

Residual feed intake (RFI) is a measure of net feed efficiency, an economically important trait in livestock. The RFI of an animal depends on the ability of the animal to consume less feed than expected based on their weight gain and weight maintained during the feed testing period. Recent work has implicated mitochondrial function as being involved in the feed efficiency of livestock. The objective of this study was to identify genes involved in mitochondrial function that may affect net feed efficiency in cattle. Several quantitative trait loci (QTL) affecting feed efficiency were previously mapped in Jersey × Limousin double backcross progeny in three sire families. Based on the QTL mapping results, ten candidate genes related to mitochondrial function and energy metabolism were identified: *ALDOB*, *AKI*, *CAT*, *GHRL*, *HADHB*, *NDUFA8*, *NDUFB5*, *SOD1*, *SOD2*, and *SUCLG1*. All ten genes were sequenced in three Jersey × Limousin sire families in order to locate DNA variants in the genes for association studies. A total of 58 DNA variants were discovered, which included six insertion/deletions (in/dels) and 52 single nucleotide polymorphisms (SNPs). Fourteen SNPs were selected for genotyping in the 366 progeny from the three sire families. Genotyping results were analysed to observe the effect of the SNPs with 27 RFI related traits and specific fat depot traits. Only four SNPs in the candidate genes were associated with residual feed intake, three of which were in the *HADHB* gene. The haplotype of *HADHB* from these three SNPs explained 8.5% of the variation in RFI. The other SNP was in the *SOD1* gene, which had a p-value < 0.001 for residual feed intake and explained another 3% of the variation in this trait. Thus, the results indicate that DNA variants in genes involved in mitochondrial function and energy metabolism may influence RFI.

Key Words: residual feed intake, feed efficiency, mitochondrial function, cattle, candidate genes

MT78 Impact of genomic selection for feed efficiency on heifer reproduction and calf performance traits. E. Akanno^{*1}, C. Ekine-Dzivenu¹, M. Abo-Ismaïl^{1,2}, M. MacNeil^{3,4}, C. Li^{1,5}, C. Fitzsimmons^{1,5}, J. Basarab^{1,6}, and G. Plastow¹, ¹Livestock Gentec, AFNS, University of Alberta, Edmonton, AB, Canada; ²Department of Animal and Poultry Production, Damanshour University, Damanshour, Egypt; ³Delta G, Miles City, MT, USA; ⁴Department of Animal, Wildlife and Grassland Sciences, University Free State, Bloemfontein, South Africa; ⁵Agriculture and Agri-Food Canada, Lacombe Research and Development Centre, Lacombe, AB, Canada; ⁶Alberta Agriculture and Forestry, 4Lacombe Research and Development Centre, Lacombe, AB, Canada.

Genetic improvement in feed efficiency is economically important in cow-calf operations but measuring feed intake is an expensive and difficult process particularly on large numbers of cows. Thus, genomic selection (GS) offers opportunities to improve feed efficiency in cow-calf herds but the potential impact of selecting for improved feed efficiency on maternal traits is unknown. Therefore, the objective of this study was to evaluate a short-term correlated response in heifer reproduction and calf performance traits due to a GS scheme that incorporates genomic breeding values (GBV) for residual feed intake (RFI) in either a maternal or feedlot productivity index. A total of 981 replacement heifers in their first calving bred between 2012 and 2014 were collated from three experimental herds namely Angus (AN; 285), Charolais (CH; 182) and Kinsella Composite (KC; 514). All replacement breeding stock for AN and CH were selected for feed efficiency using GBV within multi-trait maternal and feedlot profitability indexes, respectively, while the KC population was randomly split into feed-efficient and control herds contributing 264 and 250 heifers, respectively. Replacement breeding stock for the KC control herd was subjected to traditional selection, while the KC-efficient replacements were selected similarly to the Angus herd. In order to examine the impact of GS on

pre-breeding weight (PBW), calving date (CD), calf birthweight (CBW) and calf weaning weight (CWW), a multiple linear regression analysis was performed using R statistical software. Except for CBW (36 – 35 kg), the results showed a significant ($P < 0.01$) phenotypic trend for PBW (337 - 362 kg), CD (209 - 163 days), and CWW (202 – 223 kg), on average, in heifers from the efficient herds (AN, CH, KC) bred over the course of three years. Within a selection year, there was no difference ($P > 0.05$) observed for maternal traits between the control and efficient herd in the KC population. Despite the short-term selection experiment and the limited sample size used in this study, it appears that a genetic improvement program that incorporates RFI in a selection index will have no adverse effect on maternal traits in a cow-calf operation.

Key Words: beef cattle, feed efficiency, genomic selection, maternal traits

MT79 Bilateral iridal hypopigmentation in Holstein Friesian cattle. A. K. Hollmann¹, M. Bleyer², A. Tipold³, J. N. Nebler³, W. E. Wemheuer¹, E. Schütz¹, and B. Brenig^{*1}, ¹Institute of Veterinary Medicine, University of Goettingen, Goettingen, Germany; ²Pathology Unit, German Primate Center, Leibniz-Institute for Primate Research, Goettingen, Germany; ³Dept. Small Animal Medicine and Surgery, University of Veterinary Medicine Hannover, Hannover, Germany.

Eye pigmentation abnormalities in cattle are often related to syndromes like albinism, Chediak-Higashi or Tietz. However, also mutations that solely affect the pigmentation of body and eye have been described. These discolorations of the iris, either mono- or bilateral, complete or partial are usually referred to as heterochromia iridis. A total of 20 cattle (10 male, 10 female) with bilateral hypopigmentation of irises were observed. 18 cases were of Holstein Friesian (HF) breed, two other affected animals were crossings of Red cattle and Fleckvieh. Ophthalmological and neurological examination did not reveal any signs of an underlying syndrome or anomalies other than the iridal hypopigmentation. All cases showed an iris coloration with two differently coloured parts of varying colour intensity. The central regions were silvery-blue to grey-blue with darker and lighter parts and the peripheries were light brown to grey with occasional light grey zones. Coat colour of affected cattle was characteristic of the breed without any obvious colour deviations. Histological evaluation revealed a reduction in iris pigmentation mainly affecting the anterior border layer and the iridal stroma. Differences in pigmentation of other uveal structures, iridal thickness or stromal density were not detected. To analyse the genetics of the iris hypopigmentation, a genome-wide association study was performed using genotyping data of the 20 cases and 172 randomly selected HF cattle. Three loci with p-values above the Bonferroni genome-wide significance level of $-\log_{10}(p) = 6.65$ were detected on bovine chromosome (BTA) 8 (position 60,990,733, $-\log_{10}(p) = 9.2$), BTA4 (position 7,186,971, $-\log_{10}(p) = 6.81$) and BTA9 (position 77,442,550, $-\log_{10}(p) = 6.95$). Further analysis of genotypic and allelic dependences between the 20 cases and 316 randomly selected HF cattle using 3x2 or 2x2 contingency tables and Fisher's exact or chi-squared statistics (df = 2) were performed. The presence of the A-alleles at each of the 3 loci are leading to a 6- (BTA8), 9.04- (BTA4) and 5.47- (BTA9) times higher chance to develop an iridal hypopigmentation.

Key Words: cattle, genome-wide association, animal health

MT80 The price of looking for something no one wants to talk about: The search, quantification, and cost of genetic diseases in Ireland. J. McClure^{*1}, P. Flynn², S. Waters³, M. Mullen⁴, T. Pabiou¹, R. Schnabel⁵, J. Taylor⁵, F. Kearney¹, R. Weld², and M. McClure¹, ¹The Irish Cattle Breeding Federation, Highfield House, Shinagh, Bandon, Co. Cork Ireland; ²Weatherbys DNA Laboratory, Johnstown, Co. Kildare; ³Animal & Grassland Research and