Session 25

Genetic correlations between type traits of young Polish Holstein-Friesian bulls and their daughters
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The objective of this study was to estimate the genetic correlations of conformation traits of Polish Holstein-Friesian bulls and similarly defined type traits of their daughters. Young bulls were evaluated as required for registration in the herd book and for entering progeny testing. Data were 7 linearly scored (1-9 scale) and 3 descriptive (scored from 50 to 100) conformation traits of 933 young bulls born between 2005 and 2008, and the same traits evaluated in their 65,479 daughters. A two-trait animal model was used to estimate genetic correlations between the type traits of bulls and their daughters. (Co)variance components were estimated by a Bayesian method via Gibbs sampling. Two linear models were used: the linear model for bulls included fixed linear regressions on age at evaluation, fixed effects of herd and classifier, and random additive genetic effect; the linear model for cows contained fixed effects of herd-year-season-classifier, lactation stage, fixed linear regression on age at calving, and random additive genetic effect. Estimates of bulls’ heritabilities for all analyzed traits ranged from 0.07 for feet and legs to 0.25 for body depth. Heritabilities of cows were lowest for rear legs rear view (0.05) and foot angle (0.06), and highest for size (0.43). The genetic correlations between similarly described traits of bulls and their daughters were moderate to high (0.42-0.91). The lowest genetic correlation (0.42) was for chest width, and the highest (0.91) for rump angle. The magnitude of genetic correlations between pairs of type traits of sires and daughters were sufficiently high to suggest that bulls’ own conformation evaluations could contribute to breeding value estimation of bulls based on relatives.

Session 25

Estimation of dominance variance with sire-dam subclass effects in a crossbred population of pigs
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The most important nonadditive effect is probably dominance. Prediction of dominance effects should allow a more precise estimation of the total genetic merit, particularly in populations that use specialized sire and dam lines, and with large number of full-sibs, like pigs. Computation of the inverted dominance relationship matrix, D¹, is difficult with large datasets. But, D¹ can be replaced by the inverted sire-dam subclass relationship matrix F¹, which represents the average dominance effect of full-sibs. The aim of this study was to estimate dominance variance for longitudinal measurements of body weight (BW) in a crossbred population of pigs, assuming unrelated sire-dam subclass effects. The edited dataset consisted of 20,120 BW measurements recorded between 50 and 210 d of age on 2,341 crossbred pigs from 89 Plétrain sires and 169 Landrace dams. A random regression model was used to estimate variance components. Fixed effects were sex and date of recording. Random effects were additive genetic, permanent environment, sire-dam subclass and residual. Random effects, except residual, were modeled with linear splines. Only full-sib contributions were considered by using uncorrelated sire-dam classes. Estimated heritability of BW increased with age from 0.40 to 0.60. Inversely, estimated dominance decreased with age, from 0.28 to 0.01. Ratio of dominance relative to additive variance was high at early age (58.3% at 50 d) and decreased with age (2.6% at 200 d). Those results showed that dominance effects might be important for early growth traits in pigs. However, this need to be confirmed and dominance relationships will be included in the next steps.

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