microarray, skeletal muscle

LB5 Growth, DXA skeletal traits, and spinal curvature are compromised within four weeks in pigs fed diets with no supplemental vitamin D. L. A. Rortved^{*}, Z. Hassen, and T. D. Crenshaw, University of Wisconsin, Madison.

Recent necropsies from commercial operations implied vitamin D (D) deficiencies in young pigs, which are not typical. In 2010, we reported that kyphosis, an abnormal spine curvature, was induced in young pigs fed D-limited diets for 9 or 13 wk. The current objective was to evaluate relationships among dietary D, Ca, and P on skeletal traits and assess methods for early detection of kyphosis. In 2 trials (n = 72 ea) pigs weaned at ~3 wk were fed diets with no supplemental D for 1 wk then 1 of 8 diets (corn-SBM) for 4 wk. Treatments included supplementation with D, 0 (-D) or 280 (+D) IU/kg; Ca, 75% (0.53%) or 150% (1.05%); P, 95% (0.57%) or 120% (0.72%) of requirements. On d 28 pigs were killed and scanned using DXA (GE Lunar Prodigy) to determine bone mineral content (BMC, g/pig) and density (BMD, g/cm²). Gain was depressed (P < 0.01) in pigs fed -D and tended (P < 0.12) to be altered by interactions between D, Ca, and P. Differences in BMC were detected due to D (P < 0.01). Expected responses to Ca and P (P < 0.01) were observed, but dependent on D (P < 0.01). Differences in BMD, which accounts for size, were also detected. Pigs fed -D had reduced BMD (P < 0.01). Excess P suppressed BMD in pigs fed -D, but increased BMD in pigs fed +D (P < 0.07). Differences were detected in serum Ca and P at 4 wk due to D, Ca, and P (P < 0.01). Two methods to assess spinal curvature involved angle measurements from digital images versus a polynomial fit derived from lateral DXA scans. No differences among treatments were detected using angle measurements. Differences (P < 0.02) due to D were detected in all polynomial coefficients. Thus, a polynomial fit of the spine offers a method to detect differences due to D within 4 wk.

Table 1.

Vit D, IU/kg	0	0	0	0	280	280	280	280	
Ca, %	75	75	150	150	75	75	150	150	
P, %	95	120	95	120	95	120	95	120	SEM
Gain, kg/d ^a	0.407	0.375	0.348	0.353	0.567	0.572	0.542	0.619	0.023
Serum Ca, mg/dL ^{a,b,c}	8.18	7.39	9.07	9.71	11.01	11.64	14.02	12.49	0.87
Serum P, mg/dL ^{a,b,c}	8.40	10.25	8.21	10.07	11.40	12.53	9.28	12.36	0.67
BMD, g/cm ² ^{a,d}	0.428	0.398	0.500	0.410	0.615	0.654	0.662	0.753	0.048

a. D, P < 0.01; b. Ca, P < 0.02; c. P, P < 0.01; d. D × P, P < 0.05; e. D × Ca × P, P < 0.02.

Key Words: kyphosis, calcium, phosphorus

LB6 Effect of trans-palmitoleic acid (trans-16:1 n-7) on lipid metabolism and cellular proliferation in primary bovine adipocytes. A. K. G. Kadegowda^{*}, T. A. Burns, M. Miller, and S. K. Duckett, Clemson University, Clemson, SC.

Trans-palmitoleic acid (t-16:1) has been suggested to have beneficial effects on human health including lower adiposity. Objectives were to quantify the amounts of t-16:1 in meat samples and to determine the effect of t-16:1 on cellular proliferation and lipid metabolism in bovine primary adipocytes. For the first objective, t-16:1 in LM samples from steers finished on 2 different forage-finishing systems were analyzed by GC. For the second objective, bovine primary preadipocyte cultures were isolated from intermuscular fat of 18 mo-old Angus

crossbred heifers (n = 2). Preadipocytes were differentiated (D0) in differentiation media [DMEM containing 10% fetal calf serum, 2.5 µg/mL insulin, 0.25 µM dexamethasone (DEX), 20 µM troglitazone, 0.5 mM isobutylmethylxanthine (IBMX), and 10 mM acetate] for 2 d. Cells were further differentiated from D2 to D6 in media without DEX and IBMX. From D0 to D6, cells were treated with 1 of 4 levels (0, 50, 150, or 300 µM) of *t*-16:1 and for fatty acid analysis by GC and gene expression by RT-qPCR. The effect of *t*-16:1 on cell proliferation of pre-differentiated and differentiated cells was assayed using Cell Counting Kit-8. The treatment effects were analyzed by ANOVA using Proc Mixed (SAS). The *t*-16:1 content in meat samples varied from 0.56 to 1.18 g/100 g total FA. Increasing *t*-16:1 supplementation linearly increased ($P < 0.05$) total cellular FA, decreased ($P < 0.01$) C18:1c9, increased *t*-16:1 ($P < 0.01$), its elongation product t11 18:1 ($P < 0.01$) which was desaturated to c9t11 CLA ($P < 0.01$). Decreased C18:1c9 was probably due to increased availability of alternative FA (t11–18:1) for desaturation. *Trans* 16:1 increased ($P < 0.01$) FASN and ELVOL6 (at 50 µM) but did not affect SCD1. *t*16:1 affected cell proliferation of pre-differentiated cells ($P < 0.05$) but did not affect the differentiated cells. Results showed that meat samples are a source of *t*-16:1 and the effects of *t*-16:1 are probably mediated through c9t11 CLA in the differentiated adipocytes.

Key Words: *trans*-palmitoleic acid, adipocyte, lipid metabolism

LB7 Ferric citrate decreases ruminal hydrogen sulfide production in feedlot cattle fed diets high in sulfate. M. E. Drownoski¹, P. H. Doane², and S. L. Hansen¹, ¹Iowa State University, Ames, ²ADM Research, Decatur, IL.

Sulfate content of ethanol co-products often limits inclusion in cattle diets. Dissimilatory reduction of sulfate by sulfate-reducing bacteria in the rumen produces sulfide, which can lead to a buildup of the toxic gas hydrogen sulfide (H₂S) in the rumen, resulting in reduced performance and occasionally toxicosis. We hypothesized that adding ferric ions would competitively inhibit ruminal sulfate reduction. The objectives of these studies were to determine the effects of ferric citrate on ruminal fermentation, ruminal sulfate reduction, and DMI of cattle. The effects of 5 levels (0, 25, 50, 100, 150, 200 mg/kg of additional Fe in the in vitro fluid) and 2 sources (ferric citrate or ferric ammonium citrate) of ferric ions on in vitro H₂S production, IVDMD, total gas production, and fluid pH were examined (n = 6 per treatment). Rumen fluid was collected from a steer that was adapted to a high concentrate, high sulfate diet (0.51% S) and mixed with an equal volume of McDougall's buffer, without the reducing solution. Addition of either source of ferric ions decreased ($P < 0.01$) H₂S concentration without affecting gas production ($P = 0.38$), fluid pH ($P = 0.80$), or IVDMD ($P = 0.38$) after a 24 h incubation. An in vivo experiment was conducted using 8 ruminally fistulated steers (455 kg) in a replicated Latin square design with 4 periods and 4 treatments. The treatments included a high concentrate, high S control diet (0.46% S) or the control diet plus ferric ammonium citrate at 200, 300, or 400 mg Fe/kg diet DM. Each period lasted 11 d with a 3 d washout period where all cattle were fed the control diet, and an 8 d period in which steers were fed their experimental diet. Intake was determined during the last 4 d in a period. Inclusion

of ferric ions in the diet of steers did not affect DMI ($P = 0.21$) or ruminal pH ($P = 0.48$). There was a linear ($P < 0.01$) decrease in the concentration of ruminal H₂S as ferric ion addition increased. Ferric citrate appears to be an effective way to decrease ruminal production of H₂S, which could allow producers to safely increase inclusion of co-products containing elevated sulfate.

Key Words: distillers grains, iron, sulfur

LB8 Adding an anti-inflammatory lactic acid bacteria to a Bacillus-based direct-fed microbial improves calf performance. M. Duersteler^{*1}, K. N. Novak¹, C. A. Wehnes¹, M. E. Davis¹, D. R. Shields², and A. H. Smith¹, ¹Danisco USA Inc., Waukesha, WI, ²Merri-*rick's Inc., Union Center, WI.*

Enhanced immune development in calves was observed when scouring calves were treated with an electrolyte containing a *Bacillus*-based direct-fed microbial (DFM) selected for reducing bacterial pathogens. The objective of this experiment was to determine the effect of adding anti-inflammatory lactic acid bacteria (LAB) to the *Bacillus*-based DFM on immunity and calf performance. *Enterococcus faecium* ID7 was selected for anti-inflammatory activity from a library of LAB isolated from healthy calves. Rat intestinal epithelial IEC-6 cells (3×10^5) were treated with *Bacillus* spores (10^7 cfu), high and low dose *E. faecium* ID7 (10^8 cfu, 10^7 cfu), or *Bacillus* spores with high and low dose *E. faecium* ID7 for one hour. *Bacillus* spores increased ($P < 0.05$) expression of inflammatory cytokines (IL-1β, IL-6, TNF-α and MIP-2). High and low dose ID7 reduced ($P < 0.05$) expression of inflammatory cytokines caused by *Bacillus* spores. Calves (72) were randomly assigned to 3 treatments; control, *Bacillus*-based DFM (2×10^9 cfu/head/day) or *Bacillus*-based DFM plus *E. faecium* ID7 (2×10^9 *Bacillus*, 1×10^9 ID7 cfu/head/day). Treatments were administered in non-medicated 20:20 all milk replacer fed at 1.25 lbs/day until weaning at 6 weeks, and calves were given starter feed ad libitum throughout the 8 weeks of the trial. The *Bacillus* DFM plus *E. faecium* ID7 increased average daily gain over wk 5–6, 7–8 and over all 8 weeks ($P = 0.03$) compared with the control calves. These results indicate that providing a balanced immune response by adding an anti-inflammatory LAB to a pathogen reducing *Bacillus*-based DFM improves calf performance.

Table 1. Average daily gain (kg) per period and over trial

Week	Control ± SE	<i>Bacillus</i> DFM	<i>Bacillus</i> DFM plus ID7
1-2	0.23 ± 0.03	0.26 ± 0.03	0.31 ± 0.03
3-4	0.58 ± 0.04	0.60 ± 0.04	0.63 ± 0.04
5-6	0.78 ± 0.03 ^a	0.86 ± 0.03 ^{ab}	0.91 ± 0.04 ^b
7-8	1.01 ± 0.05 ^a	1.06 ± 0.05 ^{ab}	1.16 ± 0.05 ^b
Overall ADG	0.65 ± 0.03 ^a	0.70 ± 0.03 ^{ab}	0.75 ± 0.03 ^b
Total Gain	36.39 ± 1.49 ^a	38.94 ± 1.52 ^{ab}	42.18 ± 1.56 ^b

Means with different letters are significantly different ($P < 0.05$) within rows; means separation by least square difference. Statistical analysis by Proc Mixed procedure (SAS 9.1.3).

Key Words: direct-fed microbial, calf, immunity