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Modelling metabolic efficiency Do we need to understand the biological meaning of residual feed intake breeding values?

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ABSTRACT

Nordic Cattle Genetic Evaluation NAV (Denmark, Finland, Sweden) has included the efficiency traits metabolic body weight (MBW) and residual feed intake (RFI) into the Nordic Total Merit index in 2020 and continues improving the single-step genomic evaluations to increase reliability of genomic enhanced breeding values (GEBV). For the MBW, carcass weight will be included as correlated trait, and for RFI more data from commercial herds with the 3D camera system CFIT are under way. In this attempt, we have recognized that partial regression coefficient estimates may vary significantly across environments and parities. Furthermore, partial regression coefficients also differ from regression coefficients developed in nutrition studies for feeding recommendations. This was observed both on research farm data and CFIT data.

To explore the effect of this on GEBV, four different evaluations have been compared. Method A: same as the current RFI evaluation where at first dry matter intake (DMI) is regressed on energy sinks to get RFI observations, which then are used for the genomic evaluation. Method B: same as Method A but instead of regressing DMI on energy sinks, DMI was regressed on expected DMI. Method C: same as Method A, but RFI observations were calculated as DMI minus expected DMI. Method D: a multiplicative random regression genomic prediction model where DMI was regressed on expected DMI. Expected DMI values were calculated based on a review article on energy requirements for dairy cows. The methods were tested with data from four Danish Jersey herds that comprised 46 822 first and later lactation records from 1 211 cows.

Estimated heritability was 0.22, 0.20, 0.15 and 0.17 for RFI defined in methods A, B, C and efficiency regression in D, respectively, and additive genetic standard deviation was 1.1 kg, 1.2 kg, 1.2 kg and 5.7 %, respectively. The correlation between GEBV from Method A with GEBV from Method B, C and D was 0.93, 0.76 and 0.55, respectively indicating significant re-ranking. The differences in GEBV were a result of how

the expected DMI is modelled. Method A models the expected DMI by partial regression coefficients and represents the approach of geneticists to model RFI from a mathematical point of view. In contrast, Method D models the expected DMI from a biological point of view. Method B and C are intermediate approaches. Studying the biological implications of using GEBV from these different methods will be helpful for improving genomic predictions for metabolic efficiency. :