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