

Session 15

Theatre 7

Estimation of genetic variation in residual variance in female and male broiler chickens

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Robustness of animals and uniformity of end product can be improved by exploiting genetic variation in residual variance in breeding programs. Residual variance (V_R) can be defined as environmental variance after accounting for all identifiable effects. The aims of this study were to estimate in broilers genetic variance in V_R of body weight by different methods and to estimate genetic correlations between mean body weight and V_R and between female and male V_R . The data sets comprised 26,972 female and 24,407 male body weight records. Estimates of the heritability of V_R were in the range of 0.033 – 0.088 based on variation in V_R among sire families. Lower heritabilities (0.012 - 0.037) were found when analyzing log-transformed squared residuals. Heritabilities were higher in females than in males. Genetic correlations between mean body weight and V_R were -0.41 and -0.45, respectively in females and males. The genetic correlation between female and male V_R was 0.11, indicating that female and male V_R are different traits. Results indicate good opportunities to simultaneously increase the mean and improve uniformity of body weight of broilers by selection.

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Theatre 8

A gene flow strategy for defining unknown parents groups in beef cattle genetic evaluations

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The definition of unknown parents groups (UPG) is usually based only on time periods and flows of foreign founders. A method to account for national flows of reproducers is proposed, which is particularly relevant for beef cattle populations. It assumes that unknown parents belong to the same phantom group when their progeny are bred in herds that are similar in terms of origin of their known reproducers. This method was applied to the French Charolaise population. It pointed out three main criteria to appreciate genetic differences: the birth period, the region and AI use of the herd. The robustness of the defined UPG was tested, under a sire model, in terms of numeric stability and consistency of the group effects. The impact of accounting for UPG in an animal model was evaluated on EBV for morphology traits: muscular and skeletal developments (MD and SD). For a given time period, female UPG and corresponding male UPG may have quite different genetic levels. Concerning MD, male UPG estimates were always larger than female ones: the genetic gap reached $0.75 \sigma_g$. No major re-ranking was observed for EBVs across models with or without UPG for this first trait. Surprisingly, some female UPG estimates for SD were larger than male ones ($+0.3 \sigma_g$). On this latter trait, changes in ranking of cows EBVs modified the choice for the renewal of natural service bulls. Including UPG enlarged by 108% genetic origins on the maternal side, but it concentrates origins towards AI sires on the paternal side.