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Genomic national evaluation of dairy cattle using SNP markers on 50K Illumina Beadchip is routinely applied for production traits and somatic cells score where the test-day random regression model is used. Conformation and reproduction traits are evaluated by single trait animal model and longevity is evaluated by survival kit. Data included 1.3 mil of cows records with ~25 mil. of test-day records and 5,500 genotypes of animals. A single-step procedure is used and thus genotyped and non-genotyped animals are evaluated together across the whole population. National procedure is validated by Interbull organisation. A positive genetic trend is observed in last 35 years in milk production, but the negative one in reproduction traits. The genetic trends of evaluated traits are similar for period 1980 - 2010 but after 2010 when the genomic evaluation is used values increase. Distribution of genomic enhanced breeding value (GEBV) has similar range for subpopulations of cows, non-genotyped bulls, proven genotyped bulls, and young genotyped bulls. Average GEBV for proven genotyped bulls is slightly higher than for other groups in milk production. Czech population is strongly influenced by import of foreign bulls and therefore young animals have weak connection to domestic production records and low reliability of prediction of genetic evaluation. Evaluation is improved by implanting international MACE (Multiple Across Country Evaluation) values into domestic evaluation. Interbull MACE values were deregressed into test-day records and added to the database of domestic animals. Validated reliabilities of young bulls were calculated using for prediction partial data until the year 2012 and for verification a whole data until year 2016. Single-step evaluation on combined data including a whole domestic population and all available Interbull values of genotyped and non-genotyped bulls (MACE values of 100 000 bulls) has higher validated reliability of evaluation of young bulls than evaluation on only domestic population.

**Key Words:** single-nucleotide polymorphism (SNP), genomic prediction, milk production, animal breeding, population genomics

**MT75 Identification of hypotrichosis in Kazakh White-headed beef cattle breed in Kazakhstan.** T. Yechshzhanov<sup>\*2</sup>, R. Uskenov<sup>1</sup>, Y. Mukhanbetkaliyev<sup>1</sup>, S. Zhamaliyeva<sup>2</sup>, and A. Smakova<sup>1</sup>, <sup>1</sup>*S.Seifullin Kazakh AgroTechnical University, Astana, Kazakhstan*; <sup>2</sup>*L.N.Gumilyov Eurasian National University, Astana, Kazakhstan*.

Hypotrichosis is autosomal recessive hereditary disorder, which has had significant economic effect on beef cattle breeding worldwide. The prevalence of carriers of disorder has not been reported before in Kazakhstan. The objective of the study was to identify carriers of this disease in population and artificial insemination centre. Previously, 54 animals of different beef breeds of domestic and imported breeds from Akmola and North Kazakhstan regions were screened for 8 SNPs of glycogen storage disease, hypotrichosis, maple syrup urine disease, male subfertility and dwarfism. Our previous results revealed that the Kazakh whiteheaded bull from artificial insemination centre is the carrier of a recessive allele for genetic disease: hypotrichosis with the SNP on HEPHL1 gene. In this study, to look for distribution of recessive allele among progeny 75 offsprings of carrier bull progeny were selected for further analysis. Parentage testing with 100 SNP was used for verification. Genomic DNA was extracted from hair follicles by Qiagen DNA extraction kit with small modifications. Genotyping was performed for the following autosomal recessive diseases of beef cattle breeds: hypotrichosis with a SNP in the HEPHL1 gene. Genotyping of DNA samples for the SNPs carried out by using Illumina bovine bead chips at Labogena (France). According to the results of genotyping it revealed that the Kazakh whiteheaded breed bull is the carrier of a recessive allele for genetic disease: hypotrichosis with

the SNP on HEPHL1 gene. This study demonstrates that carriers of hypotrichosis are present in the Kazakh whiteheaded breed population, although at a low frequency. As artificial insemination is used in cattle breeding, carriers of hypotrichosis, are likely present within progeny of breeding sires. Since the mutant alleles are invisible in phenotype of animals, it is very important to detect and eliminate carriers of these diseases from breeding stock.

**Key Words:** cattle, animal breeding, genotyping, genetic disorder, genetic improvement

**MT76 Genomic profiles to assess accuracy of breed composition and hybrid vigor in crossbred beef cattle.** M. K. Abo-Ismaïl<sup>\*1,2</sup>, J. Crowley<sup>1,3</sup>, E. C. Akanno<sup>1</sup>, G. Manafiazar<sup>1</sup>, C. Li<sup>1,4</sup>, G. Plastow<sup>1</sup>, M. D. MacNeil<sup>6</sup>, D. Berry<sup>7</sup>, P. Stothard<sup>1</sup>, and J. Basarab<sup>1,5</sup>, <sup>1</sup>*Livestock Gentec, Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada*; <sup>2</sup>*Animal and Poultry Production, Damanhour University, Damanhour, Egypt*; <sup>3</sup>*Canadian Beef Breeds Council, Calgary, AB, Canada*; <sup>4</sup>*Agriculture and Agri-Food Canada, Lacombe Research and Development Centre, Lacombe, AB, Canada*; <sup>5</sup>*Lacombe Research Centre, Alberta Agriculture and Forestry, Lacombe, AB, Canada*; <sup>6</sup>*Delta G, Department of Animal, Wildlife and Grassland Sciences, Bloemfontein, South Africa*; <sup>7</sup>*Animal and Grassland Research and Innovation Centre, Teagasc, Moorepark, Co., Cork, Ireland*.

The objective of this study was to assess the effectiveness of different methods of single nucleotide polymorphism (SNP) marker selection and densities to predict breed composition for crossbred beef cattle and subsequently evaluate the use of those breed fractions to calculate retained heterozygosity (RH). A total of 8,792 individual genotypes were available from six breeds (Gelbvieh, Charolais, Angus, Simmental, Limousin, and Hereford), three commercial crossbred herds and two crossbred research herds (Kinsella composites and Lacombe Research and Development Centre [LRDC]) as well as a crossbred validation group ( $n = 102$ ) from LRDC. Genomic breed composition was predicted for all individuals using the cross-validation procedure implemented in ADMIXTURE software using different approaches in terms of number of SNPs (including ISAG parentage assignment panel), methods of SNP selection and breed information. The results indicated a strong effect for number of SNPs and SNP selection methods on breed composition and RH estimates. Genomic estimated breed composition was regressed onto the pedigree recorded breed composition in the validation group to assess accuracy ( $R^2$ ) of prediction. The ISAG SNPs had 13 percentile points lower accuracy than that obtained when using the maximum number of SNP (~7,616 SNP overlapped between SNP panels). The correlation between RH values estimated using the maximum number of SNP and other approaches ranged from 61 to 95%. Inclusion of informative SNPs using different approaches including pairwise Wright's  $F_{ST}$  and Delta statistic improved the accuracy of genomic-based breed composition and RH. Thus, predicting genomic-based breed composition was achieved using cost-effective marker panels without affecting the accuracy of estimation of RH required to optimize crossbreeding programs in beef cattle.

**Key Words:** beef cattle, admixture, breed diversity and composition, retained heterozygosity

**MT77 Residual feed intake candidate gene associations.** N. A. Zulkifli<sup>\*1,2</sup>, W. S. Pitchford<sup>2</sup>, and C. D. K. Bottema<sup>2</sup>, <sup>1</sup>*School of Environmental Science and Natural Resources, The National University of Malaysia, Bangi, Selangor, Malaysia*; <sup>2</sup>*School of Animal*