

AGBU's Approach to Across-Country Genetic Evaluation for Beef Cattle

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Introduction

Increased transfer of genetic material between countries, along with the development of better models and increased computing power, has made the implementation of across-country beef cattle genetic evaluations more feasible. The spread of genetic material across the globe has increased genetic ties between many countries, and elevated the interest of beef producers throughout the world in genetically evaluating seedstock on an international basis. The production of genetic values on a multi-country basis provides improved marketing opportunities for semen, as well as increasing the accuracy of evaluation due to the extra performance and pedigree information that is made available.

Implementation of across-country genetic evaluations is an evolving process in the beef industry. Initial applications were limited to combining data from countries in close geographic proximity with models limiting traits to be the same in all countries. Early feasibility studies indicated homogeneous genetic parameters in Canada and USA (Johnston, 1992) and Australia and New Zealand (Meyer, 1995) and little evidence of re-ranking of animals. This led to the development of the current combined North American and Trans-Tasman genetic evaluations where data from the different countries are merged to form one dataset for all traits with a single set of variance components.

In recent years several research studies have investigated the possibility of widening the scope of beef across-country genetic evaluations. Little re-ranking of animals was observed for early growth traits in Hereford cattle across North and South America (Lee and Bertrand, 2001), Charolais cattle in Australia, New Zealand and North America (Donoghue and Bertrand, 2004) and Limousin cattle in France and Australia (Phocas *et al.*, 2005) and France, Luxembourg and Ireland (Vernot *et al.*, 2006). However,

evidence of re-ranking was observed for later growth traits for Hereford cattle in intensive (North America) vs. more extensive (South America) production systems (Lee and Bertrand, 2001). Renand *et al.* (2003) found evidence of sire re-ranking for weaning weight for the Charolais breed in France, Ireland and the UK, leading to the development of an international genetic evaluation for that breed allowing genetic correlations to differ from unity. Even though many studies have found little evidence of animal re-ranking, heterogeneity of parameters was indicated in the majority of these studies, implying that assuming the same trait across countries with homogeneous genetic parameters was not the best approach.

The dairy industry has considerable experience in developing and running across-country genetic evaluations, with the current approach for international comparisons of sires being a multiple trait across country evaluation (MACE) (Schaeffer, 1994) using de-regressed proofs. Phocas *et al.* (2005) compared alternative strategies for an across-country beef genetic evaluation and concluded that an animal model on raw performance data with non-unity genetic correlations which allowed heterogeneous genetic and residual variances was superior to the MACE approach. Direct and maternal genetic correlations were underestimated by the MACE approach, most likely because MACE was restricted to a sire model in the study, thus not accounting for information in the dam proofs and the pedigree. In addition, MACE was sensitive to the lack of connectedness across countries in beef data in this study, compared to the connectedness present in dairy populations. Finally, many beef traits are commonly modelled with a maternal genetic effect included, as calves stay with their mothers until weaning (~4-9 months of age). Although the theory has been proposed (Schaeffer, 2001) to run a single MACE with direct and maternal effects, this has not yet been applied in dairy data.

Another factor impacting the priority that international genetic evaluation has been given in the Australian beef industry is related to timing of sire selection decisions, and the amount of information available when making these decisions. While the evaluation of across-country sires is important to seedstock producers, the evaluation of young domestic bulls is the most important issue for commercial beef producers, who will make selection decisions on bulls that are approximately two years of age. Some of the bigger seedstock herds in Australia are selling more than 500 performance recorded young bulls with estimated breeding values (EBVs). These EBVs are required in a timely manner; sometimes within weeks of data being recorded (eg live ultrasound scanning for carcass traits). For this reason, genetic evaluations need to occur at specific times throughout the year in Australia, usually prior to Autumn and Spring bull sales, which do not necessarily coincide with bull selling seasons in other countries. Timing and frequency of beef cattle global genetic evaluations is a logistical issue that would have to be addressed prior to implementation.

This paper summarises the research and development of across-country genetic evaluations at the Animal Genetics and Breeding Unit (AGBU), based on the well described BREEDPLAN program (Graser *et al.*, 2005), ranging from the simple Trans-Tasman genetic evaluations to the current feasibility study for a multi-trait, multi-country genetic evaluation for the Hereford and Shorthorn breeds.

Trans-Tasman Genetic Evaluations

Initial studies into the feasibility of a Trans-Tasman genetic evaluation were undertaken in the Angus breed (Meyer, 1995; Meyer and Garrick 1995). In these studies, no indication of genotype by country interactions was found, and genetic parameters were very similar for growth traits in Australia and New Zealand. These results allowed for the implementation of a simple across-country genetic evaluation, where data from both countries was merged into a single dataset. However, the implemented adjustment factors for age of calf and age of dam differ between the two countries. There are

currently BREEDPLAN Trans-Tasman genetic evaluations for 9 beef breeds in Australia and New Zealand (Angus, Charolais, Hereford, Limousin, Murray Grey, Salers, Shorthorn, Simmental and South Devon). The development of the across-country linkage files was the responsibility of the breed societies together with the Agricultural Business Research Institute (ABRI), which manages the data and is responsible for the commercial evaluation and web presentation of EBVs (<http://breedplan.une.edu.au>).

In recent years, the evaluation of overseas animals in Trans-Tasman analyses has been improved by the importation of proofs (eg expected progeny differences) from the animal's country of origin. In this case, performance information from other countries are contributing to the Trans-Tasman genetic evaluations. The natural progression from this is a global genetic evaluation, where performance information from Australia and New Zealand will contribute to evaluation of animals in other countries, and vice versa.

Pan American Hereford Genetic Evaluation

The development of the Pan American Hereford Genetic Evaluation was requested by the participating Hereford associations in Argentina, Canada, Uruguay and the USA. For this international genetic evaluation traits were assumed to be the same across countries. However, software was developed that allowed for different heritabilities by including heterogeneous residual variances across countries. A test run was conducted in early 2007 to check the feasibility with the large pedigree (~5 million animals) and data (~8 million trait records) files involved. The participating breed associations are currently in negotiation regarding the possibility of a regular commercial Pan American Hereford genetic evaluation. To be able to do this analysis, phenotypic trait records had to be transformed to the same metric scale, and EBVs (EPDs) subsequently transformed back to account for the differences between North and South America.

Global Genetic Evaluations

Several breeds have expressed interest in recent years in developing a global genetic evaluation. To facilitate this, the Hereford breed established a genetic linkage project to generate genetic connections across the key Hereford breeding countries (Donoghue, 2004). This led to a study investigating the feasibility of a global

The study by Phocas *et al.* (2005) recommended a multi-trait multi-country approach for international beef genetic evaluations. This approach requires knowledge of genetic correlations across countries. While variance component estimation is the preferred method for estimating these genetic correlations, computational demands limit the ability to apply this approach for large global populations, such as the Hereford breed. An alternative is the correlation of EBVs produced from within-country evaluations for common sires. The feasibility of this approach was tested by AGBU in a small data set. Results indicated that the alternative strategy (correlating within-country EBVs for common sires) could be useful when sufficient genetic links or connections exist, but was unreliable when connectedness was at low levels.

Software has now been developed and tested on a multi-trait, multi-country global genetic evaluation on a small data set (~1 million animals and ~328,000 trait records for 5 traits from 4 countries). In this analysis, data files from the four countries were merged and a single pedigree file was created, with across-country animals identified. While this software included the capability to fit country-specific adjustment factors and fixed effects, participating countries were requested to provide pre-adjusted phenotypes and identified management groups for their data. Within-country genetic parameters were those currently used in national genetic evaluations, while across-country genetic correlations were estimated prior to the test run. We are now working on the correlations for the Hereford dataset of 10 countries from five regions of the globe (North and South America, South Africa, Europe and Australia and New Zealand), and the software is ready to be extended to this larger data set.

Conclusions

It is possible, computationally, to implement a multi-trait multi-country beef cattle genetic evaluation in a small data set. The correlation of within-country EBVs for common sires is an acceptable alternative to estimation of variance components across countries if sufficient genetic connections exist. However, further research is needed for situations when low levels of connectedness exist between countries. From a logistical point of view, the timing of global beef genetic evaluations needs careful planning to fit all countries and their young bull selling seasons.

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