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Session 66

Theatre 13

From Genomic Applications to Societal Perception: Discussion and Feedback

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The final discussion of the “From Genomic Applications to Societal Perception” session will involve a wide range of subjects from epigenetics, genomics, quantitative genetics, and societal dimensions in implementing genomic advancements in livestock. Building on insights from presentations covering DNA methylation under environmental stress, transgenerational effects, and ethical considerations across Europe, this interactive conversation will explore how these scientific breakthroughs can be applied in real-life practices to meet sectoral and consumer needs. Participants will dive into the practical applications of genomic research—examining how genomic applications can guide breeding strategies to improve resilience and diversity while aligning with consumer expectations of improved sustainability and animal welfare. The discussion will tackle key challenges, from bridging the gap between research and farm-level application to addressing cost concerns, regulatory hurdles, and public perceptions of genomic technologies. By bringing together different actors from the livestock sector, this session fosters a collaborative exchange of ideas on how genomic and epigenetic innovations can drive value in European livestock production.

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Poster 14

Assessing the genetic contribution to intramuscular fat content in local Krškopolje pig

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Krškopolje pig is known for its advantages in meat quality traits, particularly its high but variable intramuscular fat (IMF) content. However, the genetic contribution to IMF using genotypic data has never been studied before and is crucial for evaluating the feasibility of developing a breeding program for the Krškopolje pig. DNA samples along with phenotypic data on carcass and meat quality have been continuously collected from Krškopolje pigs, out of which a total of 356 animals were selected. Samples were genotyped using the Choice Genetics custom-SNP array. SNP-based heritability, as well as genetic correlations between IMF, backfat thickness, and muscle thickness were estimated using the GREML method in GCTA software. Three models were used to estimate the genetic and environmental contributions to the studied traits, incorporating either fixed effects of 1) farm and age, 2) farm per season and age, or 3) farm per season. Preliminary analyses showed that all models exhibit similar heritability estimates for IMF (0.36-0.38), and backfat thickness (0.28-0.29). The genetic correlations between IMF and backfat thickness were -0.21 ± 0.28 for the model 1, and -0.08 ± 0.30 for models 2 and 3. The heritability for gluteus medius muscle thickness was 0.29 for model 1, and 0.19 and 0.21 for models 2 and 3, respectively. The genetic correlations between IMF and muscle thickness were 0.04 ± 0.26 , 0.03 ± 0.33 , and 0.16 ± 0.31 for model 1, 2, and 3, respectively. All models present relatively similar preliminary heritability estimates, but there is considerable uncertainty in the genetic correlations due to large standard errors. These estimates were, however, obtained from a relatively small number of animals but currently include all available phenotypic data for the Krškopolje pig. Therefore, additional phenotypic data should be further collected to improve the reliability of the estimates. Acknowledgements: Funding by Slovenian Research and Innovation Agency (grants P4-0133, Z4-60178, J4-3094) and project GeroNIMO (EU H2020 GA no. 101000236) are acknowledged.