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Augmenting saved feed index with carbon dioxide breeding values in dairy cattle

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Introduction

Including a saved feed (SF) index in total merit index selection has gained popularity in dairy cattle breeding. The originally suggested SF index (Pryce *et al*., 2015) applies appropriate index weights to two breeding values (BV), one for residual feed intake and another for metabolic body weight. However, estimating BVs for residual feed intake is challenging in dairy cattle (Stephansen *et al*., 2024), and therefore, Abdalla *et al*. (2024) suggested a simplified version of the SF index, which consists of the BVs for dry matter intake (DMI), energy-corrected milk (ECM) and body weight change. Often, feed intake data are limited, and utilizing available additional information would be beneficial.

Efficient cows consume less feed and produce less heat per unit of product, with some reservations under conditions of negative energy status. The finding that a cow's heat production and carbon dioxide (CO_2) exhalation are highly correlated (0.988; Huhtanen *et al*., 2021) has prompted studies aimed at developing feed efficiency metrics based either on the difference between measured and predicted CO_2 production (Chegini *et al*., 2025) or on efficiency ratios that include CO_2 production (Huhtanen and Bayat, 2025). However, implementing such metrics in existing total merit indices may be intricate and may limit the use of different sources of valuable data.

The aim of our study was to investigate whether an SF index could be augmented with CO_2 BV to increase the reliability of the index values. The approach is demonstrated using a pilot dataset. We developed three different SF indices to test how well a SF index can be estimated for animals with missing DMI observations and whether CO_2 production measurements can compensate for this lack of information.

Materials & Methods

Saved feed index. In its simplest form, an SF index can be defined as:

$$SF_i = -aDMI_i + \delta_M \times aECM_i + \delta_G \times aBWG_i, \quad (1)$$

where $aDMI_i$, $aECM_i$ and $aBWG_i$ are BVs of animal i for the traits DMI, ECM and body weight gain (BWG), respectively; and δ_M and δ_G are DMI requirements, based on feed requirement studies, to produce 1 kg ECM and 1 kg of BWG, respectively. Findings by Huhtanen and Bayat (2025) indicate that a cow's DMI and CO_2 production are highly correlated. If there exists a very high genetic correlation between DMI and CO_2 production, then, by assuming a genetic correlation of unity, an SF index can be augmented with BVs for CO_2 production (aSF) as follows:

$$aSF_i = -(b_1 \times aCO_{2i}) + \delta_M \times aECM_i + \delta_G \times aBWG_i, \quad (2)$$

where b_1 is the linear regression slope of DMI on CO_2 production and aCO_{2i} is the CO_2 BV of animal i.

Pilot data. To study the feasibility of the aSF index, a pilot dataset was extracted from an established feed efficiency research trial conducted at the Jokioinen dairy research farm of the

Natural Resources Institute Finland (Luke) during 2006 to 2024. The extracted 20,665 weekly records included observations on feed intake, milk production, and body weight from 537 primiparous Nordic Red dairy cows. Of these cows, the youngest 107 animals also had 2,604 weekly CO_2 observations derived from 16,395 daily measurements recorded using two GreenFeed gaseous measuring units (C-Lock Inc., Rapid City, SD) where cows had access to both units. The observations in the final dataset (Table 1) were weekly averages of daily measurements, which were prepared and validated as described in Lidauer *et al*. (2023). Body weight loss observations were excluded to enable modelling using a repeatability model.

Table 1. Descriptive statistics for the weekly averages of daily observations recorded from 537 primiparous Nordic Red dairy cows.

Trait	N	Mean	Std
Dry matter intake (kg/d)	16 904	20.0	2.87
Energy-corrected milk (kg/d)	20 665	29.5	4.49
Body weight gain (kg/d)	15 645	0.346	0.238
Carbon dioxide (kg/d)	2 604	12.6	1.59

Statistical model. A multi-trait repeatability animal model was developed for the estimation of BVs that can be presented as:

$$\mathbf{y}=\mathbf{X}\mathbf{b}+\mathbf{Z}_1\mathbf{p}+\mathbf{Z}_2\mathbf{a}+\mathbf{e}, \quad (3)$$

where $\mathbf{y}=[\mathbf{y}_1{}^T,\ldots, \mathbf{y}_k{}^T]^T$ is an $N\times1$ vector across the k traits DMI, ECM, BWG and CO_2, and N denotes the total number of observations. $\mathbf{X}$ is the design matrix for fixed effects and $\mathbf{b}=[\mathbf{b}_1{}^T,\ldots, \mathbf{b}_k{}^T]^T$ is a vector across all fixed effect levels and traits including the effects calving age, lactation stage, and production year×month interaction. $\mathbf{Z}_1$ and $\mathbf{Z}_2$ are incidence matrices for random permanent environmental and additive genetic effects, and $\mathbf{p}=[\mathbf{p}_1{}^T,\ldots, \mathbf{p}_k{}^T]^T$ and $\mathbf{a}=[\mathbf{a}_1{}^T,\ldots, \mathbf{a}_k{}^T]^T$ are $n\times1$, and $m\times1$ vectors for all the permanent environmental effects of n cows with observations, and all the breeding values of m animals in the pedigree, respectively. $\mathbf{e}=[\mathbf{e}_1{}^T,\ldots, \mathbf{e}_k{}^T]^T$ is a $N\times1$ vector including the random residuals. The random effects were assumed to follow multivariate normal distributions $\mathbf{p}\sim\text{MVN}(\mathbf{0}, \mathbf{P}\otimes\mathbf{I})$, $\mathbf{a}\sim\text{MVN}(\mathbf{0}, \mathbf{G}_0\otimes\mathbf{A})$, and $\mathbf{e}\sim\text{MVN}(\mathbf{0}, \mathbf{R}\otimes\mathbf{I})$, where $\mathbf{A}$ is the numerator relationship matrix of size m=2,693, constructed from the Nordic Red cattle pedigree by tracing cows with observations for three generations. $\mathbf{P}$, $\mathbf{G}_0$, and $\mathbf{R}$ are $k\times k$ variance-covariance matrices for permanent environmental, additive genetic, and residual effect, respectively. The required variance components were estimated by a multivariate variance component analysis applying the AI-REML algorithm implemented in the DMU software (Madsen and Jensen, 2013).

Examining the integration of CO_2 observations. To assess the applicability of the proposed approach, we estimated multiple sets of BVs for a validation cohort consisting of 92 cows. Cows in the validation cohort had at least 5 and, on average, 34 DMI and CO_2 weekly observations, which were either included in or excluded from the BV estimation datasets. Three different SF indices were constructed to estimate four SF index values for each validation animal: 1) SF index values from a standard SF index by applying Eq.1 (SF_{Eq1}), that was based on a multivariate BV analysis including the DMI, ECM and BWG observations of all cows; 2) pedigree-index SF index values (SF_{Eq1PI}) were calculated based on the standard SF index but the observations of the validation cows were excluded from the BV analysis; 3) SF index values by applying Eq.1, for which, within a four-traits multivariate BV analysis, all CO_2 observations of the validation cows were included as a correlated trait but their DMI observations were excluded (SF_{corCO2}); and 4) SF index values from an augmented SF index by applying Eq.2 (SF_{Eq2}) and using the same BVs that were estimated in 3). For Eq.1 and Eq.2, we applied the coefficients δ_M = 0.456 kg DMI/kg ECM and δ_G = 3.25 kg DMI/kg BWG as developed in

Lidauer *et al*. (2023), and a coefficient b_1 = 1.57, that was estimated from the pilot data including all DMI and CO_2 observations. We calculated the Pearson's correlations between the four sets of SF indices, as well as the Pearson's correlations of SF_{Eq1PI}, SF_{corCO2}, and SF_{Eq2} with adjusted SF phenotypes that were constructed from the cows' observations, adjusted for the fixed effects in Eq.3 ($\mathbf{y}_{adjusted}=\mathbf{y}-\mathbf{X}\hat{\mathbf{b}}+\bar{\mathbf{y}}$), and using the coefficients of Eq.1.

Results

Estimated heritabilities and genetic correlations among index BV traits are presented in Table 2. We obtained very similar heritability estimates for DMI and CO_2 and a strong genetic correlation (0.97±0.17) between the two traits. ECM had a stronger genetic correlation with DMI than with CO_2, but it should be noted that large standard errors were associated with the CO_2 (co)variance parameter estimates. The heritabilities of the two investigated SF indices, as well as their genetic correlations with the BV traits, were calculated by applying index weights of Eq.1 and Eq.2 to the estimated variance components. This resulted in an almost twice as high heritability (0.20) for the SF index augmented with CO_2 BVs compared with the standard SF index, which is most likely due to the lower correlation between CO_2 and ECM. The genetic correlation obtained between the two SF indices was very high (0.97).

Table 2. Estimated heritabilities (h^2) and genetic correlations (±standard error) for the traits dry matter intake (DMI), energy-corrected milk (ECM), body weight gain (BWG), carbon dioxide production (CO_2), and saved feed index based on Eq.1 (SF_{Eq1}) or Eq.2 (SF_{Eq2}).

		Genetic correlations				
Trait/Index	h^2	ECM	BWG	CO_2	SF_{Eq1}	SF_{Eq2}
DMI	0.30±0.08	0.72±0.10	0.21±0.19	0.97±0.17	-0.23	-0.08
ECM	0.43±0.11		-0.44±0.15	0.53±0.25	0.47	0.63
BWG	0.29±0.10			0.44±0.39	-0.68	-0.79
CO_2	0.31±0.29				-0.43	-0.31
SF_{Eq1}	0.11					0.97
SF_{Eq2}	0.20					

The Pearson's correlation between the validation cows' SF indices, based on a BV analysis that included their DMI observations, and their SF_{Eq1PI}, SF_{corCO2}, and SF_{Eq2} indices was 0.28, 0.79, and 0.82, respectively. The latter correlation was consistent with the strong genetic correlation estimated between SF and aSF, considering that the average reliabilities of the cows' SF and aSF indices were 0.47 and 0.56, respectively. The Pearson's correlation between the cows' SF_{Eq1PI}, SF_{corCO2}, and SF_{Eq2} indices and their adjusted SF phenotypes was 0.17, 0.44, and 0.43, respectively. This indicates that the increase in accuracy was similar whether CO_2 observations were included as a correlated trait or the SF index was augmented with CO_2 BVs.

Discussion

In this study, we investigated the possibility to utilize CO_2 observations as a new source of information for developing an SF index in dairy cattle. Our approach was conceived based on findings that a strong correlation exists between a cow's heat and CO_2 production (Huhtanen *et al*., 2021), and that dry matter digestibility has a low phenotypic and genetic variation (Berry *et al*., 2007; Mehtiö *et al*., 2019). This latter finding suggests that variation in DMI and metabolizable energy intake should be highly correlated when cows are fed the same diet. This is of interest because genetic variation in digestibility cannot be captured by CO_2 production, whereas variation in the proportion of metabolizable energy that is converted into heat is captured by CO_2 production. Thus, augmenting the SF index with CO_2 will be beneficial,

especially when data on direct feed intake measurements are rare and limited. Cows in this study were kept on the same research farm and fed a high-quality diet throughout the trial. All of this supports the estimated high genetic correlation between SF and aSF.
We found that SF indices in which the DMI BV of cows with missing DMI observations was augmented with a CO_2 BV (SF_{Eq2}) were more strongly correlated with the standard SF index based on full DMI data (SF_{Eq1}) than the standard SF index where the CO_2 observations were modelled as a correlated trait (SF_{corCO2}). Whether this finding is due to the in Eq.2 applied regression coefficient b_1, which has a biologically explanation, or to the limited size of the pilot dataset will require further studies. Nonetheless, the correlations of SF_{corCO2} and SF_{Eq2} with the SF phenotypes suggest that both alternatives of incorporation CO_2 observations improve the accuracy of SF indices to a similar extent when DMI observations are missing.

Conclusions

In this study, we demonstrated how CO_2 observations can be incorporated into an SF index for dairy cattle breeding. Using a pilot dataset, we found strong genetic correlations between the standard SF index and an SF index augmented with CO_2 BVs. We also found that the inclusion of CO_2 observations in an SF index can improve the accuracy of the index values when DMI observations are missing. Although the available pilot dataset was limited, our findings highlight that the use of CO_2 observations in developing SF indices may be beneficial. Future research on validating the use of CO_2 observations in an SF index, where BVs are based on genomic predictions, would be desirable.

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