

Genetic Evaluation of Enteric Methane for Sustainable Irish Beef Cattle

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Background:

Globally, livestock agriculture significantly contributes to human-induced greenhouse gas emissions, particularly through methane production. An enticing approach to effectively, durably, and progressively reduce enteric methane emissions at a reasonable cost is through animal breeding.

Methods:

Individual animal methane records were available from 1,508 multi-breed growing beef cattle using GreenFeed Emission Monitoring systems. The objective of this study was to derive genetic parameters for a series of definitions of enteric methane, carbon dioxide, and dry matter intake (DMI). Estimated breeding values (EBVs) were generated for nine alternative definitions of enteric methane and EBVs were validated against phenotypic performance (adjusted for non-genetic effects) as well as using the Legarra and Reverter (LR) method comparing EBVs generated for a part of the dataset compared to EBVs generated from the entire dataset.

Results:

The heritability estimates for methane increased with longer averaging periods, ranging from 0.09 ± 0.03 for the individual spot measurements to 0.43 ± 0.11 for the full test average. Methane exhibited moderate to strong genetic correlations with DMI (0.72) when comparing spot methane measurements with a 1-day average DMI. In the validation study, correlations (adjusted for heritability) between adjusted phenotypes and parental average EBVs varied from 0.56 to 1.14, with slopes ranging from 0.92 to 1.16 (the expected value being 1). The LR method revealed biases (level bias: -0.81 to -0.45, dispersion bias: 0.93 to 1.17) and accuracy ratios (0.28 to 0.38).

Conclusions:

The results from the study demonstrate the feasibility of genetic selection to reduce enteric methane emissions.