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Communication Nº 17-20

ESTIMATION OF CHANGES OF GENETIC PARAMETERS OVER TIME FOR TYPE TRAITS IN HOLSTEINS USING RANDOM REGRESSION MODELS. S. Tsuruta, I. Misztal, T.J. Lawlor and L. Klei. University of Georgia, Athens 30602, USA. Genetic parameters for type traits in Holsteins were estimated over time using random regression models via EM-REML and Gibbs Sampling. About 15,000 records for final scores and about 30,000 records for linear scores (including production traits provided by USDA-AIPL) were sampled from the original file in Holstein Association USA Inc. Additive genetic effects with linear, quadratic, and cubic random regressions on year at scoring were included in the model. The results from EM-REML and from Gibbs Sampling were similar although EM-REML did not converge when using small starting values. Correlations between additive genetic variances in the last year and in previous years decreased as the distance between the years increased. However, estimates with quadratic and cubic random regression models may be artifacts due to a limited amount of information.

Communication Nº 17-21

GENETIC PARAMETERS ESTIMATION USING REML, BAYESIAN METHOD AND METHOD R IN MULTIPLE-TRAIT ANALYSIS OF WEIGHT IN NELORE CATTLE. M.H. Van Melis, J.A.II de V. Silva, J.P. Eler and J.B.S. Ferraz. Universidade de São Paulo/FZEA, Cx. Postal 23, 16635-900 Pirassununga-SP, Brazil.

The objective of this study was estimate genetic parameters of Nelore cattle by restricted maximum likelihood (REML), Bayesian analysis (Bayes) and Method R. Traits were weight at 550 d (W550) and weight gain from weaning at 550 d (WG345). Animal models multiple-trait analysis were used and the models considered as fixed effects contemporary groups, linear effects of age, as covariable, only for W550) and as random effects direct animal and error. Heritability estimates were .371 \pm .014, .370 \pm .000 and .411 \pm .002 for W550 and .260 \pm .014, .260 \pm .000 and .290 \pm .002 for WG345 for each method. Genetic correlation estimates were .564, .564 \pm .000 and .632 \pm .004 for REML, Bayesian and Method R, respectively. Method R was able to estimate genetic parameters in multiple-trait analysis but genetic parameters estimated by that method were larger the estimated by REML or Bayesian analysis.

Communication Nº 17-22

BAYESIAN INFERENCE ON VARIANCE COMPONENTS USING SIMULATED DATA. G.M. Lessa de Assis, J.M. Carneiro Júnior, R.F. Euclydes and F.J. de Carvalho Corrêa. Departamento de Zootecnia da Universidade Federal de Viçosa, CEP 36571-000, Viçosa, MG, Brazil.

Genetic evaluation of animals is based on Mixed Model Methodology, which assumes the knowledge of the (co)variance components. Since these components are normally unknown, their estimation is required. Recently, Bayesian methods have been proposed as alternatives to estimate genetic (co)variance components. The objective of this paper is to estimate variance components in asimulated data set using Bayesian inference, and to compare the estimations with the real values. Genetic and residual variance components and heritability were estimated, using "Multiple Trait Gibbs Sampling for Animal Models", MTGSAM. The estimates obtained using the Bayesian inference by the MTGSAM system were not similar to the real values, but they were close to estimates obtained by REML.

Communication Nº 17-23

BAYESIAN ANALYSES OF HETEREGENEOUS VARIANCES AMONG GENERATIONS OF BRAZILIAN CANCHIM BEEF CALVES. E.N. Martins, E.O. Engler, E.S. Sakaguti, A.R. Freitas, M.M. Alencar, L.M. Nieto and A. Falcão. DZO -UEM, 87020-900 Maringá, PR, Brazil.

The purpose of this study was to evaluate the occurrence of heterogeneous variance among the first six generations of Brazilian Canchim cattle. Yearling live weights of 6,496 calves were analyzed with Bayesian procedures. The heterocedasticity was considered in the analyses by using a multi-trait model where each trait is composed by the observations in each generation. The heritability estimated by the single trait model was equal to 0.40 and ranged from 0.41 to 0.59 with multi-trait analysis. The percentage of common animals the groups selected with both models was only 62.5 and 64% when 10% of males and 30% of females were selected respectively. The results indicate that genetic evaluation of Brazilian Canchim breed should consider heterogeneous variances across generations.

Communication Nº 17-24

COMPARISON OF LINEAR AND THRESHOLD MODELS FOR PREDICTING DIRECT AND MATERNAL GENETIC EFFECTS ON NUMBER OF LAMBS WEANED IN WESTERN AUSTRALIAN MERINO SHEEP. F.D. Brien, K.V. Konstantinov and J.C. Greeff. Pastoral and Veterinary Institute, Private Bag 105, Hamilton 3300, Australia.

Two models were evaluated in terms of predictive ability for reproductive performance (number of lambs weaned) in Merino sheep. The models were a univariate linear animal (LAM) and a univariate threshold model (TAM) with maternal effects. The threshold model resulted in slightly higher heritability estimates for both direct and maternal effects (0.12 vs 0.08 and 0.16 vs 0.12, respectively). Reported correlations are the average of 20 replicates. The results obtained confirmed the slight advantage of TAM over LAM (0.57 vs 0.52) and (0.58 vs 0.54) for direct and maternal effects, respectively.

Communication Nº 17-25

ESTIMATION OF HERITABILITY FOR EGG PRODUCTION IN LAYING HENS USING MIVQUE, ML, REML AND GIBBS SAMPLING METHODS. Y. Ünver, Y. Akbas, M.Z. Firat and I. Oguz. Ege University Faculty of Agriculture Department of Animal Science, Bornova, Izmir, Turkey.

Variance components and heritabilities for three partial egg productions were estimated using MIVQUE, ML, REML and Gibbs sampling (GS) based on sire and dam model separately. Egg productions of 1980 layers from commercial sire line were used. There were no substantial differences in heritability estimates among methods based on sire component. This was not the case for heritabilities from GS and the other methods based on dam model. For initial partial egg production heritability was 0.3 and increased to 0.7 for the second partial egg production based on sire model. For total partial egg production it was 0.5. For initial partial egg production heritability was 0.5 from MIVQUE, ML and REML but 0.4 from GS. The GS method for variance component estimation can be choise because of its several advantages.

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