Genetic parameters for male fertility, skatole and androstenone in Danish Landrace boars

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The objective of this investigation was to study the genetic association between direct measures of male fertility and boar taint compounds in Danish Landrace. Concentrations of skatole and androstenone in the back fat were available for approximately 6,000 and 1000 Landrace boars, respectively. The litter size traits on female relatives of these boars, total number born (TNB), live piglets at day 5 (LP5) and survival until day 5 (SV5) were extracted from the Danish Landrace breeding program, yielding 35,715 records. Finally, the male fertility traits, semen volume, sperm concentration, sperm motility, and total number of sperms were available from 95,267 ejaculates. These ejaculates were collected between 2005 and 2012 and originated from 3,145 Landrace boars from 10 AI stations in Denmark. The traits were analyzed using single and multi-trait animal models including univariate random regression models. Skatole and androstenone concentrations were moderate to highly heritable (i.e. 0.33 and 0.59, respectively). The genetic correlation between the two compounds was moderate (0.40). Genetic variance of sperm production per ejaculate increased during the productive life of the boar, resulting in heritability estimates increasing from 0.18 to 0.31. The heritability (based on service-sire genetic component) of TNB, LP5 and SV5 was 0.02 and the correlation between these effects and the additive genetic effect on boar taint ranged from 0.05 to -0.40 (none of these correlations were significantly different from zero). Most importantly, the genetic correlations between boar taint and semen traits were low (i.e. 0.24 to -0.35) and increasingly favorable with age. In conclusion, the prevalence of boar taint may be reduced through genetic selection without negatively affecting important male fertility traits.

Theatre 11 Session 08

A novel method to visualize local variation of LD and persistence of phase for 3 Danish pig breeds L. Wang¹, P. Sørensen¹, L. Janss¹, T. Ostersen² and D. Edwards¹ ¹ Aarhus University, Blichers Allé 20, P.O. Box 50, 8830 Tjele, Denmark, ²Pig Research Centre, Danish Agriculture & Food Council, Axeltorv 3, 1609 Copenhagen V, Denmark; lei.wang@agrsci.dk

The extent of linkage disequilibrium (LD) is of critical importance for genomic selection and genome wide association studies in animal breeding. The objective of this study is to develop a novel method to investigate local LD pattern over chromosomes, and persistence of phase between pair breeds. We demonstrated the method on three Danish pig breeds (Duroc, Landrace and Yorkshire), which were genotyped by Illumina PorcineSNP60 Genotyping BeadChip. Further, we estimated local average LD level using a sliding window technique, and generated an LD map for each chromosome. Within each sliding window, we fitted pairwise $LD(r^2)$ and distance (d) between marker pairs using a generalized linear model to estimate the average level of LD, then plotted the LD estimates against the physical position on the chromosome. We also calculated local persistence of phase between breeds by common marker sets in a similar way as LD. The regions with high average LD level also appeared as long LD blocks in LD heatmaps. Our LD map showed that LD varied considerably along chromosomes. When comparing local LD between breeds, we found that the LD patterns varied substantially between breeds; some regions with high LD level across all breeds may indicate selection processes. The persistence of phase for Landrace-Yorkshire at local level was much higher than that for Duroc-Landrace and Duroc-Yorkshire. Estimation and visualization of local LD and persistence of phase gives insight into how these quantities vary along chromosomes and across breeds. The results concerning persistence of phase imply that Landrace and Yorkshire are more closely related with each other than with Duroc.

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