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Methane trait inclusion in beef terminal indices under increasing carbon pricing

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Introduction

There is a lack of consensus on the optimum method for including the carbon footprint in beef breeding objectives. One common approach where phenotypic records are limited is to use life cycle analysis (LCA) frameworks that predict greenhouse gas emissions across the entire production system using cradle-to-farm gate frameworks. These LCA approaches assign enteric methane emissions per animal from population-specific emission factors and prediction equations based on feed intake, feeding regime, and production system. When sufficient individual animal enteric methane phenotypic records exist, breeding programs can then choose to incorporate direct measures of enteric methane alongside or instead of LCA-derived estimates, therefore capturing inter-animal (genetic) variability in enteric methane emissions for the same performance as well as total greenhouse gas emissions from the system.

Ireland's national beef terminal index already includes a carbon-sub index based on a complete life cycle analysis where the carbon costs of some of the component traits are included in the index (Ryan *et al*., 2025). The present study compared different versions of Ireland's terminal index with or without the explicit inclusion of an individual animal enteric methane trait assuming a carbon price of either €80, €160, or €320/t CO_2e.

Materials & Methods

Eructated enteric methane was measured on 1,700 genetically diverse growing crossbred beef cattle using GreenFeed systems between the years 2018 and 2025 inclusive. Gross eructated methane estimated breeding values (EBVs) were calculated using a multi-trait animal linear mixed model in which both energy intake and carcass weight were included as correlated traits. Residual eructated methane EBVs were defined at the genetic level, as eructated methane production genetically independent of energy intake and carcass weight ($gRMP_{ec}$).

Residual EBVs for methane production were then calculated as

$$\mathbf{EBV}_{RMP} = \mathbf{EBV}_{methane} - \mathbf{A}_R \boldsymbol{\beta}'$$

where $\mathbf{EBV}_{\mathbf{methane}}$ was the vector of EBVs for methane production with genetic group effects removed. $\mathbf{A}_R$ is the $n \times k$ matrix of EBVs for the regressor traits with genetic group effects removed and $\boldsymbol{\beta}$ is the vector of genetic regression coefficients.

EBVs for the other traits in the terminal index were also available. The genetic standard deviation for gross eructated methane and residual eructated methane was 23.43 and 19.91 g/day, respectively. Three index scenarios were evaluated at each carbon price using AbacusBio's Selection Index Testing tool (Zhang *et al*., 2023): (1) an LCA-based carbon weighting only on all relevant traits, which is the status quo in Ireland; (2) an LCA-based weighting approach with enteric methane removed but instead where the gross eructated methane EBV was also directly included as a trait in the index; (3) the status quo LCA-based weighting plus residual eructated methane EBV.

To examine the relative contribution of individual traits to overall index rankings, correlations between component trait EBVs and the terminal index were evaluated across the 1,138 AI sires. Index performance was determined by the expected response to selection (over 10 years) and the ranking of AI sires separately across 180 Angus, 130 Charolais, 192 Limousin, and 1,138 multibreed populations. Of these sires, 438 had progeny with eructated methane records (range: 1 to 28 progeny per sire), while the remaining sires had no progeny with measured methane phenotypes.

To assess the impact of eructated methane EBV reliability on index performance and sire ranking, all analyses were repeated after stratifying sires by the number of progeny with recorded methane phenotypes. Sires were classified as having either high reliability (≥10 progeny with eructated methane records from Tully) or low reliability (<10 progeny). Contemporary groups contained, on average, 36 animals per group, with each group comprising progeny from 4 to 30 different sires. Index correlations within the high reliability and low reliability sire subsets were compared with those obtained from the complete dataset within each breed to evaluate the robustness of index performance and ranking across differing levels of progeny information.

Results

Carcass weight EBVs had the strongest within breed correlations with the terminal index (0.40 to 0.75 across the carbon prices and methane inclusion strategies). Carcass conformation EBVs also showed positive correlations within breed (0.20 to 0.60). Feed intake EBVs showed variable within-breed correlations with the terminal index depending on carbon price, ranging from -0.17 to 0.14 across breeds and scenarios, becoming more negative as carbon price increased. Within-breed correlations between age at slaughter EBVs and the terminal index were moderate to strong and negative across all breeds and scenarios, ranging from -0.46 to -0.20. Correlations between eructated methane EBVs and the terminal index were moderately negative increasing in strength with carbon price for both Limousin and Angus, strengthening from -0.11 under the status-quo LCA-based index at €80/t CO_2e to -0.33 at €320/t CO_2. In contrast, correlations between eructated methane EBVs and the terminal index for Charolais were weakly positive, decreasing from 0.11 to 0.03 with increasing carbon price.

The within breed correlations among all the three explored terminal index constructs at €80/t were >0.990 which were not different from 1 (P>0.05), indicating minimal sire re-ranking. The within breed correlations among just the carbon sub-index components of the three explored indexes was also >0.990. At €80/t CO_2e, the current LCA-based carbon weighting is projected to generate breed-specific methane responses of +0.32 g methane/day for Charolais, -0.50 g methane/day for Limousin and -1.39 g methane/day for the multibreed over 10 years from a population mean of 252.70 g methane/day, with expected carcass weight gains of up to 8.50 kg after 10 years. Although gross eructated methane EBVs had a SD of 21.90 g/day across the 1,138 AI sires, directly including eructated methane EBVs in the terminal index at €80/t CO_2e provided minimal additional methane response (<0.1 g/day change, equivalent to 40g methane over a 100 day finishing period) over and above the status quo, with no expected impact on genetic gain in carcass weight.

At €160/t, the status quo LCA-based carbon weighting were expected to generate enteric methane responses from -1.54 (Angus) to -0.63 (Limousin) g methane/day to +0.26 g methane/day (Charolais) after 10 years, while expected genetic gain in carcass weight was 90% of the current index (i.e., €80/t). Relative to the status quo at €160/t, replacing the LCA-based methane weighting with gross eructated methane EBVs resulted in additional changes in methane response ranging from -0.05 g/day (Charolais) to -0.20 g/day (Angus) after 10 years. In Charolais, this reduced the predicted increase from +0.27 to +0.22 g methane/day. Carcass weight gains increased by up to 0.74 kg over 10 years when methane traits were directly

included compared to the €160/t LCA-only scenario. Including residual eructated methane EBVs in the index while retaining the LCA-based methane weightings on feed intake and carcass weight produced similar additional responses to those achieved with a direct gross methane EBV.

At €320/t, the status quo LCA-based carbon weighting were expected to deliver enteric methane responses ranging from -1.71 g methane/day (Angus) to +0.21 g methane/day (Charolais) after 10 years, with expected genetic gain in carcass weight at 77 to 96% of baseline (i.e., €80/t). Relative to the €320/t LCA-only scenario, replacing the LCA-based methane weighting with gross eructated methane EBVs delivered additional methane reductions in Angus and Limousin (by -0.44 and -0.18 g methane/day respectively), while in Charolais it reduced the predicted increase from +0.21 to +0.09 g methane/day after 10 years, with carcass weight gains maintained at 93-100% of baseline. Including residual eructated methane EBVs in the index while retaining the LCA-based methane weightings on feed intake and carcass weight achieved similar responses to those achieved with gross eructated methane EBVs with carcass weight gains at 97-107% of baseline (i.e., €80/t).

When stratified on methane EBV reliability, correlations among the different terminal index constructions remained strong within each breed and within both high- and low-reliability sire subsets at €80/t CO_2e, indicating negligible sire re-ranking across index definitions. At €320/t CO_2e, correlations between each alternative index construction and the status quo weakened slightly within breeds for high-reliability sires (0.981 to 0.987), while remaining very strong for low-reliability sires (0.988 to 0.993), reflecting increased differentiation among sires with more reliable eructated methane EBVs as carbon price increased.

Discussion

While the potential for direct genetic selection to reduce methane emissions is well established, beef breeding objectives must include multiple traits to deliver balanced genetic progress across economically and biologically important characteristics. Accordingly, most beef cattle breeding objectives already include feed intake, carcass weight, average daily gain, and metabolic liveweight due to their established economic importance (Berry, 2022). A key consideration when undertaking multi-trait selection is the strength and direction of genetic correlations among goal traits, as these not only impact potential genetic gain for each trait in the index (Cole and VanRaden, 2018) but also determine the additional response achievable by directly including a trait in the breeding objective. Because methane production is genetically correlated with feed intake (Ryan *et al*., 2024; Donoghue *et al*., 2020), changes in feed intake will result in correlated changes in enteric methane production in the same direction. Ireland's current terminal index attempts to exploit these genetic relationships through LCA-based carbon weightings that assign economic penalties to feed intake and other production traits based on their associated carbon emissions, thereby creating indirect selection pressure for lower methane production.

However, this LCA-based approach captures only the component of methane emissions that is systematically associated with production traits. When methane production was genetically adjusted for energy intake and carcass weight in the present study, the genetic standard deviation reduced from 23.43 g/day to 19.91 g/day, corresponding to a reduction in the coefficient of genetic variation from 9.27% to 7.87%, indicating that 28% of the genetic variance in methane is explained by genetic associations with these traits, leaving 72% genetically independent. This residual variation reflects differences in daily methane production among animals of similar intake and carcass weight that are not captured by the LCA framework but can be identified through direct measurement. The extent to which this independent variability influences selection outcomes therefore depends on how strongly methane is weighted relative to production traits within the breeding objective.

The present study compared two approaches to incorporating this independent variation: replacing the LCA-based methane weighting with gross eructated methane EBVs or retaining the LCA-based methane weightings while adding residual eructated methane EBVs (genetically independent of intake and carcass weight). Both approaches produced nearly identical selection responses and sire rankings across all carbon prices evaluated, with correlations exceeding 0.990 at €80/t CO_2e. This similarity demonstrates that the choice between gross and residual methane definitions has minimal impact on index performance. Consequently, under the carbon prices and weighting schemes evaluated in the present study, the more relevant consideration is not which methane definition theoretically captures independent variation more effectively, but rather which definition integrates most practically with the existing index structure. For breeding programs already applying LCA-based carbon weightings to intake and carcass weight, including residual methane EBVs avoids the necessity to recalculate the carbon weightings. Conversely, replacing the LCA methane component with gross methane EBVs offers conceptual simplicity by directly measuring the trait of interest, though this requires removing methane-related weightings from correlated traits to prevent double counting. However, this equivalence may not hold if substantially greater economic weight is placed on methane reduction. Under scenarios where carbon prices are considerably higher or where methane is prioritized more heavily in the breeding objective, the choice between gross and residual methane definitions could have greater impact on selection outcomes, as the additional independent genetic variation captured by direct measurement would exert stronger influence on index rankings.

Conclusions

Although minimal sire re-ranking occurred between index scenarios, having access to eructated methane EBVs enables farmers to differentiate among bulls of comparable economic merit and select those with superior genetic merit for reduced enteric methane emissions.

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