

## ORAL

### Technical Session 14

### **Beef Cattle - Genetic Evaluation and Recording**

## **Implementation of genetic evaluation for intramuscular fat in Norwegian beef cattle using ultrasound measurements**

Furre Siri<sup>[1]</sup>, Wetten Marte<sup>[2]</sup>, Svihus Cecilie<sup>[2]</sup>

[1] Tyr, [2] Aninova

There is an increasing demand from the beef market and breeding programs for reliable selection tools for intramuscular fat (IMF). The objectives of this study were to estimate genetic parameters for IMF and related traits and to establish a robust routine evaluation model for Norwegian beef cattle.

Ultrasound records from 12,748 animals of the Hereford (n=1,928), Charolais (n=4,990), Angus (n=2,489), Limousin (n=2,003) and Simmental (n=1,338) breeds collected between 2008 and 2022 were analyzed. Linear animal models were applied including fixed effects of classification year, breed-sex, ultrasound device, classifier, image interpreter and a regression on age within breed-sex, and random effects of herd or herd-year and animal. Across-breed multivariate analyses showed moderate heritabilities for IMF, fat depth and muscle depth, and a strong genetic correlation between IMF and fat depth (0.94), while correlations with muscle depth were low and negative (-0.15 and -0.04). Increasing the number of herd×year levels reduced the IMF heritability from 0.23 (310 herd levels) to 0.06 (964 herd×year levels), demonstrating strong environmental and data-structure effects. Within-breed heritabilities for IMF were 0.34 (Hereford), 0.13 (Charolais), 0.12 (Angus), 0.09 (Limousin) and 0.22 (Simmental). Corresponding estimates for fat depth were 0.45, 0.18, 0.15, 0.20 and 0.25, and for muscle depth 0.27, 0.37, 0.15, 0.30 and 0.34. Systematic differences between ultrasound devices introduced in 2017 and between image interpreters affected phenotypic means and variances.

Routine breeding values are now published for IMF. To increase accuracy, a bivariate animal model is used where fat depth is included as a correlated trait. (Co)variance components are based on the across-breed analyses, where the model includes herd as the environmental random effect. The results demonstrate that IMF can be evaluated with sufficient accuracy for selection, provided continued standardization of ultrasound interpretation.