Genomic Validation of National Systems

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Background information

Traditional evaluations: National evaluation centers began testing their estimated breeding values several decades ago to determine optimum statistical methods and to convince their breeders that the chosen methods work properly. In 1998, validation of traditional EBVs became more formal when 3 tests of genetic trend were required by Interbull. These tests measure only trend bias and not the accuracy of EBVs. Each country must still remember to check correlations, reliabilities, other biases, and properties of cow EBVs when choosing optimal methods.

Genomic Evaluations: Genomic EBVs for young bulls (and heifers) are now a major focus of genomic selection. Removal of bias is important because traditional parent averages for elite young stock often were inflated due to over-evaluated dams. Statistical methods and data sets used to compute genomic EBVs are evolving rapidly, and breeders have little experience with calculations before they are revised or new data introduced. Tests for genomic evaluations help ensure that optimal methods are chosen and that breeders can be confident that the predictions are accurate.

Objectives for this discussion group

1) Validation methods should be convenient, convincing, and helpful in choosing an accurate model. The current validation method of Mantysaari *et al.* (2010) detects problems with scaling but not necessarily accuracy or bias.

2) One goal of validation is to ensure that consistent data is input into genomic multi-trait across country evaluation (GMACE). Secondly, validation is used as a trade barrier by the EU. Embryos, cows, heifers, and live young bulls can be marketed internationally using parent averages or EBVs, but if a country's GEBV validation for protein is not within tolerance, semen from their genomic tested young bulls is banned from the EU. Interbull now has an official role in setting the EU standards. Most other countries allow open importation of young bull semen.

Questions for the discussion group:

1) What experiences have evaluation centers had with the current test?

2) Are the expected regressions and adjustments for selection well understood?

3) How can we validate traits introduced very recently or test inclusion of cows in the reference population if most of the genotypes are from young animals?

4) Should the validation model include only a regression and no intercept so that a single parameter captures both the bias and problems with slope?

5) For countries that share reference bulls, should the validation bulls include only the domestic or also foreign bulls to improve power of test?

6) What other tests or demonstrations could help breeders to understand the properties of GEBVs?

Answers from the discussion group:

1) Use of a 4-year data cut-off in the current test is not optimum for new traits or small populations. Also, if genotyped cows are included in the reference population, very few may have records > 4 years ago. Different cut-off years may be needed for different traits or

populations, and more guidance may be needed on how best to choose a balance between sufficient reference and test animals.

2) The expected regressions account for selection only within test bulls but not for pre-selection from the training population. Countries use different adjustments to convert observed R^2 into published reliability, and this makes reliability comparisons across countries difficult.

3) Previous studies have detected bias in EBVs of elite cows, and currently only US includes cows in the reference group after pre-adjusting for bias. Independent predictions could be computed (such as cows-only vs. bulls-only) to check if different data sources are consistent.

4) Inclusion of both a regression and intercept is recommended, however a problem in just the regression may also cause the intercept to differ from 0. Interbull validation currently focuses all attention on the regression, however practical breeders may also be concerned with intercepts because these affect rankings of young vs. old bulls. Regressions greater than expected were viewed as not being a reason for rejection because in this case the GEBVs deliver more than advertised, leading to breeders being pleasantly surprised rather than disappointed.

5) Use of foreign validation bulls to improve power of test sounds appealing, but three main problems can decrease their usefulness. Parent averages on domestic scale from 4 years ago probably are sub-optimal, second-country bulls may be highly selected, and their proofs potentially contain some biases. Thus, validation should include only domestic bulls if sufficient numbers are available, however, validation including foreign bulls is better than no validation.

6) Extension and communication to the industry is a major opportunity. Current validation results are too science based to be easily understood by breeders. Validation studies include fewer reference bulls than routine evaluations, and the extrapolation process may not be appreciated. Terminology may also need to be more precise. An animal may have a domestic PA computed from traditional EBV of parents, another PA that includes MACE of sire and/or converted EBV of foreign dam, another PA computed from GEBVs of parents, and then its own GEBV that may be labelled differently than a GEBV that includes own records or progeny records. With GMACE, even more terms may be needed to keep track of GEBVs from national vs. foreign sources.

Expected outcomes

Recommendations:

1) Validation tests should be useful to other researchers in documenting the properties of evaluations.

2) Validations, documentation, and educational materials should also be useful to breeders and breeding companies in purchasing decisions. National evaluation centers need to build more confidence by improving and refining the whole system of genomic evaluation.

3) Ongoing monitoring will be needed for 2-3 years after implementing official genomic evaluations and after changing models or input data to verify that calculations work as intended. After each evaluation or at least each year, predictions from the initial GEBV should be compared to PA to demonstrate how effective each is in predicting new data of new bulls. Such comparisons can use simple means of selected bulls instead of the parametric tests used in model selection and validation.

Reference

Mäntysaari, E., Liu, Z. & VanRaden, P.M. 2010. Interbull validation test for genomic evaluations. *Interbull Bulletin 41*, 17-21.