INTERBULL BULLETIN NO. 61. 21-22 June 2025, Louisville, Kentucky, USA

Quantifying the effective contribution of phenotypic records to genetic evaluations: a case study on enteric methane emissions

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Abstract

In the context of data sharing for genetic evaluation, such as enteric methane emissions in cattle, quantifying the effective contributions of phenotypic records to genetic evaluations is essential. This research introduces a framework for estimating the effective contribution of phenotypic records to genetic evaluations, using the concept of effective record contributions (ERCs). Our three-step approach involves: 1) computing reliabilities of a pedigree-based genetic evaluation using phenotypic information, 2) approximating ERCs due to own records, free of contributions due to relationships, from reliabilities of phenotyped animals using a reverse reliability algorithm, and 3) calculating the total effective contribution of phenotypic records as the sum of ERCs associated with all phenotyped animals. We apply this approach to a Dutch dataset comprising 187 219 records of weekly enteric methane emissions from 8 668 Holstein cows measured between March 2019 and April 2024. The pedigree spans five generations. Estimated heritability and repeatability were 0.18 and 0.47, respectively. We evaluate the effective contribution of weekly enteric methane emission records using: 1) the entire dataset, 2) a subset spanning until October 2023, instead of April 2024, 3) a dataset reduced by over 30% and limited to 20 records per animal, and 4) the entire dataset but considering the weekly enteric methane trait as an indicator trait genetically correlated to a hypothetical trait of interest with a heritability of 0.20 and a genetic correlation of 0.80. Results show that the entire dataset corresponds to 12 671 ERCs for the weekly enteric methane emission trait, which remains similar after reducing the number of weekly records by over 30%. The subset spanning until October 2023 corresponds to 10 870 ERCs. The reduction of ERCs can be explained by a smaller amount of records, but also by a smaller amount of recorded animals. Finally, when calculating the effective contribution to a correlated trait of interest, the entire dataset with weekly methane emission records corresponds to only 3 286 ERCs. Our approach provides a flexible framework for quantifying the effective contribution of phenotypic records to genetic evaluations. The proposed framework can be extended for optimizing data collection schemes when aiming to optimize the accuracy of genetic evaluations.

Key words: effective record contribution, phenotype, genetic evaluation, methane emissions

Introduction

Global climate changes pose significant threats to ecosystems and human societies, with rising temperatures and altered weather patterns. Livestock, particularly ruminants, contribute to greenhouse gas emissions, with enteric methane emissions accounting for a considerable portion of their emissions. Several strategies have been proposed to mitigate enteric methane emissions, including management practices, feed additives, vaccination, and genetic selection (Knapp et al., 2014). Genetic selection is particularly appealing due to its low implementation costs as well as its permanent and cumulative effects (Bishop and Woolliams, 2004). However, the success of genetic selection in breeding programs depends on several factors. A key factor is the definition of the breeding objective that will guide the designs of the breeding program and of the trait recording schemes (Banks, 2024). For traits difficult or expensive to measure, such as methane emissions in ruminants, a special attention for the design of the trait recording scheme is required, as the main limiting factor is the availability of sufficient phenotypes to create a reference population to estimate sufficiently reliable genetic parameters and breeding values required for informed breeding decisions.

Worldwide, research groups and breeding organizations are exploring the integration of methane mitigation into breeding programmes, requiring a clearly defined trait that is recordable, cost-effective, exhibits phenotypic variation, and is heritable. Recent studies (e.g., Manzanilla-Pech et al., 2021; van Breukelen et al., 2023) have explored various phenotyping methods and trait definitions. For instance, van Breukelen et al. (2023) compared daily and weekly means of methane production (grams/day) by GreenFeed units and of methane concentration (ppm) by sniffers, recorded on commercial dairy farms in the Netherlands. These differences in terms of phenotyping methods and trait definitions may limit the effectiveness of collaborations across research groups and breeding organizations, hindering the success of genetic selection for methane mitigation (Manzanilla-Pech et al., 2021).

In this context, the Global Methane Genetics (**GMG**) initiative (https://www.wur.nl/en/project/global-methane-genetics-initiative.htm) was launched in 2024 as a global initiative to accelerate genetic progress in reducing methane emissions in ruminants (Gredler-Grandl et al., 2024). The GMG initiative is coordinated by Wageningen University and Research-Animal Breeding and Genomics and funded by the Global Methane Hub and the Bezos Earth Fund. It aims to enhance genetic progress by establishing standard operating procedures for data collection, harmonizing protocols, facilitating the sharing of methane phenotypic and genotypic data, and increasing methane data recording in large and small ruminants across the world.

A key task of the GMG initiative is to first establish a GMG database for sharing data and protocols to support research, reference population expansion, breeding program design, and genetic evaluations for enteric methane reduction. The effective amount of information of phenotypic records provided by any party to the GMG database varies, impacting the composition of reference populations and the effectiveness of genetic evaluations and breeding programs with clearly defined breeding objectives. Factors that influence the effective amount of information of phenotypic records for a genetic evaluation are, of course, the number of phenotypic records provided, but also the definition of the recorded trait, the recording scheme and associated factors (e.g., the contemporary group sizes), and the accuracy of recording (reflected by heritability and repeatability), among others.

The objective of this research is to develop a framework to quantify the effective contribution to a genetic evaluation of phenotypic records submitted to a database. The framework considers the number of records provided, recording scheme properties, and the accuracy of recording (heritability and repeatability). Then, we apply our framework to a Dutch dataset including individual cow enteric methane emissions measured with sniffers in automatic milking systems (**AMS**). Results demonstrate the flexibility of our framework to quantify the effective contribution of phenotypic records to a genetic evaluation.

Materials and Methods

This section introduces the framework for quantifying the effective contribution of phenotypic records to genetic evaluations. We first define the concept of effective record contribution (**ERC**) to quantify the effective amount of information of phenotypic records. Second, we outline our proposed framework which leverages this concept. Finally, we present various scenarios assessing the framework using a Dutch dataset.

Effective amount of information

The concept of effective amount of information contributing to a genetic evaluation was introduced in the 80s to approximate reliabilities (**REL**) associated with estimated breeding values (e.g., Wilmink and Dommerholt, 1985; Robinson, 1986; Misztal and Wiggans, 1988; Meyer, 1989). The main goal of all these approaches is to summarize all information of an individual in a single value that is a diagonal element of a diagonal matrix **D** such that the diagonal elements of the inverse of ($\mathbf{D} + \mathbf{A}^{-1}\lambda$) are approximately equal to the prediction error variances obtained from the inverse of the absorbed coefficient matrix, ($\mathbf{Z'MZ} + \mathbf{A}^{-1}\lambda$), where **Z** is the incidence matrix relating phenotypes to animals, **M** is the absorption matrix including all fixed and random effects other than the random additive genetic effect, $\mathbf{A}^{-1}$ is the inverse of the pedigree relationship matrix, and λ is the ratio between the residual variance and the additive genetic variance.

Several measures have been proposed for summarizing the effective information, varying by application context. For sire evaluations, these measures focus on the records of progeny of a sire, and are called "daughter equivalent" (VanRaden and Wiggans, 1991), "effective number of daughters" (Wilmink and Dommerholt, 1985; Van Vleck, 1987), or even "effective daughter contribution" (Fikse and Banos, 2001). Similarly, for animal models, the proposed measures focus on the records of the animals themselves and are called "record equivalent" (VanRaden and Wiggans, 1991), "effective number of records" (Misztal and Wiggans, 1988) or "effective record contribution" (Meyer, 1989; Přibyl et al., 2013).

In line with VanRanden and Wiggans (1991), and for our context of quantifying the effective contribution of phenotypic records to genetic evaluations, we define one ERC as the amount of information contributed by a standard animal to its genetic prediction. This standard animal is defined as having one record and an infinite number of contemporary group mates. The total ERC for a standard animal (**ERC_total**) can be computed for a trait of interest using its REL, as follows:

$$\text{ERC\_total} = (1-h^2)/h^2 * \text{REL}/(1-\text{REL}),$$

with h^2 being the heritability of the trait of interest.

Notably, ERC_total is the sum of two components: ERC due to own records (**ERC_own**) and ERC due to relationships (**ERC_rela**). ERC_own represents the amount of information contributed by the own records of an animal, excluding information from relatives. ERC_own is influenced by factors such as the number of records, the contemporary group size, and the repeatability, among others (Misztal and Wiggans, 1988; VanRaden and Wiggans, 1991). In contrast, ERC_rela represents the amount of information contributed by relatives (through the parents and progeny) to the genetic prediction of an animal.

From a phenotypic dataset, algorithms for approximating REL and ERC_total involve accumulating information from an animal 's performance records or those of its relatives, and adjusting for finite contemporary group sizes, and potentially accounting for other fixed and random effects, such as random permanent environment effects in case of repeated records (Misztal and Wiggans, 1988; VanRaden and Wiggans, 1991; Tier and Meyer, 2004).

From REL, algorithms for approximating ERC_own and ERC_rela involve reversing REL or ERC_total (Harris and Johnson, 2010; Vandenplas and Gengler, 2012; Ben Zaabza et al., 2022). Such algorithms are often used to calculate appropriate weights for integrating deregressed proofs in a genetic or genomic evaluation (Harris and Johnson, 2010; Vandenplas and Gengler, 2012) or approximating genomic reliabilities (Ben Zaabza et al., 2022; Bermann et al., 2022).

Quantification of the effective contribution of phenotypic records to genetic evaluations

The framework for quantifying the effective contribution of phenotypic records to genetic evaluations consists in a three-step approach: (1) approximation of REL using a pedigree-based evaluation and the model associated with the phenotypic records; (2) estimation of ERC_own using a reverse reliability algorithm; and (3) calculation of the total effective contribution of phenotypic records by summing the ERC_own of all phenotyped animals.

Step 1: Approximation of pedigree-based reliabilities

The first step consists of approximating pedigree-based REL for the trait of interest using the provided phenotypic records, the pedigree, and the associated model and variance components. If the phenotypic records are available for an indicator trait correlated with the trait of interest, pedigree-based REL for the trait of interest can be approximated using genetic correlations between the indicator trait and the trait of interest, and the heritability of the trait of interest. For this study, pedigree-based REL are approximated using the Tier and Meyer (2004) algorithm, as implemented in the software MiX99 (Lidauer et al., 2013) and MiXBLUP (Vandenplas et al., 2022).

Step 2: Estimation of ERC due to own records

The second step involves estimating the ERC_own for animals with phenotypes, using pedigree-based REL of the trait of interest approximated in the first step. We assume these REL are from a univariate animal model including only the additive genetic and residual effects, and with variance components reflecting the heritability of the trait of interest. The estimation of ERC_own is performed using a reverse reliability algorithm, which aims to estimate ERC_own for phenotyped animals, independent of ERC due to relationships (that is, contributions through the parents and progeny). For this study, ERC_own for phenotyped animals are estimated using the reverse reliability algorithm proposed by Ben Zaabza et al. (2022) and based on Tier and Meyer (2004).

Step 3: Calculation of the total effective contribution of phenotypic records

The final step involves calculating the total effective contribution of phenotypic records to a genetic evaluation for a trait of interest by summing the ERC_own associated with all phenotyped animals. This measure allows for a comprehensive understanding of the overall impact of the phenotypic records on genetic evaluations.

Data and software

Enteric methane emissions were recorded by sniffers (WD-WUR version 1.0, Carltech BV) installed in AMS on 62 commercial dairy farms located throughout the Netherlands, between March 2019 and April 2024. Pedigree and other cow information were provided by CRV (Arnhem, the Netherlands). For further details on the data recording scheme and data editing, see van Breukelen et al. (2024).

After editing, the dataset used in this study comprises 187 219 records of weekly averaged enteric methane emissions for 8 668 animals in 62 herds. The pedigree, extracted from the animals with phenotypes, spans five generations and includes a total of 31 471 animals.

The same model and variance components as estimated by van Breukelen et al. (2024) are used in this study. It is worth noting that the model includes as random effects, additive genetic, within-lactation permanent environment, across-lactation permanent environment and residual effects. The heritability is 0.18, and the repeatability is 0.47, respectively (van Breukelen et al., 2024). The software MiXBLUP (Vandenplas et al., 2022) was used for approximating pedigree-based REL and for reversing REL to estimate ERC_own.

Description of the scenarios

Using the Dutch dataset with weekly enteric methane emissions, the proposed framework is investigated using four scenarios. The first scenario simulates an initial submission of the entire Dutch dataset (i.e., 187 219 records for 8 668 animals) to a database.

The second scenario simulates a subsequent submission of a second dataset to a database. In this scenario, the entire Dutch dataset is submitted to a database in two subsets: 1) the first subset includes 125 169 records up to October 2023 for 8 034 animals, and 2) the second subset includes 62 050 records from October 2023 to April 2024, including 634 animals that are not present in the first subset.

The third scenario simulates a subsequent submission of a dataset with additional records for animals that already have some records in the database. In this scenario, the entire Dutch dataset is submitted to a database in two subsets: 1) the first subset includes 125 484 records for all the 8 668 animals, with at most 20 records per animal, and 2) the second subset includes the remaining 61 735 records. It is worth noting that the subsets have a similar number of records in the second and third scenarios.

For the first three scenarios, the weekly enteric methane emission trait is considered as the trait of interest. In the fourth scenario, the weekly enteric methane emission trait is considered as an indicator trait genetically correlated to a hypothetical trait of interest with a heritability of 0.20 and a genetic correlation of 0.80. In this scenario, the proposed framework is applied on the entire Dutch dataset to estimate its effective contribution to genetic evaluations for the hypothetical trait of interest.

Results & Discussion

Scenario 1 – Entire Dutch dataset

Applying the first and second steps of the framework on the entire Dutch dataset results in ERC_own ranging from 0 to 2.7 ERCs per animal with phenotypes, with an average of 1.5 ERCs (Table 1). First, ERC_own equal to 0 indicate that certain animals and their associated phenotypic records do not contribute to a genetic evaluation at all. This can be explained, for example, by animals being part of contemporary groups that are too small.

Second, these ERC_own illustrate that the number of phenotypic records, ranging from 1 to 80 records per animal, and averaging 21.6 ERCs (Table 1) does not linearly translate to an effective contribution of a dataset to genetic evaluations. This can be also observed in Figure 1 showing that, beyond a certain threshold (approximately 8 to 10 records), ERC_own no longer increases substantially with an increase number of records, indicating diminishing returns on investment in collecting more records.

Table 1. Number of records, and effective record contributions due to own records for the entire Dutch dataset.

	Min.	Average	Max.	Total
Number of records	1	21.6	80	187 219
ERC_own[1]	0.0	1.5	2.7	12 671.4
ERC_total[2]	1.0	3.2	6.3	25 724.0

[1]ERC_own = Effective record contributions due to own records.

[1]ERC_total = Effective record contributions due to own records and due to relationships.

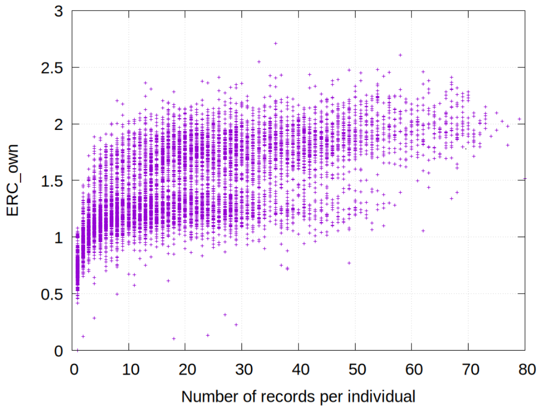

Figure 1. Effective record contributions due to own records (ERC_own) according to the number of records per animal.

Applying the third step of the framework on the entire Dutch dataset results in a total effective contribution of phenotypic records to a genetic evaluation for weekly methane emissions equal to 12 671 ERCs (Table 1). This sum of ERC_own is substantially lower than the number of records in the entire Dutch dataset (i.e., 187 219 records; Table 1), illustrating again that additional records do not linearly translate into effective contribution to genetic evaluation.

It is worth noting that ERC_own are lower than ERC_total because it include both contributions due to own records and due to relationships. Computed from the REL as ERC_total = $(1-h^2)/h^2$ * REL/(1-REL), the ERC_total range from 1 to 6.3 ERCs per animal with phenotypes, with an average of 3.2 ERCs (Table 1). The additional ERCs are due to relationships (ERC_rela), depend on contributions of relatives, and will therefore vary with a new submission of phenotypic records to the database.

Scenario 2 – Two subsequent submissions

For the second scenario, the entire Dutch dataset is divided into two subsets, with the first subset up to October 2023, and the second subset from October 2023 until April 2024. The first subset includes 8 034 animals and 125 169 records, and corresponds to a total effective contribution of phenotypic records of 10 870 ERCs, as estimated with the proposed framework.

The second subset dataset includes the remaining records of the entire Dutch dataset, as well as 634 animals that were not included in the first submission. Given that the entire Dutch dataset comprises 12 671 ERCs, we can estimate with the proposed framework that this second subset corresponds to 1 801 ERCs, calculated as the difference between the total effective contribution of the entire Dutch dataset (i.e., 12 671 ERCs) and the total effective contribution of the first subset (i.e., 10 870 ERCs). This effective contribution of the second subset can be explained by the additional records and also by the addition of 634 newly recorded animals.

Scenario 3 – Two submissions with no new animals

The framework is further investigated by dividing the entire Dutch dataset into two submissions, such that no new animals with phenotypes are added to the database. The first subset comprises 125 484 records for 8 668 animals with at most 20 records per animal and corresponds to a total effective contribution of 12 137 ERCs. Notably, this total effective contribution is comparable to that of the entire Dutch dataset, despite this first subset representing only 67% of the entire dataset.

Given that the entire dataset comprises 12 671 ERCs, the second subset corresponds to 534 ERCs only, calculated as the difference between the total effective contribution of the entire dataset (i.e., 12 671 ERCs) and the total effective contribution of the first subset (i.e., 12 137 ERCs). These total ERCs illustrate that this second subset will have a limited contribution to a genetic evaluation that already includes the first subset, even if it includes 61 735 records.

Scenario 4 – A hypothetical trait of interest

For the fourth scenario, the weekly methane emission trait is considered as an indicator trait genetically correlated to a hypothetical trait of interest with a heritability of 0.20 and a genetic correlation of 0.80. Applying the proposed framework on the entire Dutch dataset results in a total effective contribution of the Dutch phenotypic records to a genetic evaluation for this hypothetical trait of interest of 3 287 ERCs. This sum of ERC_own represents the effective contributions that flow from the indicator trait to the trait of interest through the genetic correlation.

A flexible framework

The different scenarios demonstrate the flexibility of the proposed framework to quantify the effective contribution of phenotypic records to genetic evaluations for a trait of interest. Our scenarios involve submission of datasets that include either records for a trait of interest, or records for an indicator trait.

Our framework can be easily extended to datasets that include records both for the trait of interest and for indicator traits. In such a scenario, pedigree-based REL for the trait of interest are approximated using phenotypic records of all traits with the first step of the proposed framework. Then, ERC_own are approximated for the trait of interest with the second step by reversing REL of the trait of interest assuming that they are approximated from an univariate model. The obtained ERC_own for the trait of interest include therefore ERC_own of the trait of interest, but also ERC_own of the indicator traits transferred through genetic correlations. Finally, the sum of all ERC_own of the trait of interest represents the effective contribution of all records of the trait of interest and of indicator traits to a hypothetical univariate genetic evaluation for the trait of interest.

Our framework can be also easily extended for estimating the effective contribution of phenotypic records to genetic evaluations of relatives of the phenotyped animals, such as selection candidates. By focusing on ERC_own of phenotyped animals, this study illustrates how individual phenotypic contributions can be aggregated to understand their cumulative impact on their genetic evaluations for a trait of interest. However, the aggregate effective contribution obtained from our framework does not reflect the effective contribution or phenotypic records to genetic evaluations of another group of animals, such as selection candidates. It has been shown that the accuracy of genomic prediction for selection candidates depends on the relationships among the reference animals and on the relationships between the reference animals and the selection candidates (Pszczola et al., 2012). Such contributions can be easily considered with our framework by estimating ERC_own for the selection candidates using the phenotypic records of the reference population with the second step of the framework, and then by aggregating these ERC_own to estimate the effective contribution of phenotypic records to genetic evasluations of selection candidates. The ERC_own of a non-phenotyped selection candidate is 0. However, the second step will estimate for selection candidates non-zero ERC_own that represent the effective contribution of relatives' phenotypic records to their genetic evaluations, without considering ERC_rela among them.

Finally, future research could aim to adapt the proposed framework for designing optimal recording schemes when aiming to optimize the accuracy of genetic evaluations. Such an optimization framework could integrate prior knowledge on the traits to be recorded (e.g., heritability, repeatability), but also prior knowledge on environment, management (e.g., seasons and herds), and recording costs (Banks, 2024). Future research could also aim to extend the proposed framework to consider genomic relationships, instead of pedigree relationships, in the first step of the framework. Considering genomic relationships will allow, for example, to estimate the effective contribution of phenotypic records of one breed to the genetic evaluation of another breed. That is currently not possible with the proposed framework because it is based on pedigree information only.

Conclusions

This study presents a flexible and comprehensive framework to quantify the effective contribution of phenotypic records to genetic evaluations using the concept of effective record contribution. This method relies on reversing reliabilities of estimated breeding values for a trait of interest by accounting for finite contemporary group sizes, and potentially other fixed and random effects, such as random environment permanent effects, as well as genetic correlations among the trait of interest and indicator.

Acknowledgments

This work is part of the Global Methane Genetics Initiative, funded by Bezos Earth Fund and the Global Methane Hub. The use of the HPC cluster has been made possible by the RegioDeal Foodvalley (through Shared Research Facilities Wageningen UR).

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