



Dr David Johnston

David is a quantitative geneticist and Senior Scientist at the Animal Genetics and Breeding Unit (AGBU) where he has been employed for the past 11 years. David is program manager of the beef genetics research and is responsible for overseeing all beef genetics research at AGBU. This involves managing work programs, ensuring project milestones are met, doing research and securing new funding. David is also currently responsible for overall design and maintenance of the Beef CRC II Northern breeding project and will be responsible for much of the genetic analyses from that project.

David's work is mainly in the area of mixed model estimation and prediction for beef cattle traits and the implementation of this research into the national genetic evaluation scheme BREEDPLAN. A major focus of his work has been in the development and implementation of genetic evaluation procedures for several new traits. These have included important developments in the female fertility trait days to calving, mature cow weight, abattoir carcass and meat quality traits, and more recently research into the incorporation of genotypic data into EBVs.

A GLOBAL HEREFORD GENETIC EVALUATION – MAKING IT HAPPEN!

Introduction

Routine production of global estimated breeding values for Hereford cattle (polled and horned) will require considerable effort from seedstock breeders, breed associations, scientists and genetic evaluation providers. The actual requirements will depend on the method chosen to deliver the new values (as outlined in the preceding paper by Graser) however there are some universal features that will be required for any of the methods to be implemented. This paper aims to briefly describe each of these features and outlines their importance in the development of a global evaluation for Hereford and Poll Hereford cattle.

1) Unique animal identification

Permanent and unique animal identification is the most important component of any within country genetic evaluation system and will have increased importance in global analyses. All animals, especially those parents used across populations, must be correctly and uniquely identified such that their progeny are correctly assigned. The correct identification of sire progeny across countries is critical in establishing genetic linkage (see below). Therefore it is imperative that all countries wishing to participate in global evaluations record in their system the original identification number of an overseas animal. To do this effectively and efficiently we propose that an Internet based system is developed to maintain cross reference tables for the identification numbers of animals used in more than one country. The system would need to be available to download into cooperating countries databases and genetic evaluation systems. Setting up this system will require cooperation between breed associations and recording agencies across countries but will greatly reduce the time and errors currently required to match animals.

2) Trait definition

The exact definition of all traits in each country must be examined to determine if they are the same trait across countries. Variables that would be considered include: adjustments that are made for systematic fixed effects, time and method of measurement, covariates and genetic modelling (e.g. partitioning of maternal effects). To combine data across country on a trait into a single analysis (i.e. considering them as the same trait) may simply be done by determining that the definitions are the same but most likely will require research to estimate the genetic similarity of the 2 traits. If the correlation between the 2 traits measured in the different countries is high then they could be combined and analysed as the same trait (after converting the data in the same units of measurement). However, if the correlation is significantly less than one (or has different variances) then they may be analysed as 2 correlated traits.

Table 1 presents the current list of traits evaluated by different countries that may be considered in the initial development of a global Poll/Hereford genetic evaluation. The weight and ultrasound scanning traits in Australia/New Zealand and the US/Canada are taken at similar ages and are likely to be the same trait.

However the abattoir carcass records are expressed on a different basis and in some cases are different measures (e.g. IMF% versus USDA marbling scores). The other point to note is that some countries have their own specific traits (e.g. days to calving in Australia/NZ) and how these are handled in a global analysis will need to be resolved.

Table 1. Traits currently included in Poll/Hereford genetic evaluations of each country

Trait	Australia/New Zealand	US/Canada	South America
Calving ease	yes	yes	
Gestation length	yes		
Birth weight	yes	yes	yes
Weaning weight	yes – 200d	yes – 205 d	yes – 200d
Pre-weaning gain	no		
Yearling weight	yes – 400d	yes – 365 d	yes – 400d
Post-weaning gain	no		
Final weight	yes –600d		yes –600d
Cow weight	yes		
Scan rib fat – heifers/steers	yes	yes	yes
Scan P8 fat – heifers/steers	yes	yes	
Scan EMA – heifers/steers	yes	yes	yes
Scan IMF% - heifers/steers	yes	yes	
Scan rib fat – bulls	yes		
Scan P8 fat – bulls	yes		
Scan EMA – bulls	yes		
Scan IMF% - bulls	yes		
Carcass weight	yes	yes	
Carcass rib fat	yes – wt basis	yes – age basis	
Carcass P8 fat	yes – wt basis	yes – age basis	
Carcass EMA	yes – wt basis	yes – age basis	
Carcass Yield	Yes – % wt basis		
Carcass Marbling	yes – IMF% wt basis	yes – MS age basis	
Scrotal size	yes	yes	yes
Days to calving	Yes – Nat. and AI		
Feed efficiency	Yes – NFI + IGF1		
Selection Indexes	yes		
Temperament	?	?	
Carcass tenderness	?	?	
Structural traits	?	?	
Longevity	?	?	

3) Genetic Linkage across countries

To establish global EBVs, the separate analyses (or breeding values) will need to be combined and their bases aligned. This can only be achieved through genetic links. Linkage occurs when the same animals have breeding values estimated in each country's genetic analysis. Linkage is commonly achieved through AI where a sire has offspring performance recorded in more than one country. It is important that sires are well evaluated in both countries. Commonly in the beef industry young sires or embryos are transferred across countries. Although the animal may have a breeding value estimated in its home country the accuracy is very low because it does not have any performance records (or progeny). Mid-parent values don't contribute to effective linkage.

The WHC linkage project was designed to help strengthen the genetic linkage across countries. The aim was to generate approximately 30 progeny on at least 4 sires from Australia and North America and progeny test them for the range of traits recorded in those countries. This data will be combined with the existing linkage to allow the first steps towards global EBVs. However this data alone will not be enough! The number of sires and progeny is only relatively small and the calves were mostly generated in commercial herds (to get steers) but this means we are unlikely to generate much data for maternal traits. Therefore if global evaluation is truly a desire of world Hereford breeders then the issue of linkage will need to be addressed further. In particular, there is a need to develop further linkage (across all traits) and an effort by participating countries to maintain the linkage over time. I suspect this will require the

drafting of formal arrangements that will ensure the generation of minimum numbers of linkage progeny (similar to the WHC linkage project) by nominated sires across participating countries. Sires will need to have high accuracy EBVs across as many of the traits evaluated and there will be added merit in choosing sires that link other important international beef genetics projects that used Hereford sires (e.g. US MARC GPE, Australian Beef CRC, WH Linkage Project). At the present I see a real need to generate progeny of non-North American progeny in performance recording straightbred seedstock herds in Canada and the US.

4) Genotype x country interactions

Prior to the development of global EBVs it will be important to establish the presence and magnitude of genotype x country (GxC) interaction (i.e. the re-ranking of animals across countries). Several studies have been undertaken in the past decade between countries with similar production systems (see Graser). In general the results showed little evidence of GXC interactions for growth related traits, however few, if any, studied traits such as body composition, fertility, or calving ease. If significant GxC interactions exist across countries then both sources of data can still be used in a global evaluation but the interaction will need to be accommodated in the genetic model. It is also likely that only one of the EBVs will be reported in each country. In this case the value to the home analysis of the outside country's information declines according to the magnitude of the interaction. To accurately estimate GxC effects requires large numbers of sires with progeny in more than 1 country (i.e. good linkage)

5) Operational and reporting issues

Several operational issues will be important when evaluating the methods for a global evaluation. The likely most important variable will be computer requirements and associated data handling and storage issues. Other considerations include: timing of data submittal to coincide with the data collection of the different countries; timing of the evaluation to requirements of countries (e.g. timing of seasonal sales); the basis of expressing global EBVs; models used (including both fixed and random effects)

Conclusions - Likely first step

The first step is for breeders and their associations to establish which countries are likely to participate in the initial development of a global evaluation. Once this is determined then data managers and scientists will need to work on quantifying the data structure between the countries. This will primarily involve matching the identification numbers of across country animals. Some countries have taken the important step of dual recording of overseas registration numbers, however this is likely to need to be expanded. The across country animals can be stored in a linkage file that can be used to quantify the amount of across country linkage. Conversion formulas may be sufficient in the short term but as computer power increases and sharing of data occurs it is likely that MACE or joint analyses will be the preferred method. The linkage developed by WHC linkage project and existing across country sires should be sufficient to develop an across country evaluation now for some countries however it would not be possible for all traits. The cooperating countries would have to decide whether a sub-set of traits would suffice or whether attempts should be made to further develop linkage across additional traits.