



Guidelines on Including External MACE Proofs in National Genetic Evaluations

Background

Since 1995, Interbull has conducted international genetic evaluations for dairy cattle using the MACE approach. MACE breeding values and their associated reliabilities provide valuable information that national evaluation centers can leverage to enhance their domestic evaluations.

At the 2025 Interbull Open Meeting in Louisville, USA, discussions highlighted the growing adoption of single-step models and various approaches to incorporating external data (i.e. MACE proofs) into national genetic evaluations. Following these discussions, the ITC recommended developing standardized guidelines to harmonize the use of external MACE breeding values across national genetic evaluation systems. The Working Group (WG) identified three main approaches through which external proofs can be integrated: (1) as prior information within a Bayesian framework; (2) via the pseudo-records approach; and (3) via the correlated-trait approach. The specific implementation requirements of each method will be described in the guidelines.

Therefore, the objectives of the WG are to review and summarise existing methods for incorporating external and MACE proofs into national genetic evaluations; to evaluate the strengths, limitations, and practical applicability of each approach; and to compile an inventory that distinguishes between theoretical possibilities and practical feasibility across member countries. The WG will also formulate recommendations on documentation standards, reporting requirements, and potential new data outputs to the Interbull Steering Committee, with the aim of supporting effective data integration.

The WG on Guidelines for Including External/MACE Proofs in National Evaluations was formally established by the Interbull Steering Committee on 1 October 2025. A kick-off online meeting was held on 6 November 2025 to review the Terms of Reference (ToR), which were formally approved at the Interbull ITC and SC meeting on 27 November 2025. The WG convenes bi-monthly online meetings to monitor progress and discuss ongoing tasks.

On 8 April 2026, an online meeting was held to discuss the survey instrument. The WG agreed to first circulate the draft questionnaire among its own members before





distributing it more broadly to other countries and member organizations. To date, four WG member institutions have submitted completed responses.

An in-person session is scheduled for June 2026 at the Interbull Meeting in Verona to review progress.

Work Performed and Achievements

Investigations of the PREPdb and GenoForm databases revealed that existing records lack sufficient methodological detail to fully characterize the approaches to integrating external information that is currently in use across member institutions. Accordingly, the WG decided to develop a structured survey questionnaire to collect standardized information on current practices, covering both methodological approaches and their practical implementation across trait groups. The questionnaire was first circulated among WG members prior to broader distribution to all national evaluation centers. The responses received to date are summarized below.

Four WG members submitted completed survey responses: NAV (DFS — Finland, Denmark, Sweden), Qualitas AG (Switzerland), INIA (Uruguay), and CDCB (USA). All respondents confirmed no objections to the publication of their responses.

Of the four respondents, only Qualitas AG (Switzerland) reported using MACE proofs within a traditional pedigree-BLUP evaluation framework, and exclusively for production traits.

All four institutions incorporate MACE proofs into their genomic evaluation systems. Qualitas AG and CDCB cover all seven trait groups; INIA incorporates MACE proofs for production, longevity, fertility, and udder health; and NAV/DFS currently covers production traits only.

All four institutions use the pseudo-records approach as their primary method for incorporating MACE proofs, applying it within a single-step model framework. Qualitas AG additionally applies a weighted-average combination of MACE and direct genomic EBVs in a multi-step approach to derive a genomically optimized breeding value.

Results and Impact

The survey results confirm that the pseudo-records approach, with MACE reliabilities converted to equivalent record contributions (ERCs) via the reverse reliability method, is the dominant methodology among responding institutions. All respondents apply an explicit double-counting correction, using either the Pitkänen et al. (2020) or the Bonifazi





et al. (2023) approach. Eligibility criteria for the inclusion of MACE proofs, however, vary considerably across institutions, reflecting the current absence of a common standard.

The survey also revealed that, with the exception of Qualitas AG, all responding institutions operate exclusively within a genomic single-step framework. No institution reported using the correlated-trait or Bayesian prior-information approaches.

The WG plans to: (i) expand the survey to additional Interbull member organisations; (ii) conduct a systematic literature review on methods for incorporating external information into genetic and genomic evaluations; and (iii) develop draft guidelines based on responses from national genetic evaluation centres, for discussion at the next ITC/SC meeting.

References

Pitkänen, T. J., et al. "Integration of MACE breeding values into domestic multi-trait test-day model evaluations." *Proceedings of the 71st Annual Meeting of the European Federation of Animal Science*. Vol. 31. 2020.

Bonifazi, Renzo, et al. "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 (2023): 41.

