European Bovine Evaluation – building joint genetic evaluations across Europe

J. Heise[1], Z. Liu[1], I. Croué[1,2], A. Michenet[1,2], R. Reents[1,3], J. Baltissen[1,4], A. Levring[1,5], H. Splittorff[1,8], L. Schibler[1,9], and J.-Y. Dréau[1,10]

[1] European Bovine Evaluation F.M.B.A., Agro Food Park 12, 8200 Aarhus N, Denmark

[2]Eliance, 149 rue de Bercy, 75012 Paris, France

[3] Vereinigte Informationssysteme Tierhaltung w.V. (vit), Heinrich-Schröder-Weg 1, 27283 Verden, Germany

[4] Rinder-Union West eG, Schiffahrter Damm 235a, 48147 Münster, Germany

[5] Landbrug & Fødevarer F.m.b.A, Vesterbrogade 4A, 4. sal, 1620 København V, Denmark

[6] Växa Sverige ek. för, Box 288, 751 05 Uppsala, Sweden

[7] Faba co-op, P.O. Box 40, FIN-01301 Vantaa, Finland

[8] NAV – Nordic Cattle Genetic Evaluation, Agro Food Park 15, 8200 Aarhus N, Denmark

[9] Gènes Diffusion, 3595 Route de Tournai, 59500 Douai, France

[10] Synetics, 4 Rue Eric Tabarly, 35530 Noyal-sur-Vilaine, France

Corresponding author: Johannes Heise (johannes.heise@ebe-centre.eu)

Abstract

In 2025, Partners from France, Germany and the Nordics (Denmark, Finland, Sweden) founded European Bovine Evaluation FMBA (EBE) to develop joint single-step genetic evaluations for Holsteins by 2028. These evaluations cover 9 countries across Europe, i.e., additional to the Partners' countries: Austria, Belgium (Walloon region), Luxembourg, and Norway. Number of offspring of bulls in the different countries that participate in Interbull MACE are routinely reported by the countries. A comparison of these figures between the EBE countries on the one side and the currently largest Holstein population under joint routine genetic evaluations worldwide on the other side shows that the Holstein population under joint routine genetic evaluations at EBE will become one of the largest worldwide as soon as routine evaluations are established at EBE.

Key words: Holstein, European collaboration, single-step, genetic evaluation, joint evaluation, large populations

Introduction

With the establishment of European Bovine Evaluation FMBA (EBE) in 2025, Partners from France, Germany and the Nordics (Denmark, Finland, Sweden) have joined forces to develop joint routine single-step genetic evaluations covering cattle populations from 9 European countries: in addition to the Partners' own countries, the collaboration covers populations from Austria, Luxembourg, Norway, and Wallonia (Belgium). The development of joint single-step genetic evaluations will serve three main goals:

1) make GEBVs for individual traits directly comparable across countries,
2) increase the reliabilities of GEBVs
3) leverage cross-country synergies to deliver better genetic evaluations more efficiently, including the development of genetic evaluations for new traits.

As its first mission until 2028, EBE will develop joint single-step evaluations for the Interbull traits, additional health traits (claw health, metabolic health, reproductive disorders), and young stock survival for Holsteins. After this, joint single-step evaluations will follow for other breeds, e.g.,

Jersey, Red Dairy Cattle, Normande, as well as for other traits that are not covered by the first mission. Furthermore, EBE will be open to new Partners.

In the following paper, we present the expected size of the Holstein population under genetic evaluation at EBE for different Interbull traits and compare it to the currently largest Holstein population under genetic evaluation worldwide.

Materials and Methods

EBE will merge phenotypic, genomic, and pedigree data of Holsteins from currently four different national genetic evaluation centres (NGEC) to develop and conduct joint single-step genetic evaluations. Currently, these NGECs provide data from Holsteins to Interbull MACE (Interbull 2026; Schaeffer, 1994) independently: DEU (Germany, Austria and Luxembourg; VIT, 2026), FRA (France; GenEval, 2026), DFS (Denmark, Finland, Sweden, Norway; NAV, 2026), and BEL (Walloon region of Belgium; Vanderick et al. 2025). Due to the early stage of development of genetic evaluations at EBE, analyses from joint data were not available at the time of this study. Therefore, we used information provided to Interbull by the different countries to give an indication of the future Holstein population size under joint genetic evaluation at EBE once those are established.

For Holstein bulls, we analysed number of offspring reported by the different countries in the Interbull bull evaluations (MACE) as of April 2026. Within birth year classes of bulls, we compared number of offspring reported by DEU, DFS, FRA (incl. BEL) with the USA and EBE, i.e., the sum of DEU, DFS, FRA (incl. BEL). This comparison was conducted for all 39 Interbull traits evaluated in Interbull MACE separately. In this paper, we only present numbers for protein yield and calving ease direct.

Results & Discussion

Comparison of number of offspring for protein yield across countries

Figure 1 shows the total number of offspring with phenotypes of Holstein bulls for the trait protein yield (PRO) in comparison for EBE, USA, DEU, FRA and DFS. EBE countries have reported higher numbers of offspring for most historic sire birth years until 2018, e.g., for sires born in 2012, EBE countries have reported

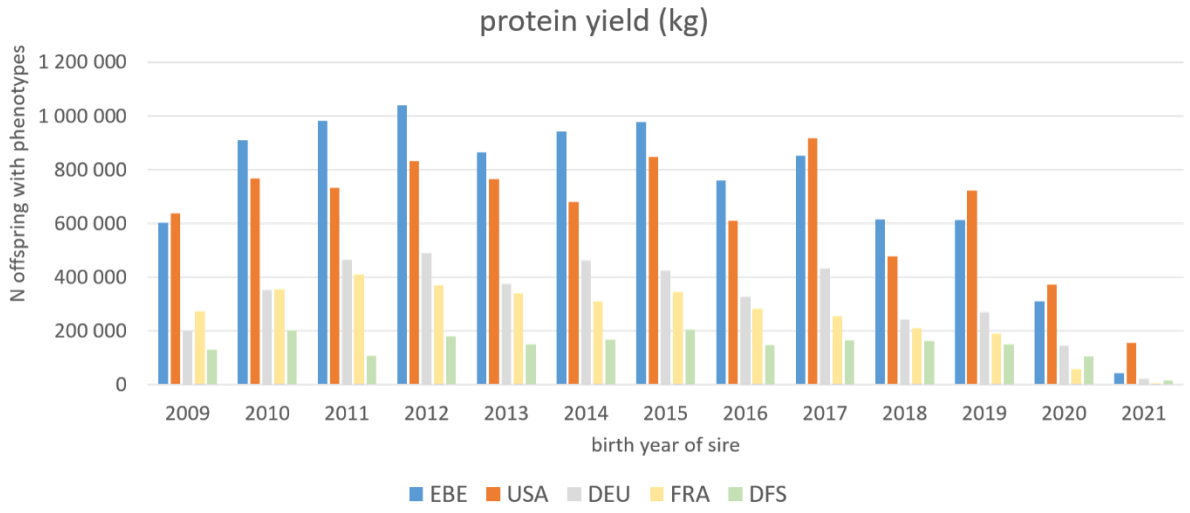


Figure 1. Total number of offspring with phenotype for protein yield of all Holstein bulls included in Interbull MACE as of April 2026 for EBE (sum of DEU, DFS, FRA, BEL), USA, DEU, FRA (incl. BEL), DFS.

1,039,877 offspring with phenotypes in total, while the USA have reported 832,473 offspring with phenotypes. For the most recent sire birth years (2019 to 2021), a slightly higher number of offspring was reported by the USA compared to the EBE countries. Similar patterns were also found for the trait groups somatic cell scores, female fertility and longevity (results not shown).

Comparison of calf counts for direct genetic effect of calving ease between countries

In contrast to most dairy cattle traits, where phenotypes are recorded on cows, for calving ease direct (DCE) phenotypes of calves contribute to estimated breeding values. Figure 2 therefore shows calf counts by birth years of their sires for EBE, USA, DEU, FRA and DFS for the trait DCE. EBE countries have reported substantially larger numbers of calves with phenotypes than USA, e.g., for sire birth year 2012 (year with the highest number of calves), the total number of calves of Holstein bulls reported by the EBE countries is 2,109,781, while only 1,311,709 calves are reported by the USA, which is 62% amount of calves reported by the EBE countries.

Similarly, a much lower number of calves was also observed for stillbirth direct in the USA population than in the EBE population (results not shown).

Interpretation of number of offspring of bulls reported by different countries

NGECs only send EBVs of bulls that have offspring in at least 10 herds in their national evaluation to Interbull MACE, but national evaluations also include sires with offspring in less herds, and often also include natural service sires. Therefore, the actual number of animals with phenotypes included in the national evaluations are usually somewhat higher than the total number of offspring with phenotypes reported for bulls that participate in MACE at Interbull. Although the actual gap might differ between countries due to differences in sire usage patterns across herds and proportions of natural mating, it remains small compared to the size of the population. Therefore, the number of offspring of bulls participating in Interbull MACE which are reported by the different countries can serve as a good indicator for the actual population size.

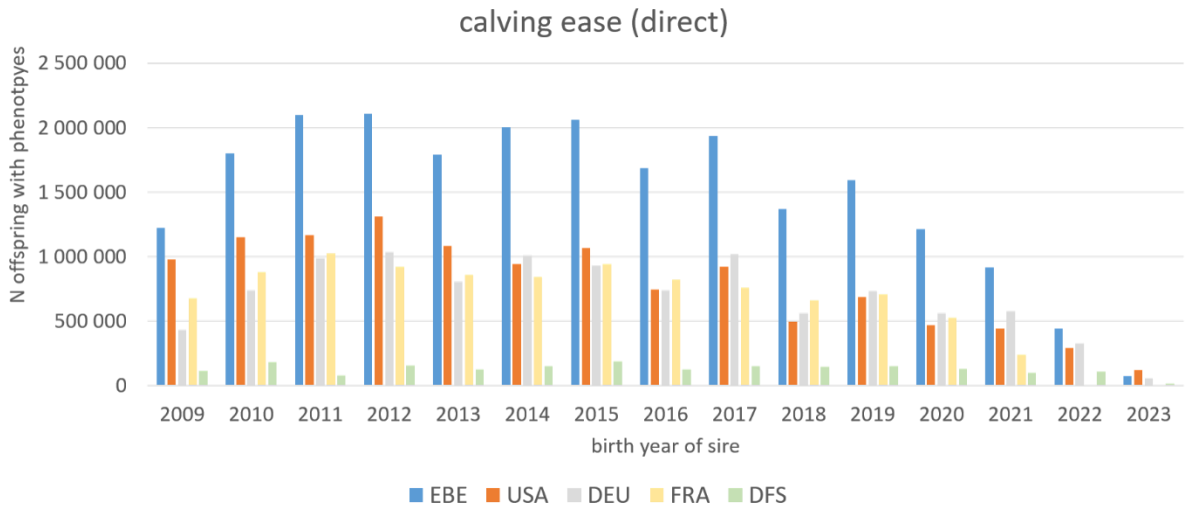


Figure 2. Total number of offspring with calving ease (direct) phenotype of all Holstein bulls included in Interbull MACE as of April 2026 for EBE (sum of DEU, DFS, FRA, BEL), USA, DEU, FRA (incl. BEL), DFS.

Conclusions

With EBE, the EBE Partners aim to set the European Standard for genetic evaluations of cattle. Our analysis shows that the expected size of the Holstein population under joint routine single-step genetic evaluations at EBE will be mostly comparable to the currently largest Holstein population under joint genetic evaluations worldwide. In addition, EBE builds upon a long history of high-quality data recording in the European countries, which includes also well-established data recording for many relatively new traits. Equipped with these core foundations, EBE has the potential to match and even exceed its aim to set the European Standard for genetic evaluations of cattle.

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