The M3GE project: developing beef cattle multi-trait multi-breed multi-country genomic evaluations for sustainability traits and small populations

R. Bonifazi[1], S. Aivazidou[1], R.F. Veerkamp[1], F. Macedo[2], R. Evans[3], T. Pabiou[3], K. Quigley[3], K. Matthews[4], H. Bunning[4], G.M. Tarekegn[5], M. Cassandro[6,7,12], R. Finocchiaro[7], J. Layton[7], R.G.M.F. Damai[7], A. Quaglia[8], D. Vicario[9], L. Degano[9], M. Piazza[10], F. Tiezzi[13], T. Roozen[2], M. Coffey[5], M. Burke[11] and J. Vandenplas[1]

[1] Animal Breeding and Genomics, Wageningen University & Research, P.O. Box 338, 6700 AH Wageningen, The Netherlands.

[2] Interbull Centre, Department of Animal Biosciences, SLU, Box 7023, S-75007 Uppsala, Sweden.

[3] Irish Cattle Breeding Federation, Link Rd Ballincollig, P31 D452 Cork, Ireland.

[4] Agriculture and Horticulture Development Board, Middlemarch Business Park, Siskin Parkway East, CV3 4PE Coventry, England.

[5] Scotland's Rural College (SRUC), Peter Wilson Building, The King's Buildings, West Mains Road, EH9 3JG, Edinburgh, Scotland, United Kingdom.

[6]National Federation of National Breeders Associations, XXIV Maggio 43, 00187 Roma, Italy.

[7]Associazione Nazionale Allevatori della Razza Frisona, Bruna e Jersey Italiana, Via Bergamo 292, 26100 Cremona, Italy.

[8]Associazione Nazionale Allevatori Bovini Italiani da Carne, Strada del Vio Viscioloso 21, 06132 Perugia, Italy.

[9]Associazione Nazionale Allevatori Bovini di Razza Pezzata Rossa Italiana, Via Ippolito Nievo 19, 33100 Udine, Italy.

[10]Associazione Nazionale degli Allevatori delle razze bovine Charolaise e Limousine Italiane, Via Ventiquattro Maggio 44/45, 00187 Roma, Italy.

[11]International Committee for Animal Recording, Arthur van Schendelstraat 550, 3511 MH Utrecht, The Netherlands.

[12]University of Padova, DAFNAE, Agripolis, viale dell'Università 16, 35020 Padova, Italy.

[13] University of Florence, DAGRI, via delle Cascine 23, 50144 Florence, Italy.

Corresponding author: renzo.bonifazi@wur.nl

Abstract

Sustainability traits, such as feed efficiency and enteric methane emissions, are difficult and expensive to measure. Establishing a large national reference population is therefore challenging, and pooling data across countries in a joint international evaluation would be beneficial. In beef cattle, data on sustainability traits are collected across multiple breeds and in small populations, including crossbred animals of various breed composition. In such scenarios, genomic prediction requires modelling the individuals' different genetic background. Additionally, including available data on correlated indicator traits could improve the accuracy of genomic prediction for sustainability traits. However, current international beef cattle evaluations led by Interbeef are pedigree-based, performed within each breed separately, and use data from one trait, or one group of traits, at a time. The "M3GE" project aims to develop multi-trait multi-breed multi-country genomic evaluations for beef cattle, focusing on sustainability traits and small populations. The project is the result of a collaboration between WUR, ICAR (the Netherlands), Interbull Centre (Sweden), ICBF (Ireland), AHDB, SRUC (Great Britain), and FedANA (Italy), involving six national breeding organisations from three countries. The aims of this paper are to: i) present the M3GE project and its objectives, ii) give an overview of the status of collecting and modelling feed efficiency across participating organisations, and iii) present the first

results of the project. Pedigree, phenotypic, and genomic data for feed efficiency, longevity, and associated indicator traits have been collected using the Interbull Centre's GenoEx-GDE and IDEA platforms. Initial work will focus on feed efficiency for which individual direct measures have been collected on ~13K phenotyped animals (~9K of which are genotyped), from over 15 different breeds and crossbreds recorded in Great Britain, Ireland, and Italy. The first steps include the imputation of collected genotypes to a common reference panel, population structure analysis, estimation of connectedness measures across populations, and estimation of genetic correlations across countries. The final step is to develop an international multi-breed single-step evaluation for feed efficiency including crossbred animals. This project contributes to the development of sustainable genomic evaluations in beef cattle for large and small populations.

Key words: beef cattle, international evaluations, multi-trait, multi-breed, genomic evaluations, feed efficiency

Introduction

Novel and sustainability traits, such as feed efficiency and enteric methane emissions, are difficult and expensive to measure, making it challenging to establish large reference populations at the national level. Hence, combining data across countries into a single international genomic evaluation is an attractive solution to build a large reference population for genomic predictions.

International beef cattle evaluations led by Interbeef involve up to fifteen countries worldwide and are carried out for five major popular breeds (Angus, Charolais, Hereford, Limousin, Simmental), and four trait groups: growth (composed by weaning weight), calving (composed by calving ease and birth weight), and carcass (composed by weight, conformation and fat) (Macedo, 2023; Venot et al., 2014; Vesela et al., 2019). Interbeef evaluations are performed within each breed separately and use data from one group of traits at a time. In Interbeef, raw national data (pedigree and phenotypes) are pooled at the international level and modelled using a pedigree-based evaluation following the AMACI model (Animal Model Accounting for Across Country Interactions) (Phocas et al., 2005). The resulting estimated breeding values (EBVs) and reliabilities (RELs) are distributed back to each participating country according to their national scale for a list of publishable sires (Bonifazi et al., 2023). Bonifazi et al. (2022) showed the feasibility and advantages of also including SNP genotypes at the international level to implement a joint single-breed single-step beef cattle genomic evaluation for a group of traits at a time.

In the Interbeef context, national beef cattle evaluations face different challenges that could be addressed through international collaboration. Firstly, the implementation of genetic evaluations for novel traits is highly desirable; however, the high costs associated with data recording hinder their widespread adoption. Consequently, genetic progress on new traits remains limited or is delayed, primarily due to the small size of the available reference populations at the national level. Second, small and local breeds risk becoming non-competitive in favour of more popular ones. Indeed, small and local breeds are not yet considered in current international, and sometimes even national, evaluations. Third, although crossbreeding is already widely used in some countries (e.g., Ireland) and is becoming more popular in others with the increased use of beef-on-dairy, international evaluations are still defined per breed and focus on purebred animals. In particular, in the presence of crossbred animals of various breed composition, genomic prediction requires

modelling of the individual's different genetic background. Thus, there is a need to develop new and improved services for countries and to expand the current Interbeef portfolio to allow the inclusion of genomic data, new breeds and crossbreeds, and new (novel) traits.

We conducted a preliminary survey to identify which (novel) trait groups were of interest to Interbeef participating countries and which breeds already had data collected at the national level. Results revealed that feed efficiency and longevity were the most interesting trait groups to implement, alongside consideration of crossbred information (e.g., beef-on-dairy). Furthermore, the survey emphasised that pedigree, phenotypic, and genomic data are already available at the national level, but collected on different purebred and crossbred animals across different countries.

Based on the survey results, the project called "M3GE" (multi-trait multi-breed multi-country genomic evaluations) has been launched in 2024. This paper aims to: i) present the M3GE project and its objectives, ii) give an overview of the status of collecting and modelling feed efficiency across participating organisations, and iii) present the first results of the project.

The M3GE project

The M3GE project aims to develop a multi-trait multi-breed multi-country genomic evaluation for beef cattle, focusing on sustainability traits and small populations. Through such an evaluation, the project aims to unlock several potential advantages. First, including data on new purebred and crossbred animals would help expand the reference population for genomic prediction, potentially increasing the accuracy of genomic EBVs (GEBVs) and providing international GEBVs for both purebred and crossbred animals. Second, the evaluation would facilitate pooling data for new suitability traits at the international level, effectively harnessing collaboration among countries for novel and complex traits such as feed efficiency. Third, by involving new numerically small and local breeds, the project would increase the use of local genetic resources that are currently unexplored at the international level, as is the case for local transboundary breeds (local and genetically similar populations separated by national borders). Fourth, by leveraging the joint international reference population, the evaluation could allow countries to deliver GEBVs to their breeders for traits that are not yet evaluated at the national level due to the small size of their national reference population.

The M3GE project is a private-public-partnership (PPP) supported by the Dutch Ministry of Economic Affairs and is a collaboration between Wageningen University & Research (WUR), the International Committee for Animal Recording (ICAR), the Interbull Centre, the Irish Cattle Breeding Federation (ICBF), the Agriculture and Horticulture Development Board (AHDB), Scotland's Rural College (SRUC), and the National Federation of National Breeders Associations (FedANA). The project involves a total of six national breeding organisations from three countries: Ireland (IRL), Great Britain (GBR), and Italy (ITA). Next to ICBF (IRL), and AHDB and SRUC (GBR), there are four Italian national organisations involved in the project through FedANA: ANABIFJ (Associazione Nazionale Allevatori della Razza Frisona, Bruna e Jersey Italiana), ANAPRI (Associazione Nazionale Allevatori Bovini di Razza Pezzata Rossa Italiana), ANABIC (Associazione Nazionale degli Allevatori delle razze bovine Charolaise e Limousine Italiane), ANACLI (Associazione Nazionale degli Allevatori delle razze bovine Charolaise e Limousine Italiane).

Materials and Methods

Data collection

Individual pedigree, phenotypic, and genomic information was collected at the Interbull Centre (Uppsala, Sweden). Pedigree and phenotypic repeated records were collected using IDEA, which was adapted to support the submission of repeated records. Genomic information was collected using GenoEx-GDE (Interbull Centre, 2025a). Data were collected for two new traits (feed and longevity) and their associated indicator traits. Therefore, two new trait groups were defined as follows:

- **FEED**, composed of feed itself (FEF) and its associated indicator traits: carcass traits (weight (CAW), fat (CAF), and conformation (CCO)), liveweight (LW), and growth traits (average daily gain (ADG) and average daily carcass weight (ACG)).
- **LONG**, composed of longevity (LON) and its associated indicator traits: calving traits (age at first calving (AFC), and calving interval (CAI)).

Data for FEED were collected for purebred beef animals, crossbred animals (both beef-on-beef and beef-on-dairy), and growing purebred dairy males, such as bulls and steers. Data for LONG were collected for purebred beef, crossbred (beef-on-beef and beef-on-dairy) animals.

Genomic information

Individual genomic information in the form of (imputed) single-nucleotide polymorphisms (SNPs) was available at medium-high density at the national level. Genomic information was collected for any animal with genomic and/or phenotypic information and their relatives (ancestors and sibs) to be later used in a single-step approach (Legarra et al., 2014). Different genotyping chips (i.e., panels) may be used within and across organisations. In total, eleven chips were collected among all participating organisations, with densities ranging from 30,111 to 777,962 SNPs. For each chip, a map file with information on the SNPs' commercial names, their physical positions on the genome (chromosome and base pair position), and their genome assembly version was collected. Chips and associated genomic information were validated to ensure that the collected genomic information followed the same Illumina AB coding (Illumina, 2006), and that genotype information would agree within- and across-country as well as within- and across-breed. Finally, all genotypes were mapped to the UMD3.1 genome assembly (Zimin et al., 2009).

Population structure

A Principal Component Analysis (PCA; Patterson et al., 2006; Chang et al., 2015) for FEF was performed using only SNPs overlapping across all chips (~4,000 SNPs) and including genotyped animals with phenotype and their genotyped ancestors. The PCA included about 18,000 genotyped animals, of which about 9,000 had a FEF phenotype.

Modelling of FEF at the national level

National information on FEF trait and model definitions, including (genetic) parameters, were collected using Interbeef 603 files (Interbull Centre, 2025b) and extended national genetic evaluations forms (Interbull Centre, 2025c).

Results & Discussion

Data collected

Table 1 shows an overview of the number of phenotypes and genotypes collected within the M3GE project for each organisation and trait group. Overall, data from GBR and IRL are collected on both purebred and crossbred animals, while data from ITA are collected only on purebred animals.

For the FEED trait group, about 98.5 thousand FEF repeated records have been collected across all organisations and breeds.

The number of records collected on FEED indicator traits ranges from 12.9 thousand for ADG to 12.9 million for CFA and CCO, with the majority of indicator traits' phenotypes being collected in IRL for carcass and live weights (Table 1). For FEED indicator traits, LW records are available in all organisations and countries, except for the Italian local breeds. Other indicator traits for FEED are only collected in either one or two countries. For the LONG trait group, approximately 10.7 million LON records have been collected from IRL and ITA, with the majority of phenotypes originating from the former. For LONG indicator traits, phenotypes have been collected for IRL and ITA with ~3.3 million and ~9.5 million records, respectively.

A total of about 3.1 million genotypes have been collected across organisations for both purebred and crossbred animals (Table 1). The majority of the genotypes are from IRL (~3 million), followed by GBR (~106 thousand), and ITA (~35 thousand).

Recording and modelling feed in different national organisations

Ireland

ICBF collects FEF at the Tully research station next to other novel phenotypes (e.g., enteric methane emissions). FEF is collected on commercial beef animals from targeted candidate sires, specifically the offspring of AI bulls, ensuring genetic connectedness to the rest of the IRL population. FEF recording is done close to the finishing period, mainly for steers

Table 1. Overview of the number of collected phenotypes (repeated records included) and genotypes [1].

Country	**GBR**	**IRL**			**ITA**		
Organization (breeds) [2]	AHDB&SRUC (PBD & XBD)	ICBF (PBD & XBD)	ANAFIBJ (HOL)	ANAPRI (SIM)	ANABIC (ITA breeds)	ANACLI (LIM & CHA)	
Trait [3]							**Total**
FEED							
FEF	28.4K	8.4K	8.8K	900	27K	24K	98.5K
CWE		12.9M				42K	13M
CFA		12.9M					12.9M
CCO		12.9M					12.9M
LW1	581K	1.0M	26K	7.6K		6K	1.6M
LW2		1.0M				192K	1.0M
LW3		1.3M					1.3M
ADG				7.6K	5.3K		12.9K
CDG					355K		355K
LONG							
LON		10.2M			248K	239K	10.7M
CAI		8.5M			912K		9.5M
AFC		3.1M			255K		3.3M
Genotypes	106K	3.0M	5.3K	3.3K	13.3K	12.9K	3.1M

[1] K = thousands, M = millions. [2] PBD = purebred, XBD = crossbred, HOL = Holstein-Friesian, SIM = Simmental, ITA breeds = Chianina, Marchigiana, Romagnola, Podolica, Maremmana, LIM = Limousin, CHA = Charolais. [3] FEED = feed trait group, FEF = feed, CWE = carcass weight, CFA = carcass fat, CCO = carcass conformation, LW1, LW2, LW3 = live weights (different definitions), ADG = average daily gain, CDG = carcass daily gain, LONG = longevity trait group, LON = longevity, CAI = calving interval, AFC = age at first calving.

and heifers, and a few young bulls. The age at recording ranges from about 200 to 900 days. While recording was initially focused on purebred animals, it is now mostly conducted on crossbred animals. Initially, when recording focused on purebred individuals, the diet was *ad libitum* (concentrate and hay), while nowadays is a TMR (Ryan et al., 2022). A single record

per animal is available, with FEF defined as the average daily dry matter intake (Kg DMI/day) over the whole testing period. The minimum length of the testing period is 30 days and the average length is 109 days. The national model used is a multi-breed, multi-trait, two-step genomic animal evaluation including purebred and crossbred data for: FEF, three live weights (365-450 days, 450-550 days, 550-700 days), skeletal development, and three carcass traits (CWE, CFO, CCO). In this evaluation, FEF is modelled as:

$$FEF = hrbxb + hrbxd + dhrbxb + dhbxd + dfrac + afi + a2fi + a3fi + damage + dampar + byr + twin + hysfi + a + e,$$

where: *FEF* = daily DMI, *hrbxb* = heterosis beef x beef (covariate), *hrbxd* = heterosis beef x dairy (covariate), *dhrbxb* = dam heterosis beef x beef (covariate), *dhrbxd* = dam heterosis beef x dairy (covariate), *dfrac* = dam breed fraction (covariate), *afi*, *a2fi*, and *a3fi* = age at feeding fitted as a linear, quadratic, and cubic covariate, respectively, *damage* = age of the dam (covariate), *dampar* = parity of the dam (fixed), *byr* = birth year of the animal (fixed), *twin* = twinning (fixed), *hysfi* = hear-year-season (random), *a* = animal genetic effect (random), *e* = residual effect (random).

Great Britain

AHDB collects FEF data from research and mostly commercial farms, using the provided equipment and protocol. Recording is done over a 63-day period with animals having an *ad libitum* diet. FEF is collected during the testing period on purebred and crossbred steers with age at recording ranging from about 170 to 560 days. FEF is defined by SRUC as the average daily dry matter intake (kg DMI/day), with one record per week, for up to 7 weeks in total. At the national level, FEF is modelled using a single-trait, multi-breed, ssGBLUP repeatability animal model, defined as:

$$FEF = fdg + brl + aaf + lve + h13 + h23 + h34 + r12 + r13 + r23 + pe + a + e,$$

where: *FEF* = daily DMI, *fdg* = feeding group (fixed), *brl* = birth location (fixed), *aaf* = age at feeding (covariate), *lve* = live weight (covariate), *h13*, *h23*, *h34*, *r12*, *r13*, and *r23* = heterosis (*h*) and recombination (*r*) covariates between dairy breeds (1), beef breeds (2), continental breeds (3), and UK beef breeds (4), *pe* = animal permanent environment effect (random), *a* = animal genetic effect (random), *e* = residual effect (random).

Italy

In Italy, national breed organisations independently collect and model FEF recorded at their own test centre for (young) male selection candidates.

Holstein. ANAFIBJ collects FEF on purebred Holstein growing male selection candidates. The age at recording ranges from about 100 days to 600 days. Repeated records are collected over a minimum 30-day period. FEF is defined as daily dry matter intake (Kg DMI/day). FEF is modelled using a single-trait, genomic BLUP (GBLUP) repeatability animal model, defined as:

$$FEF = aaev + bidt + dtpt + pe + a + e,$$

where: *FEF* = daily DMI, *aave* = age at phenotyping (covariate), *bidt* = birth date (covariate), *dtpt* = date at phenotyping (random), *pe* = animal permanent environment effect (random), *a* = animal genetic effect (random), *e* = residual effect (random).

Simmental. ANAPRI collects FEF on purebred Simmental male selection candidates. The age at recording ranges between about 280 and 340 days. Repeated records are collected over a 60-day period and summarised into a single record per animal. FEF is defined as daily residual feed intake (RFI; Kg DMI/day). FEF is

modelled using a single-trait, single-step GBLUP animal model as:

$$FEF = cg + weight + a + e,$$

where: *FEF* = daily RFI, *cg* = contemporary group (fixed), *weight* = animal live weight (covariate), *a* = animal genetic effect (random), *e* = residual effect (random).

Italian local beef breeds, Limousin, and Charolais. ANABIC collects FEF on purebred male selection candidates for three Italian local beef cattle breeds: Chianina, Marchigiana, and Romagnola. FEF is available over a 30-day testing period, and the age at recording ranges between about 200 and 400 days. FEF is defined as residual feed intake (RFI; kg DMI/day). FEF data for the three local beef breeds are jointly modelled using a multi-breed, single-trait, ssGBLUP repeatability animal model as:

$$FEF = cg + breed + weight + pe + a + e,$$

where: *FEF* = daily RFI, *cg* = contemporary group (fixed), *breed* = breed effect (fixed), *weight* = animal weight (covariate), *pe* = animal permanent environment effect (random), *a* = animal genetic effect (random), *e* = residual effect (random).

ANACLI collects FEF on purebred Limousin and Charolais male selection candidates at the ANABIC test centre using the same procedure. FEF is defined as residual feed intake (kg DMI/day). For FEF and Limousin individuals, a single-trait, ssGBLUP repeatability animal model was recently developed as:

$$FEF = cg + weight + pe + a + e,$$

where: *FEF* = daily RFI, *cg* = contemporary group (fixed), *weight* = animal weight (covariate), *pe* = animal permanent environment effect (random), *a* = animal genetic effect (random), *e* = residual effect (random). The FEF data from ANACLI was not included in the PCA as it was not yet available.

Table 2 shows a summary of the national trait definitions of FEF, evaluations and model used, and genetic parameters estimated at the national level by the different organisations. Overall, FEF heritabilities are moderate (average across organisations of 0.22), ranging between a minimum of 0.05 for the Italian local beef breeds and 0.32 for IRL. Repeatability ranged between 0.22 for the Italian local beef breeds and 0.50 for the Italian Holstein.

Population structure

The first two principal components (PC) explained a large proportion of variance (24.4 % and 15.3%, respectively). Figure 1 shows the PCA for purebred individuals. The first PC separated purebred individuals into several main breed clusters independent of the country providing the genotypes: from left to right, Holstein, Limousin, Angus, and Simmental. The local Italian breeds clustered together and separately from other purebred individuals following the second PC. The remaining purebred individuals clustered closely with either the Limousin or the Angus breed cluster. Finally, Figure 2 shows the PCA including crossbred animals, demonstrating how crossbred individuals form a continuum across purebred animals, except for the local Italian breeds, which remain distinct as they were not crossed with other breeds. Such a pattern was expected as the majority of the crossbred animals are from unstructured crosses.

Table 2. Summary of national models and genetic parameters for the feed trait group across different countries.

Country	GBR		IRL		ITA	
Organization	AHDB&SRUC	ICBF	ANAFIBJ	ANAPRI	ANABIC	ANACLI
Breeds[1]	PBD & XBD	PBD & XBD	HOL	SIM	ITA breeds	LIM & CHA
Trait[2]	DMI	DMI	DMI	RFI	RFI	RFI
Model[3]	ssGBLUP multi-breed single-trait	two-step genomic multi-breed multi-trait	GBLUP single-trait	ssGBLUP single-trait	ssGBLUP multi-breed single-trait	ssGBLUP single-trait
Heritability	0.14	0.30	0.32	0.29	0.05	0.13
Repeatability	0.26		0.50		0.22	0.24

[1] PBD = purebred, XBD = crossbred, HOL = Holstein-Friesian, SIM = Simmental, ITA breeds = Chianina, Marchigiana, Romagnola, LIM = Limousin, CHA = Charolais. [2] DMI = Dry Matter Intake, RFI = Residual Feed Intake. [3] ssGBLUP = single-step genomic BLUP, GBLUP = genomic BLUP.

Next steps and implications

The next steps in the project are to impute the collected genotypes to a common reference panel, and to estimate connectedness and genetic correlations across populations and breeds. Then, an international multi-breed single-step evaluation for FEF, including crossbred animals, will be developed. Later, the project will focus on developing similar multi-breed single-step evaluations for LON. In the final phase, the project will focus on including indicator traits for both FEF and LON using a multi-trait approach.

The M3GE project is expected to improve current and future Interbeef evaluations by optimising existing services and developing new ones. Such improvements include, for instance, adapting pipelines to accommodate repeated records as well as identifying possible bottlenecks, such as the efficient upload and routine handling of large volumes of genomic data from individuals with diverse breed composition. Overall, the M3GE project contributes to the development of sustainable international genomic evaluations in beef cattle across both large and small populations, thereby enhancing Interbeef's capacity to meet future demands.

Conclusions

The M3GE project is an international collaboration between different partners, including six national breeding organisations. The project aims to develop beef cattle multi-trait multi-breed multi-country genomic evaluations for sustainability traits and small populations. In the first phase, data (pedigree, phenotypes, genotypes) have been collected for feed, longevity, and their associated indicator traits, for both purebred and crossbred animals, including (small) local populations. The next step is to develop a multi-breed, multi-country genomic evaluation for feed efficiency.

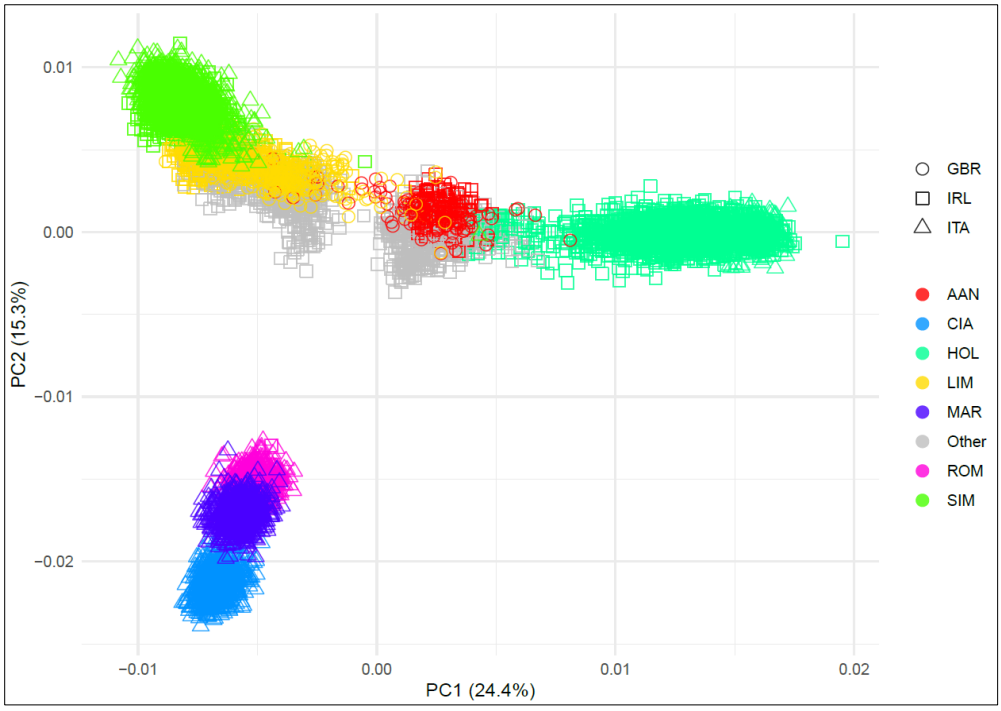

Figure 1. Plot of the first two principal components (PC) and percentage of explained variance (within brackets) of the genomic relationship matrix for purebred animals. Shapes indicate the country sending the genotype and colours indicate the breed (Other = other purebred breeds). GBR = Great Britain, IRL = Ireland, ITA = Italy.

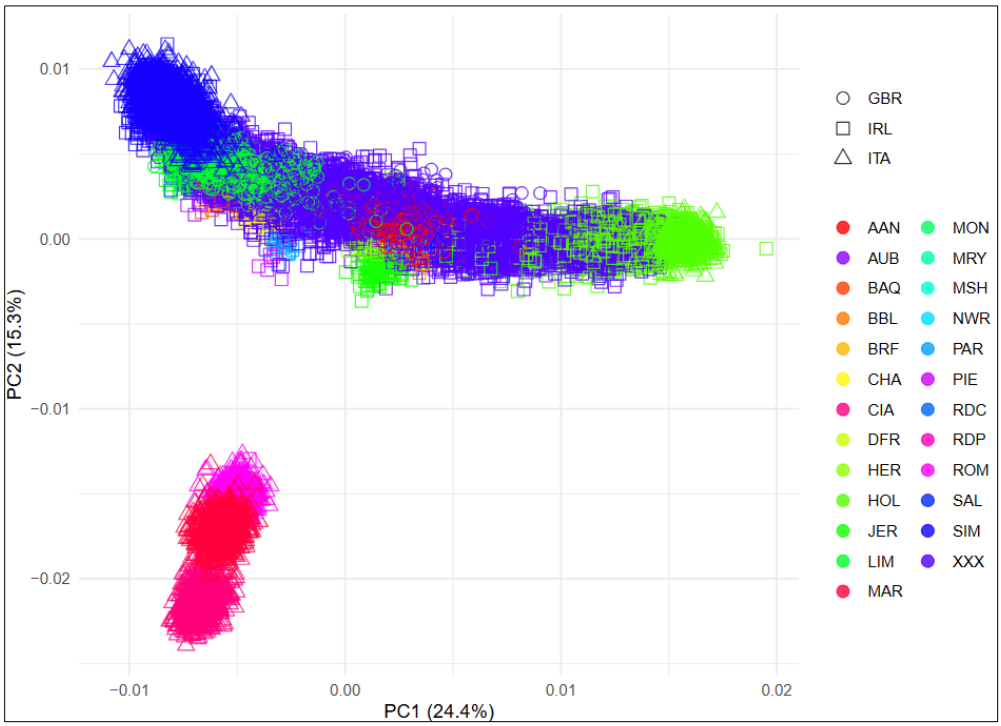

Figure 2. Plot of the first two principal components (PC) and percentage of explained variance (within brackets) of the genomic relationship matrix for purebred and crossbred animals. Shapes indicate the country sending the genotype and colours indicate the breed. GBR = Great Britain, IRL = Ireland, ITA = Italy.

Acknowledgments

This study was financially supported by the Dutch Ministry of Economic Affairs (TKI Agri & Food Project LWN23062) and the M3GE partners ICAR (Utrecht, the Netherlands), SLU (Uppsala, Sweden), AHDB (Coventry, United Kingdom), SRUC (Scotland, United Kingdom), FedANA (Rome, Italy), and ICBF (Cork, Ireland).

References

Bonifazi, R., Calus, M. P. L., ten Napel, J., Veerkamp, R. F., Biffani, S., Cassandro, M., Savoia, S., and Vandenplas, J. (2023). Integration of beef cattle international pedigree and genomic estimated breeding values into national evaluations, with an application to the Italian Limousin population. *Genetics Selection Evolution*, *55*(1), 1–18. https://doi.org/10.1186/s12711-023-00813-2

Bonifazi, R., Calus, M. P. L., ten Napel, J., Veerkamp, R. F., Michenet, A., Savoia, S., Cromie, A., and Vandenplas, J. (2022). International single-step SNPBLUP beef cattle evaluations for Limousin weaning weight. *Genetics Selection Evolution*, *54*(1), 57. https://doi.org/10.1186/s12711-022-00748-0

Chang, C. C., Chow, C. C., Tellier, L. C., Vattikuti, S., Purcell, S. M., and Lee, J. J. (2015). Second-generation PLINK: rising to the challenge of larger and richer datasets. *GigaScience*, *4*(1), 7. https://doi.org/10.1186/s13742-015-0047-8

Illumina. (2006). *Technical note. "TOP/BOT" Strand and "A/B" Allele*. Illumina Inc. https://www.illumina.com/documents/products/technotes/technote_topbot.pdf

Interbull Centre. (2025a). *GenoEx-International Genotype Exchange platform for Animal Breeding*. Interbull Centre-Department of Animal Biosciences, Swedish University of Agricultural Sciences. https://genoex.org/ [Accessed date 2025/09/15]

Interbull Centre. (2025b). *Interbeef guidelines* [Wiki]. https://wiki.interbull.org/public/beef_guidelines

Interbull Centre. (2025c). *PREPdb-Performance Recording, Evaluation and Publication database*. Interbull Centre, Department of Animal Biosciences-Swedish University of Agricultural Sciences. https://prep.interbull.org/ [Accessed date 2025/09/15]

Legarra, A., Christensen, O. F., Aguilar, I., and Misztal, I. (2014). Single Step, a general approach for genomic selection. *Livestock Science*, *166*, 54–65. https://doi.org/10.1016/j.livsci.2014.04.029

Macedo, F. (2023). International beef evaluation for Carcass traits. *Interbull Bulletin*, *59*, 197-201.

Patterson, N., Price, A. L., and Reich, D. (2006). Population structure and eigenanalysis. *PLoS Genetics*, *2*(12), 2074–2093. https://doi.org/10.1371/journal.pgen.0020190

Phocas, F., Donoghue, K., and Graser, H. U. (2005). Investigation of three strategies for an international genetic evaluation of beef cattle weaning weight. *Genetics Selection Evolution*, *37*(4), 361–380. https://doi.org/10.1051/gse:2005006

Ryan, C. V., Pabiou, T., Purfield, D. C., Conroy, S., Kirwan, S. F., Crowley, J. J., Murphy, C. P., and Evans, R. D. (2022). Phenotypic relationship and repeatability of methane emissions and performance traits in beef cattle using a GreenFeed system. *Journal of Animal Science*, *100*(12), skac349. https://doi.org/10.1093/jas/skac349

Venot, E., Pabiou, T., Hjerpe, E., Nilforooshan, M. A., Launay, A., and Wickham, B. (2014). Benefits of Interbeef international genetic evaluations for weaning weight. *10th World Congress of Genetics Applied to Livestock Production Benefits*, *August*, 17–22.

Vesela, Z., Brzakova, M., Svitakova, A., Vostry, L., and Bucek, P. (2019). Interbeef international genetic evaluation for calving traits. *ICAR Technical Series*, 49–54. https://www.icar.org/Documents/technical_series/ICAR-Technical-Series-no-24-Prague/Vesela.pdf

Zimin, A. V., Delcher, A. L., Florea, L., Kelley, D. R., Schatz, M. C., Puiu, D., Hanrahan, F., Pertea, G., Van Tassell, C. P., Sonstegard, T. S., Marçais, G., Roberts, M., Subramanian, P., Yorke, J. A., and Salzberg, S. L. (2009). A whole-genome assembly of the domestic cow, Bos taurus. *Genome Biology*, *10*(4), R42. https://doi.org/10.1186/gb-2009-10-4-r42