PRESENTING *BREEDPLAN* VERSION 4.1

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SUMMARY

New features of the BREEDPLAN Version 4.1 analytical software are described, with emphasis on new methodology for analysing carcase traits. Other include accounting for sire x herd interactions and heterogeneous variances; incorporating overseas breeding values; new genetic grouping strategy; mature cow weight EBV; and the ability to analyse crossbred data and the methodology to produce across breed EBVs when data are available. BREEDPLAN Version 4.1 has been in use in the Australian beef industry since December 1998.

Keywords: Genetic Evaluation, BREEDPLAN

INTRODUCTION

BREEDPLAN Version 4.1 analytical software is the culmination of several years of AGBU research, primarily funded under Meat Research Corporation (now Meat and Livestock Australia) projects. The new version is written in FORTRAN 90. In addition to the features of previous versions, BREEDPLAN V4.1 includes new traits, new methods for analysing and expressing carcase traits, and several new analytical enhancements. BREEDPLAN V4.1 is not breed specific, in fact it has the capacity to simultaneously run several breeds. This paper briefly describes the new features of BREEDPLAN V4.1.

NEW BREEDPLAN VERSION V4.1

Development and testing of BREEDPLAN V4.1 analytical software was recently completed at AGBU. The new features include:

- accounting for sire x herd interactions
- accounting for heterogeneous variances across herds
- incorporation of genetic information from one or more overseas evaluation(s)
- new genetic grouping strategy
- a new carcase trait module - new methods of analysis, new EBVs for retail beef yield percentage (RBY %) and intramuscular fat % (IMF %), fat depth (p8 and rib) and eye muscle area (EMA) on a 300 kg steer carcase basis, and for carcase weight on an age-constant basis
- an EBV for mature cow weight
- methodology for including crossbreds with straightbreds in genetic evaluation, and for deriving across-breed EBVs once suitable data become available

All traits in BREEDPLAN V4.1 are run in a multiple-trait animal model BLUP with direct and maternal effects fitted for traits influenced by maternal effects. The new features are each briefly outlined below, with the new carcase trait module being described in more detail.

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NEW FEATURES OF BREEDPLAN V4.1

Accounting for sire x herd interaction. Sire x herd interaction effects can be an important source of variation in field performance records (Notter *et al.* 1992; Bradfield *et al.* 1997). These can arise from mis-recording of management groups, unreported preferential treatment, sire by dam line interactions and true sire by environment interactions. EBVs are more accurately predicted when procedures used account for any sire x herd effects. Sire x herd variances of between 2-10 % of the phenotypic variance for BREEDPLAN traits have been estimated from several breed databases. The effect is included in the mixed model equations as an additional random effect with a particular variance for each trait. Additive and residual variances are reduced to maintain the same phenotypic variance for each trait. The paper of Graser *et al* (1999) described some results of including this effect in BREEDPLAN.

Accounting for heterogeneity of variances. Prediction of EBVs in BREEDPLAN Version 4.1 is also improved by accounting for heterogeneity of residual variances that can occur for records in different herd | year | sex groups. Reverter *et al* (1997) showed this can improve prediction of EBVs across herds. Heterogeneity can arise due to scale effects across herds, season/paddock and misrecording of management groups. Adjustment for this heterogeneity occurs by solving and adjusting for a scaling factor after each round of computations in the iterative analyses used to compute EBVs. A scaling factor of unity results in no changes to the data. A factor less than one reflects increased variation in that group and the scaling acts to reduce the variation. Conversely, a scaling factor of greater than one reflects small group variation and the scaling acts to increase the group variance. Scaling factors for four traits from a recent BREEDPLAN analysis are presented in Table 1. Scaling factors for scan fat traits are generally the largest and result in an increase in the variance of the scan fatness records of the groups.

Table 1. Example of scaling factors for heterogeneous variance adjustment for four traits

Trait	no. levels	mean	std	min.	max.
Birth weight	7,246	1.004	0.007	0.92	1.12
200d weight	3,393	1.003	0.011	0.93	1.16
Heifer scan p8 fat	41	1.092	0.090	0.98	1.43
Bull scan p8 fat	49	1.143	0.071	1.00	1.35

New genetic grouping strategy. Specifying animals as belonging to different genetic groups within a BREEDPLAN analysis is designed to account for differences that may exist between groups of 'base animals'. Base animals are animals in the pedigree of the population who do not have identifiable parents. The new strategy for forming groups takes account of the fact that base animals come from a number of sources, and that new base animals occur all the time (both from new herds entering BREEDPLAN and new base animals occurring in old herds). The new strategy groups animals on the basis of geographic location, and time of entry into the evaluation. Base animals from different breeds can be grouped separately in multi-breed evaluations.

Incorporating overseas information. BREEDPLAN has previously not been able to exploit the information known about the performance of animals overseas. This is particularly important for imported animals for traits like 200-day milk where records are slow to accumulate. BREEDPLAN

V4.1 converts overseas genetic evaluations to local units, and using knowledge of models, genetic parameters and overseas accuracies generates conceptual observations that give the animal a starting level of accuracy (up to 60 %) in BREEDPLAN analyses. As local performance records become available, these overwhelm the conceptual records and the EBV moves to reflect more performance in the local population. A full description of the methodology is contained in Tier *et al* (1999).

New carcase EBVs. As a consequence of industry interest in progeny testing for carcase traits and the accumulation of abattoir carcase data in the Cattle and Beef Industry Cooperative Research Centre (CRC), there was a need to develop new methods for incorporating abattoir and live animal scan data to derive carcase trait EBVs. This was not simple, as scan measures are taken on seedstock (bulls and heifers) while abattoir records are taken on commercial carcases, predominantly from finished steers. It was recognised that the trait ultimately of interest is that on the carcase of the slaughter animal, and that this is perhaps best evaluated at a constant carcase weight. New methods were developed to achieve these goals. The opportunity was taken to allow for overseas carcase information to also be included in analyses (as described in the previous section).

METHOD

a) Scan measures (p8 and rib fat depths, EMA, IMF %) on seed-stock bulls are considered separately from the same measures on heifers and some steers. Previous BREEDPLAN versions assumed these to be the same trait after an adjustment for the mean difference between sexes. All records are pre-adjusted to 500 days of age.
b) Abattoir carcase records (p8 and rib fat, EMA, IMF %, and RBY %) are pre-adjusted to a 300 kg carcase weight using regressions developed from CRC data. Carcase weight is pre-adjusted to 650 days of age (the average age of CRC slaughter animals).
c) Genetic correlations between scans on bulls and heifers and between these and the 300 kg adjusted carcase traits were determined using the adjusted records. These correlations are utilised in the BREEDPLAN analysis to predict EBVs for the 300 kg adjusted carcase traits. The 300 kg adjusted carcase traits are the traits for which BREEDPLAN EBVs are published.
d) The scan data, abattoir data, available overseas information and all other traits are run in the multi-trait BREEDPLAN prediction model along with all other traits.

The development of the IMF % EBV from live animal ultrasound is described by Graser *et al* (1998). Records from scanning are only accepted from technicians who have passed a proficiency test for each trait. The new carcase EBVs will be quite different to previous age adjusted EBVs for some animals. Contributing to this are differences in the variances for steer carcase and scanned seed-stock traits, the adjustment to 300 kg carcase weight rather than to a constant age, and other factors, such as the simultaneous incorporation of overseas data on carcase traits.

Mature cow weight EBV. Selection for early growth has correlated effects on cow size, with implications for cow herds and potentially also for the long-fed feedlot sector. Johnston *et al* (1996) showed cow weights taken at weaning can be used to evaluate genetic differences in mature cow weight. Up to four records on a cow's weight at weaning are utilised along with correlations with other traits in multi-trait analyses to derive the EBV. Cow weight records are pre-adjusted for age using a quadratic adjustment.

Across breed and crossbred EBVs. The new methodology for analysing crossbred data is also the methodology that will be used to produce across-breed EBVs when this is possible. Sufficient data for deriving across-breed EBVs are not yet available. Records on crossbreds are pre-adjusted for individual and maternal heterosis using literature estimates for the breeds involved. Base animals for different breeds are assigned to separate genetic groups, one implication being that grade of dam (i.e. F1 vs pure) no longer contributes to the definition of contemporary group. The facility to derive across-breed EBVs will be further tested when data become available.

NEW BREEDOBJECT FOR V4.1

A new version of BREEDOBJECT is now available that can use the new BREEDPLAN V4.1 EBVs. Changes made, and under test, include adding marbling score to the breeding objective (Barwick and Henzell 1997), allowing for the new EBVs in indexes, and allowing for breed differences in the speed of transition to BREEDPLAN V4.1.

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