S11.O-06

EXPLORING OPPORTUNITIES TO EVALUATE GENOMICALLY MIR-PREDICTED RESIDUAL CH$_4$ EXPLOITING CORRELATIONS TO MACE TRAITS

Hadi Atashi[1], Amélie Vanlierde[2], Frédéric Dehareng[2], Hélène Soyeurt[3], Nicolas Gengler[3].

[1]Shiraz University, Shiraz, Iran; [2]CRA-W, Gembloux, Belgium; [3]ULiège-GxABT, Gembloux, Belgium.

Breeding has been identified as a promising strategy to reduce methane (CH$_4$) emissions in dairy cows. However, trait definitions and setup of efficient genetic evaluation systems remain important issues despite availability of genomic data. The aim of this study was to demonstrate an optimized computational single step genomic model setting, hereafter called ssGBLUP, exploiting correlations to traits evaluated in an international context by INTERBULL through Multiple Across Country Evaluation (MACE). Objective was to generate genomically enhanced estimated breeding values (GEBV) for the trait "Residual CH$_4$" (RCH4) defined on a genetic level as the deviation of "MIR-predicted CH$_4$" (MCH4) from "Expected CH$_4$" (ECH4) obtained from traits available internationally through MACE. The trait MCH4 was obtained as a prediction from milk mid infrared (MIR) spectra with a model based on 1,089 reference values showing a R² and a standard error of calibration of about 0.73 and 53g/d respectively. Genetic parameters and GEBV for MCH4 were estimated using test-day MCH4 records on 229,465 first-, 151,726 second-, and 90,484 third-parity Walloon Holstein cows, a ssGBLUP model and Gibbs sampling. Mean (SD) MCH4 yields were 327 (68), 356 (70), and 358 (72) g/day and mean (SD) h2 estimates for daily MCH4 were 0.12 (0.04), 0.14 (0.05), and 0.13 (0.05), for the first three lactations, respectively. For 1,129 bulls with at least 30 daughters (727 genotyped), GEBV for 305-d MCH4 of each lactation (and average of first three lactations) were regressed on published EBV of MACE evaluated milk, fat and protein yields, derived fat and protein percentages, and linear type traits. The used (G)EBV of ECH4 were defined as predictions combing the MACE evaluated traits using the obtained regression equations. Correlations between (G)EBV of 305-d MCH4 and ECH4 ranged from 0.57 to 0.61 in the first three lactations and was 0.60 for the averaged three lactations EBV of 305-d MCH4. Linear type traits including body depth, chest depth, teat placement, udder support, bone quality, and udder texture, the two later traits being non-MACE trait available locally, showed significant association to MCH4. An innovative evaluation setup is possible considering direct MCH4 data and, as external information, EBV for ECH4 combined in a bivariate ssGBLUP exploiting the indirect extra information provided by correlated traits that are available for sires based on daughters found internationally. Different settings to include external information for ECH4 are currently being tested. Final (G)EBV of RCH4 could then be predicted by subtracting ssGBLUP recomputed 305-d G)EBV for ECH4 from (G)EBV for MCH4, but alternative strategies are under review. Breeding using RCH4 could avoid complex weighting of all involved traits and simplify development of an efficiency sub-index in the setting of the Walloon genomic evaluation system.