

**W34 Weaning performance of Charolais calves.** F. Szabó<sup>1</sup>, A. Fördös<sup>1</sup>, Z. Domokos<sup>2</sup>, and S. Bene<sup>1</sup>, <sup>1</sup>University of Pannonia, Keszthely, Hungary, <sup>2</sup>National Association of Hungarian Charolais Breeders, Miskolc, Hungary.

Weaning weight (WW), preweaning daily gain (PWDG) and 205-day weight (205DW) of 23010 Charolais calves (10696 male and 12314 female) born between 1990 and 2005 from 10098 cows mated with 149 sires were analyzed. Breeding region, year and season of birth, age of dam, and sex of calves were fixed effects, and sire was random effect. Data were analyzed with Harvey (1990) Least Square Maximum Likelihood Computer Program, and two animal models were used for breeding value estimation. Variance, covariance components, heritability, correlation coefficients and the effect of the maternal environment on genetic parameters and breeding values were examined. The overall mean value and standard error of WW, PWD and 205DW were 219±7.60 kg, 939±40.63 g/day and 227±8.58 kg, respectively. Significant (P<0.005) region, year, season, sire and dam age effects, and sire × herd interaction were found. Weaning performance increased with increasing dam age up to six years of age. The direct heritability (h<sub>2d</sub>) of the evaluated traits was between 0.54 and 0.59. The maternal heritability (h<sub>2m</sub>) of these traits was 0.32 and 0.38. The direct-maternal correlations (rdm) were strong and negative (-0.84). Contribution of maternal heritability and maternal environment to phenotype was smaller than that of direct heritability (h<sub>2m</sub> + c<sub>2</sub> < h<sub>2d</sub>). The proportion of the variance of maternal permanent environment in the phenotypic variance (c<sub>2</sub>) changed from 0.02 to 0.03. The rank of animals based on breeding value for weaning traits was not changed whether the maternal environmental effect was modeled. The genetic value for weaning results of Charolais population has increased since 1993.

**Key Words:** weaning weight, environmental effects, heritability

**W35 Improving the profitability of beef from pastures: A case study of Tasmania's Circular Head Beef Business Group.** A. E. O. Malau-Aduli<sup>1</sup>, I. D. Bruce<sup>1</sup>, B. Doonan<sup>2</sup>, and P. A. Lane<sup>1</sup>, <sup>1</sup>School of Agricultural Science, University of Tasmania, Hobart, Tasmania 7001, Australia, <sup>2</sup>Davey & Maynard Consultants, Davenport, Tasmania 7310, Australia.

This case study on improving grazing management skills was conducted over a 12-month period in 2007 utilizing 1200 beef cattle on two properties of 60 hectares each, subdivided into 24 paddocks. The objectives were to evaluate pasture utilisation, liveweight gains and profitability using a multi-faceted economic model. Leaf emergence rate, average pasture cover, pasture growth rate, pre-grazing pasture mass, post-grazing residual and cattle liveweight gain data were collected monthly. Data were analysed using mixed (PROC MIXED) and general linear (PROC GLM) models in SAS to test for the fixed effects of property, date of sampling, cattle type and their second order interactions, while age of cattle and paddocks were fitted as random effects. Relationships between livestock and pasture variables were tested in correlation analyses using PROC CORR and significance established using Bonferroni probabilities. Results demonstrated that significant improvement in grazing management led to an increase in total pasture utilisation per hectare of over 40%, significantly greater than the set target of 7000kgDM/Ha on both properties. Pasture utilised directly for liveweight gain was positively correlated with total pasture utilised (r = 0.8686, p<0.0001). Energy partitioning for animal maintenance was found to be negatively correlated with total pasture utilised (r = -0.5927, p<0.05), and pasture utilised for liveweight gain (r = -0.8112, p<0.0001) and related to the nutritive value and species composition of the pastures. Average daily liveweight gain was found to be positively correlated with total pasture utilisation (r = 0.7302, p<0.0001) and pasture utilised for liveweight gain (r = 0.9181, p<0.0001) and negatively correlated with energy partitioned for animal maintenance (r = -0.9263, p<0.0001). It was concluded that increased pasture utilisation per hectare allowed for stocking rate increases across each property resulting in significant increases of approximately 73% in beef produced per hectare, thus increasing profitability by an overwhelming average of 250% across both properties.

**Key Words:** beef, pasture grazing, profitability

## Breeding and Genetics: Genomic Evaluation, Molecular Genetics, Statistical Methods, Sheep Breeding, and Swine Breeding

**W36 Value of genome-wide selection in Japanese dairy population.** H. Ohmiya\* and M. Suzuki, *Obihiro University of Agriculture & Veterinary Medicine, Obihiro, Hokkaido, Japan.*

Little research has been done on the genomic breeding program for the Japanese dairy cattle population. Therefore, we examined the rate of genetic gain, the rate of inbreeding increase, and the reduction of economic costs associated with the implementation of genome-wide selection in the Japanese dairy cattle population. The simulation data, which mimics the Japanese dairy population, were used to evaluate progeny testing by BLUP with an animal model and genome-wide selection scheme by improved BayesB (Meuwissen et al. 2001). These simulations were replicated 20 times with 30 chromosomes and having 100 QTLs and 101 biallelic SNP markers per chromosome. The candidate bulls in the progeny testing scheme were raised for 5 years until their semen could be used, however in the genome selection scheme candidate

bulls were selected at birth and put into service in one year. All records and pedigree information were used for calculating breeding values by BLUP, whereas only records and genotyping information of each generation were used in the BayesB scheme because of recombinant locus. The results showed that the accuracy of estimated breeding value for bulls by BayesB was a little lower than BLUP (0.82 vs 0.89), however, the reduction of generation interval and larger selection differential per generation in the genome-wide selection led to more genetic gain than BLUP. The rate of inbreeding increased 0.44 during the 10-year period in the progeny testing scheme, but the genome-wide selection scheme was 0.28. Furthermore, the economic costs in genome-wide selection scheme were reduced by 63% compared with the traditional progeny testing strategy. This suggests that genome-wide selection is effective genetically and economically.

**Key Words:** genome-wide selection, BayesB