

BREEDPLAN represents the most widely used genetic evaluation service for beef cattle internationally. While ABRI has been conducting smaller scale multi-country BREEDPLAN evaluations for over 20 years (e.g. Australia and New Zealand; South Africa and Namibia) and a number of larger scale multi-country evaluations for the last 10 years, the changing commercial context of beef cattle genetic evaluation means we have now moved towards significantly larger and more complex evaluations that combine multiple sources of pedigree, phenotypic and genomic information. Two primary initiatives have been undertaken. The first involves progression towards International evaluations, working with client countries of ABRI where performance (and genomic) data is recorded on the same breed and for which there is some degree of genetic linkage between the respective populations. The second initiative involves multi-breed evaluations, using intentionally-designed multi-breed populations that allow the wider population of component breeds to be combined for genetic evaluation within the one analysis. To date, ABRI has completed a number of International test evaluations for each of the Brahman and Hereford breeds. Each evaluation represents a multi-country, multi-trait model using Single-Step methods to integrate available genomic data. These models include a diverse range of growth, fertility and carcass quality traits within the one analysis, plus separate analyses of docility (Brahman) and calving ease (Hereford) data. Multi-breed evaluations are also being conducted for the Brahman, Santa Gertrudis and Droughtmaster breeds in Australia, with a goal towards combining all three within the one analysis.

Keywords: multi-country, multi-breed, genetic evaluation, beef cattle, BREEDPLAN

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Interbeef international genetic evaluation for calving traits

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Since 2007, Interbull Centre has developed with help of ICBF (Ireland) and INRA (France) the various tools to run Interbeef joint genetic evaluation of beef cattle. The first official run was performed in 2014 on Charolais (CHA) and Limousine (LIM) weaning weight. The second group of traits of interest were calving traits (calving ease - CAE and birth weight - BWT). The Czech Republic (Institute of Animal Science) is responsible for estimation of genetic correlations between countries and for development of international genetic evaluation for these traits. The first official routine run for calving traits was performed in 2018 for CHA, LIM and Beef Simmental (BSM). The model chosen for international genetic evaluation is an animal multiple trait model based on raw data and considering each country as a separated trait. The both calving traits (CAE and BWT) are evaluated jointly as correlated traits in multiple trait model as well. Nine countries are currently involved in international genetic evaluation for calving traits: i) for all breeds - Czech Republic, Denmark, Finland, Ireland, Sweden, ii) for LIM and CHA - France, iii) for CHA only - South African Republic, iv) for LIM only - United Kingdom and v) for BSM only - Germany. Across-country genetic correlations were estimated by two series of 2 by 2 country analysis successively: 1. Animal model with direct genetic effect (DIR) and maternal permanent environmental effect (MPE). 2 Animal model for DIR and maternal genetic effect with MPE. The resulting matrices were banded in order to make them positive definite. Average direct genetic correlation for BWT between countries were 0.7 (CHA), 0.79 (LIM), 0.84 (BSM) and for CAE 0.67 (CHA), 0.70 (LIM), 0.45 (BSM). Average maternal genetic correlation for BWT between countries were 0.47 (CHA), 0.45 (LIM), 0.49 (BSM) and for CAE 0.58 (CHA), 0.53 (LIM), 0.79 (BSM).

Keywords: beef cattle, Interbeef, calving traits, beef cattle, genetic correlation

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Optimizing mate selection: A genetic algorithms approach

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The Brazilian Association of Hereford and Braford provides to breeders a genetic evaluation and breeding program called PampaPlus. For selection, this program uses a Genetic Quality Index (GQI), which is calculated from weighted Expected Progeny Differences (EPD) for production traits. The choice of mating pairs is fundamental for the generation of the best progeny and consequent maximization of the average herd GQI. However, the number of possible combinations, defined by the product of the number of cows by times the number of bulls, and of genetic traits to be analyzed, makes the search for the best combinations of mating a difficult problem to be treated computationally in polynomial time, requiring a heuristic strategy for its resolution. This work presents an approach, based on genetic algorithm heuristics, which after the selection of bulls and cows belonging to a mating group, recommends the best combinations of mating to maximize the GQI, taking into account both: directional values of expected differences of progeny and penalizations on mating restrictions, such as inbreeding and poor expected performance on important traits. The data used to perform simulations were obtained from the Brazilian Association of Hereford and Braford breeders. Fourteen traits were available to be used in the composition of the breeding objectives: birth weight, weaning weight, weaning maternal weight, total maternal weight, post-weaning weight, post-weaning weight gain, cow weaning weight, scrotal circumference, musculature, body height, body structure, cow body condition score at weaning, navel size, and eye pigmentation. Moreover, the breeder can define a minimum and/or maximum use of each bull, for the mating period, in order to search for the best combinations of mating. The

genetic algorithm takes into account a breeder-defined inbreeding constraint, which restricts incompatible matings. The processing time of the genetic algorithm varies according to the number of cows and bulls used in the simulation. For an experiment containing 148 cows and 17 bulls, typical average amounts cattle owned by breeders belonging to the association, the average time was 49 seconds on an i7 processor with 8gb RAM, and average GQI was improved from 4,63 to 11,25, representing an improvement of 140%. Among valid matings according to breeder objectives, solutions found by our approach typically reach a GQI maximization, considering the average of initial and final values, with improvement exceeding 100%. Analyses of experiments show a satisfactory behavior of the genetic algorithm, since obtained results showed that it favors the choice of animals with the highest EPD values combination based on the weights determined by the breeding goal, while complying with the defined maximum and/or minimum use of the bulls and inbreeding restriction for mating recommendations.

Keywords: beef cattle, compensatory mating, evolutionary algorithm

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Data collection through IT-intensive phenotyping in the Hungarian Grey Cattle

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The optometric measurement of body parameters in the Hungarian Grey Cattle species started in 2001. Then – using video cameras – we have created a computer-based optometric system, which was also able to measure moving animals.

Now the system is capable of managing images coming from several video cameras which record the image of the animal from different angles [from the side, above, and front]. With the help of standard bar images defining the pixel/m ratio it is possible to perform measurements on the chosen still images.

With the method of geometric morphometrics we can describe the changes of the animals' bodies by using non-linear body parameters, concentrating on shapes. This method can also be used for performing more complex measurement tasks, such as the mathematical representation and comparison of the stages of development and the proportions of different body parts.

In the case of measurements performed on whole populations, as well as in the case of identifying different conformation types, the fast and simple VATEM-Video Aided Body Measurement Method] was a great help. For example, with the help of the archived measurement frames it was even possible to show the population-scale body parameter changes occurred during a period of 15 years, caused by the changes of the effective breeding goal and selection methods.

Such a population-scale phenotyping [4K video recordings, recording the point clouds from 3D sensors] provides a cost-effective solution which, if combined with metasyntesis, may also be helpful in the analysis and interpretation of a continuously increasing amount of data.

Our case study consists of a metasyntesis showing the genetics of the Hungarian Grey Cattle's horn colours, using NGS genotyping and phenotyping.

After the phenotyping of the animals recorded during the 2018 VATEM measuring trip we assessed the data of a genotyping performed in 2017. This was the point when we started to examine the inheritance and genetic background of the green, „cardy” [mixed green and white] and white colour types of the horn, through a common metasyntesis also using the data resulting from an earlier genotyping project.

Based on the 840 phenotypes identified with the help of the VATEM images and after processing the data of the breed registry we identified a simple Mendelian inheritance pattern. During the examination of the histological background it was proven that the green colour was not of endogenous origin. The metasyntesis started by examining the loci connected to the production and structural buildup of keratin, and the identified cause was the settlement of symbiotes in the horn. Based on our preliminary results, it seems so that the genes encoding the structure of keratin are responsible for the synthesis of structural variant which is susceptible to be infiltrated by the symbiotes.

With the cost effective method of phenotyping using the optometric method the amount of data obtained can be multiplied. Even in the case of externally kept cattle populations this method may be a safe, fast and cheap way of phenotyping, which can be performed on a large sample.

Keywords: phenotyping, VATEM, horn colour