



Technical Information Note III/1997

Calculation of Multibreed EBVs

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Introduction

BREEDPLAN Version 4, released in December 1997, has the facility to calculate multibreed or non-breed specific EBVs. These EBVs can be used to compare crossbred and purebred cattle of various breeds and crosses that have been included in the same analysis. This does not mean that from December 1997 all EBVs will be comparable. At present each breed society expresses its EBVs relative to a base which is defined within that breed. However, the ideal long term outcome would be for all breeds and crosses to have EBVs expressed relative to the same base and hence be directly comparable. An accompanying Technical Information Note (TIN II/97) explains the data needed to make valid comparisons across breeds. This note explains how multibreed EBVs will be calculated.

Statistical Model

The model currently used in BREEDPLAN for a trait without a maternal component, such as 600 day weight, is:

$$y = cg + bv + e$$

Where:

y = measured trait (eg 600 day weight)
adjusted for calf age and dam's age

bv = breeding value of the calf for
600 day weight

e = an environmental effect on 600 day
weight

The breeding values of related animals are linked so that information on one animal influences the EBVs of its relatives. The animals at the top of the pedigree, ie those

without known parents, are placed in genetic groups according to when and where (Australia or overseas) they were born. The changes in Version 4 of BREEDPLAN to make comparisons across breed possible are:

- a term for hybrid vigour or heterosis will be included in the model. This term allows for the fact that crossbreds on average perform better than the mean of their parents. Not all crosses get the same benefit from heterosis. For instance, a cross (F2) between two Angus x Hereford (F1) crossbreds receives only half the heterosis of a first cross (F1) Angus x Hereford.
- the animals at the top of the pedigree will be grouped according to breed as well as the year of birth. All animals will be traced back to purebred ancestors. There will be a number of genetic group solutions for each breed represented in the dataset being analysed and these solutions will influence crossbreds descended from that breed.

To illustrate how this will work, consider a Simmental x Hereford bull. His genetic group effect via his pedigrees will be the average of the Hereford and Simmental genetic group effects. His own performance is boosted by hybrid vigour but this will not increase his breeding value because hybrid vigour cannot be passed on to offspring - it must be created anew in each generation.

Using multibreed EBVs

To predict the performance of calves from a particular mating you take half the sire's EBV plus half the dam's EBV as at present and, if the sire and dam are not the same purebreed, add on the effect of hybrid vigour. Therefore, although an Angus and Hereford bull may have the same EBV, the Angus bull will produce heavier calves when mated to Hereford cows and the Hereford bull will produce heavier calves when mated to Angus cows.

Maternal traits

The cow through her milk supply and mothering ability makes a contribution to the 200 day and 400 day weight of her calves. This is recognised in BREEDPLAN by including a maternal effect in the model (ie the 200 day milk EBV). In Version 4 of BREEDPLAN the maternal effects will be grouped according to breed and there will be a maternal heterosis effect if the dam is a crossbred.

Estimating heterosis and genetic group effects

There are two main alternative methods for estimating effects in the statistical model. The effect can be fitted in the BLUP and estimated from the dataset being analysed. Alternatively, an estimate from other data which have already been analysed can be used to pre-adjust the measurements, as is done with age and dam age at present. This second approach is desirable if a more accurate estimate of the effect is available from outside the current data and if it applies to the data currently being analysed.

There have been many experiments carried out around the world to estimate heterosis in crosses between different breeds of cattle. It is likely that these estimates are applicable to Australian conditions. To estimate heterosis for a given cross requires comparisons between both purebreds and both reciprocal crossbreds. It will be rare to have such comparisons within data submitted to BREEDPLAN. Therefore it is proposed to use

estimates of heterosis from the published scientific literature.

There are also many published estimates of breed differences. However, it is uncertain how well these effects apply to Australian conditions. For instance, the sample of Herefords used in a sire breed comparison in USA may be quite different to modern Herefords in Australia. Therefore it is best to estimate the genetic group solutions within BREEDPLAN analyses. However, there will be some breeds that are rarely represented in breed comparisons in data available to BREEDPLAN and so will not receive an accurate estimate of their genetic group. To overcome this problem it may be best to use published estimates from the scientific literature as starting values and to update them as Australian data becomes available.

BREEDPLAN databases

Existing BREEDPLAN databases contain limited information on sire breed comparisons although hopefully this will increase in the future once the opportunity to get EBVs on crossbred cattle exists. The best data on breed differences will come from experiments such as the CRC, South Australian and Victorian/BIA crossbreeding experiments. Unfortunately the older experiments are not useful because the sires they used do not have BREEDPLAN EBVs.

This experimental crossbreeding data will be useful to all breeds because it will provide more accurate estimates of breed differences than could be obtained from any breed society or other database. Therefore a database specifically for the experimental crossbreeding data will be formed. This database will be joined with any database which is being analysed for GROUP BREEDPLAN. For instance, when the Limousin GROUP BREEDPLAN analysis is being carried out the experimental crossbreeding data will be joined to the Limousin Society database. Then, if Angus cattle occur in the Limousin datafile, the genetic group solution for Angus will be based on the Angus offspring in the

Limousin datafile and those in the experimental crossbreeding database.

Introduced animals

BREEDPLAN Version 4 can utilise an EBV or equivalent calculated on data not available to the current analyses. For instance, when a bull from USA has semen sold in Australia he usually has an American EPD based on his records and that of his relatives in USA. This EPD can be converted to the Australian EBV scale and imported into the BREEDPLAN analysis where it acts as a starting point for the bulls EBV. This methodology can also be used to import the Angus EBV of an Angus bull into the Limousin analyses. This means that the information on the genetic merit of a bull is not lost when he is used in another breed.

