

Female Inclusive MACE for Improved Genetic Evaluations in Small Populations: A Special Case for Ayrshire Dairy Herds

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Abstract

Small reference populations hinder prediction accuracy in minor breeds, thereby limiting genetic progress. In response, the World Ayrshire Federation (WAF) initiated an international collaboration through the Interbull Centre (IBC) to enhance genomic evaluations for Ayrshire-based populations across countries. This initiative is primarily to ensure breed sustainability by addressing the challenge of limited reference population sizes in individual countries, which affects the reliability of national genomic evaluations. The aim of this study is to adapt IBC's Multiple Across-Country Evaluation (MACE) to include female estimated breeding values (EBVs) alongside male data while leveraging the Interbull Data Exchange Area (IDEA) and GenoEx-GDE platforms for data management.

The participating countries initially include Australia, Canada, Colombia, the United Kingdom, New Zealand, South Africa, and the United States. A total of 22,383 genotyped Ayrshire animals (4,403 males and 18,880 females) have been identified, with Canada contributing 46% of the genotypes. Adding cow data is envisioned to accelerate reference population growth, boost genotyping returns and improve the reliability of both national and international genetic and genomic evaluations over time. The first phase of implementation involves integrating cow EBVs into MACE while sharing genotypes among participating countries using the GenoEx-GDE platform. The second phase envisions extending these evaluations through InterGenomics for interested countries and those that cannot perform their own national genomic evaluations. This collaboration paves the way to faster growth of reference population sizes and improves genetic and genomic prediction accuracy for not only Ayrshire sustainability, but also the opportunity exists for other small breed populations like Guernsey, among others.

Key words: Ayrshire, genomic evaluation, MACE, small populations, international evaluation

Introduction

As genotyping costs continue to drop, the number of genotyped animals worldwide is on the rise. This creates an opportunity to significantly accelerate genetic gain through genomic evaluations on both national and international levels. However, the reliability of genomic predictions depends heavily on the size of the reference population, which links

genotypic and phenotypic information. For numerically small dairy breeds such as Ayrshire, Guernsey, and others, a limited national reference population remains a persistent challenge that restricts the potential gains from genomic selection (Mäntysaari et al., 2010; Wiggans et al., 2011).

Traditionally, international genetic evaluations for dairy breeds have relied on the MACE system implemented by the IBC, which

integrates bull evaluations from national genetic evaluation centres (Schaeffer, 1994). However, MACE has typically excluded cow EBVs, omitting valuable data that could enhance prediction accuracy. With IBC's data sharing platforms, such as the Interbull Data Exchange Area (IDEA) and GenoEx-GDE, it is feasible to exchange raw genotype data and expand genomic reference sets across countries under agreed-upon terms.

In this context, the WAF, in partnership with the IBC, initiated a collaborative project to investigate the possibility of including cow data into MACE. We hypothesise that incorporating female EBVs into the MACE system while leveraging the IDEA and GenoEx-GDE infrastructures will enable broader, more reliable international evaluations. This work holds potential not only for Ayrshire sustainability but also as a model for other numerically small or geographically dispersed dairy breeds. This paper outlines the proposed approaches and data management strategies for an international Ayrshire-based genetic evaluation that includes female EBVs, building on existing IBC services such as MACE and thus the future possibility of InterGenomics.

Materials and Methods

The first step of the project involves the modification of the existing MACE pipeline to incorporate female EBV records. This involves evaluating the accuracy of current de-regression methods for female data and ensuring no information overlaps between bulls and cows. Contributing organisations will supply female EBVs and pedigree data, alongside bull EBVs, while the Interbull Centre will conduct the necessary research to adapt, test, and validate the MACE pipeline and its outcomes.

Data Collection and Management

Data for the proposed research will include pedigree, genotypes, and EBVs (for both cows and bulls), managed through the IDEA and GenoEx-GDE platforms. Pedigree data utilises

the Interbull International ID format, ensuring consistency across countries. Genotypes will be stored in GenoEx-GDE, with organisations controlling data-sharing permissions. Cow EBV and pedigree data uploaded to IDEA will undergo quality checks and verification of data integrity, together with bull data, before being included.

In 2023, participating countries shared genotype counts with CDCB, revealing a total of 22,383 genotypes for Ayrshire animals, with Canada contributing 46% of the total (Table 1). These data form the basis for evaluating reference population sizes and potential genomic evaluation improvements when females are added.

Table 1: Number of Ayrshire genotypes by sex and participating country

Country	Female	Male	Total
Canada	8,670	1,806	10,476
United States	3,107	1,973	4,180
South Africa	2,761	19	2,780
New Zealand	2,105	41	2,146
United Kingdom	1,175	468	1,643
Australia	1,062	96	1,158
Columbia	N/A	N/A	N/A
Total	18,880	4,403	22,383

Source: Brian Van Doormaal, 2024

MACE with Female EBVs

MACE, a multi-trait evaluation treating each country-trait combination as a separate trait, uses de-regressed proofs from national evaluations. Including female EBVs requires modifications to account for heterogeneous variance and potential double-counting of information. Proposed changes include adjusting data verification and checking programs in IDEA and establishing the threshold criteria for cow data inclusion (e.g., minimum number of daughters, herds, and status). Preliminary estimates of descriptive statistics from the data are expected to follow. Additionally, the research phase of the project will involve the investigation of the technical aspects below:

- The best method to deregress cow EBVs for MACE
- Adjustments to the MACE model
- Possible bias, double counting
- Changes in reliability
- Accurate conversion equations that include females

InterGenomics

After a successful MACE evaluation that includes cow data, international EBVs will be provided to the participating countries (Figure

1). For those countries that cannot perform national genomic evaluations, and those interested in international genomic evaluations, they might then have an opportunity to participate in a new InterGenomics service from IBC. With InterGenomics, MACE EBVs are used as phenotypes, and together with GenoEx-GDE genotypes, international genomic breeding values and their reliabilities can be estimated and provided to countries that request the service. It is also possible to obtain information on duplicate genotypes, SNP conflicts, and parentage conflicts.

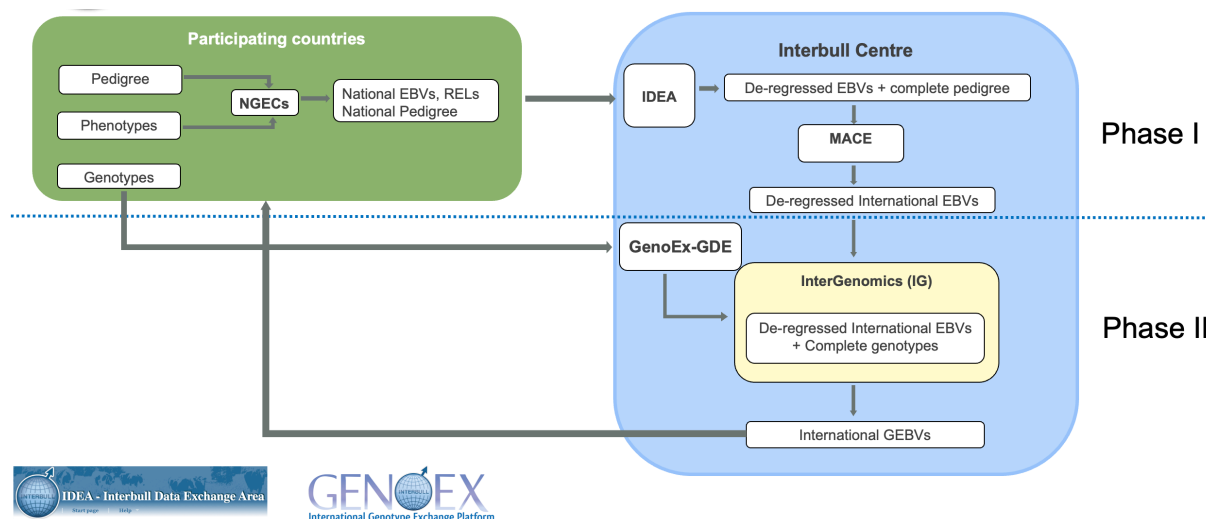


Figure 1. Proposed workflow showing the two implementation phases of including females in MACE project.

Results and Discussion

The international collaboration to enhance genomic evaluations for Ayrshire populations, as proposed by the participating countries involved in the World Ayrshire Federation (WAF), represents a significant step toward improving the reliability of genomic predictions for a breed with historically small reference populations in many countries. The initiative leverages the Interbull Centre's infrastructure and expertise to integrate genotypic and phenotypic data from multiple countries, including Australia, Canada, Colombia, the United Kingdom, New Zealand, South Africa, and the United States. The preliminary data

reveal a substantial pool of 22,383 Ayrshire genotypes currently available, with 84% being females, providing a robust foundation for expanding national genomic reference populations.

This section discusses the potential benefits, challenges, and considerations of the proposed methodologies, adapting MACE to include female EBVs while addressing their implications for Ayrshire breed sustainability.

Benefits of International Collaboration

The primary advantage of this collaboration is the significant increase in reference population size, which directly enhances the accuracy of genomic predictions. National evaluations for Ayrshire populations often suffer from limited

reference populations, resulting in lower reliabilities for genomic estimated breeding values. By pooling genotypes from across countries, the reference population for bulls alone exceeds 2,900, a marked improvement over any single country's capacity. This aligns with findings from Bonifazi et al. (2020), who demonstrated that increasing the number of genotyped animals in international evaluations improves across-country genetic correlation estimates, thereby enhancing prediction accuracy.

For countries like Colombia and South Africa, where genomic evaluations are not yet established, this collaboration could enable the implementation of genomic selection, fostering breed sustainability. The inclusion of female EBVs in MACE further amplifies the reference population by incorporating cow data, which is particularly valuable given the high proportion of genotyped females, allowing faster genetic gains. Mäntysaari et al. (2011) showed that de-regressed cow EBVs can be effectively used in national genomic evaluations, suggesting potential for international applications.

The IDEA and GenoEx-GDE platforms facilitate secure permission-based data sharing, allowing countries to control access while benefiting from collective data (Figure 1). This infrastructure supports the standardisation of data formats and quality control, critical for ensuring evaluation consistency across diverse national systems (Nilforooshan and Jorjani, 2022).

Challenges in MACE with Female EBVs

Adapting MACE to include female EBVs presents technical challenges, particularly the risk of double-counting information from cows and their sires. This issue arises because cow EBVs may partially reflect sire contributions already included in MACE, potentially biasing results. Thus, careful de-regression methods are needed to mitigate bias. The Interbull Centre has outlined steps to address this, including defining thresholds for cow data inclusion, such as minimum daughter numbers, the type of cow,

among others. These modifications involve research to develop de-regression techniques and validate data integrity. Additionally, heterogeneous variance across countries must be addressed, as differences in national evaluation models could affect the standardisation of EBVs (Nilforooshan and Jorjani, 2022).

Including cow data also necessitates updates to the IDEA database and verification programs, such as those in the *CheckProofsPara.py* and *verify_proofs.F90* programs to accommodate cow-specific metrics like genotyping status (codes "00" or "40" for non-genotyped or genotyped animals, respectively). These updates need to ensure that only valid female records are included and are subject to changes as the research goes on. While these changes are feasible, they require careful coordination with participating countries to establish consistent data submission protocols.

Strategic Considerations

Both methodologies require agreements on data sharing and result distribution, which involve political and legal considerations. The GenoEx-GDE platform allows countries to control data access, but consensus on sharing female genotypes and EBVs is critical. The IBC's experience with InterGenomics for Brown Swiss and small Holstein populations provides a model for establishing an Ayrshire-specific service, potentially managed by a Global Ayrshire Services Management Committee. This committee would facilitate ongoing discussions to address emerging opportunities and challenges, ensuring alignment with national priorities.

The choice to participate in MACE or InterGenomics with cow data depends on computational resources, data availability, and country preferences. MACE is less computationally intensive and leverages existing infrastructure, making it a faster option. However, InterGenomics may offer superior accuracy for small populations by directly

incorporating genomic data (Bonifazi et al., 2023). A hybrid approach, combining MACE with InterGenomics, could balance feasibility and accuracy, as proposed for Brown Swiss (CDCB 2024).

Implications for Ayrshire Sustainability

This collaboration has the potential to transform Ayrshire breeding by enabling genomic evaluations in countries without national systems and enhancing existing ones. By maximising reference population sizes, the initiative addresses the breed's risk of declining relevance due to limited genomic progress.

Conclusions

This study presents a novel and collaborative approach to enhancing genomic evaluations for numerically small dairy breeds by adapting the IBC MACE system to include cows. Future research will focus on optimising the integration of female EBVs into MACE and on piloting InterGenomics services tailored to the Ayrshire population. Currently, a data call has gone out to participating countries, together with an agreement for collaboration that includes data sharing. This work may reshape how global evaluations are designed for underrepresented breeds.

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