Advanced genetic evaluation for the Australian Beef Industry

Project number BFGEN.100
Final Report prepared for MLA by:

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ABSTRACT

This three year project (BFGEN.100), conducted by the Animal Genetics and Breeding Unit (AGBU), has contributed significantly to the increased rate of genetic improvement for profitability of Australian beef cattle primarily through the development and enhancement of the BREEDPLAN and BreedObject systems. The latest estimate of beef industry rate of genetic progress for commercial profitability has continued to increase and is likely to double in the next few years. Australian beef producers have access to the state-of-the-art genetic evaluation technologies, and the project has ensured these technologies and associated knowledge were delivered and implemented in breeding programs throughout Australia.

EXECUTIVE SUMMARY

This project, through its research and development, has ensured beef producers in Australia have first class genetic evaluation and breeding objective technologies and associated services. The implementation and adoption of outputs from this project by industry have contributed significantly to faster rates of genetic gain in profitability of Australian beef cattle. This improvement has been achieved by ensuring Australian beef industry has an effective, flexible and improving genetic evaluation system that is able to adapt to the changing needs of its users and be able to incorporate new knowledge in genetics, animal breeding, recording practices, statistics and computing.

The most recent (August 2004) estimates of beef industry rate of genetic progress for commercial profitability, summed across breed, market x production systems, show that this rate has increased by 1.58 times when comparing animals born in the periods 1998-2003 to 1992-1998. The increase in estimated genetic progress for the most recent year (i.e. 2002-2003) compared to animals born in 1992-98 was 1.97 times, which is very close to the MLA's strategic plan target to double (i.e. 2.0 times) the rate of genetic progress by 2006. Importantly, the benefits from the project's R&D will continue to contribute to further increases in the rate of gain over coming years as adoption and further implementation occurs.

Throughout the project the operational integrity of the BREEDPLAN and BreedObject systems have been maintained and enhancements were made to the evaluations of specific breeds based on their developing requirements. New genetic parameters were estimated from the complete Beef CRC carcase and meat quality database consisting of over 7,500 animals and these parameters were incorporated in the variance/covariance matrices of all temperate breeds in 2001, and of tropically adapted breeds in 2002. Also, for the first time, estimation was completed of a full genetic covariance matrix for 22 traits for the Hereford/Poll Hereford breed. These developments ensure BREEDPLAN analyses are using the most up to date estimates of critical parameters, thus ensuring selection decisions are based on the most accurate information possible.

In early 2003, the project delivered to beef industry the first across-breed BREEDPLAN EBVs. This research was undertaken using data from the MRC Victorian Multi-breed EBV project and the Beef CRC Northern crossbreeding project to derive breed differences and the necessary base adjustments for their existing breed BREEDPLAN evaluations. A simple table of adjustments was published that allows Australian beef producers to directly compare the EBVs of four prominent British (Angus and Hereford) and European (Limousin and Simmental) breeds for the full range of growth traits. Commercial crossbreeders or composite developers who are using combinations of these breeds can now simultaneously exploit both within and between breed variation.

Enhancements to the BreedObject software have resulted in a very large increase in adoption of this technology by both the seedstock and commercial sectors. Twenty-four breed standard $Indexes have been developed in consultation with Industry, representing approximately 70% of Australian industry production situations. Most breeds now publish $Indexes on a regular basis via their BREEDPLAN internet facilities and the BreedObject web site. Importantly, the indexes can now be fully customised via the BreedObject web site. This gives individual producers the capacity to develop an index specifically for their own production and market system (or for that of their clients). The increased adoption of $Indexes by industry has greatly assisted seedstock breeders and bull buyers making selection decisions with the correct trait emphasis for profitability and hence has contributed to overall increases in industry

profitability. The BreedObject software was also enhanced to allow computation and reporting of the genetic trends in profitability summed across the entire industry. Genetic trends in the existing breed standard indexes show all breeds are making significant positive progress in their $Indexes and, in almost all cases, that this progress is occurring at an increasing rate.

New “StockTake” software, developed during the project, allows a genetic audit of a breed, or herds within a breed. BREEDPLAN users (e.g. Breed societies or large companies) can use StockTake to monitor changes over time in numerous breeding program variables associated with genetic improvement. The software facilitates benchmarking of genetic progress across herds through the establishment of key performance indicators (KPI) within a breed. Herds can be evaluated against the KPI to provide valuable information on the relative performance of their breeding program compared to other herds of their breed. The ability to benchmark a herd’s genetic progress against all other herds in a breed will greatly assist breeders to make improvements to breeding programs that will increase rates of genetic progress in a herd and the breed.

The emerging molecular technologies are now delivering a small number of direct markers to the Australian beef industry. Algorithms were developed in the present project for incorporating direct gene data for GeneSTAR marbling into BREEDPLAN IMF EBVs by a process of “de-regressing” the EBVs to include the marker effect. Lack of numbers of genotyped animals in BREEDPLAN recorded herds and inconsistencies in the estimates of the size of marker effects have prevented full industry implementation of this new procedure. The incorporation of markers will help increase the accuracy of EBVs, at a younger age, and by this means assist in increasing genetic progress. From an industry perspective the procedure developed simplifies the selection process by combining the two sources of genetic information.

The project has greatly advanced the ability of the Australian beef industry to improve profitability through the selection of more feed efficient cattle. The Net feed intake (NFI) EBV was developed and released to industry for the Angus and Hereford breeds. In addition, considerable work was undertaken, in conjunction with MLA project BFGEN.100a, to establish the usefulness of insulin-like growth factor I (IGF-I) as a correlated measure of NFI. As a result of this work, IGF-I testing has been adopted by the beef industry and the BREEDPLAN NFI EBVs now incorporate the available industry IGF-I data. It is expected that the number of bulls available for selection with NFI EBVs will rise greatly with the recording of IGF-I as large numbers of young animals can be tested in seedstock herds. Ultimate numbers however, will depend on the cost of the IGF-I test. The latest Angus BREEDPLAN evaluation illustrates the likely effects on numbers. It included 7,497 IGF-I records and resulted in the doubling of the number of animals with a publishable NFI EBV compared to the previous evaluation. It will be critical that selection for NFI is done within a multiple trait framework (i.e. using BreedObject). This is needed to ensure the correct emphasis is placed on the trait based on its economic importance, and to ensure that potential genetic antagonisms with other important traits (e.g. marbling and fertility) are also addressed.

The project developed a set of new procedures to allow the use of mating records from artificial insemination joinings in the genetic evaluation of female fertility (i.e. days to calving EBV). A procedure was developed to allow the days to calving record to be derived from the AI mating records collected on farm. This trait was heritable and highly correlated to the days to calving trait currently derived from paddock mating records. This development will greatly enhance the genetic evaluation of female fertility traits, especially in those breeds with large use of AI, through increased numbers of sires evaluated and increased accuracy of their days to calving EBVs. This is an important development because female fertility is a trait that commonly has a high relative economic value, suggesting it is one of the more important traits of the breeding objective.

Significant outcomes were achieved for the beef industry through the use of random regression procedures. The first outcome was the development of an analytical procedure that allowed complete analysis of over 550,000 weight records to estimate covariance functions from birth to 8 years of age. The project developed a new procedure to estimate covariance components for random regression models employing a Gibbs sampling algorithm. The other very important outcome was the development of a new method for computing prediction error covariances. This will have applications for computation of approximate accuracies for EBVs derived from random regression methods and also for BreedObject Indexes. The research showed the benefits of employing random regression techniques at a number of levels. It occurs through increased accuracy of EBVs, the ability to use records at any age (i.e. no need to age adjust) and also to potentially describe growth curves or produce EBVs that apply at any age. For the industry to exploit the new technique requires that a large proportion of animals have a minimum of approximately 6 records (e.g. weights) and that commercially viable computing strategies can be developed.

Finally, the project has implemented international research to develop a new procedure for solving the huge number of equations involved in BREEDPLAN analyses. The new solver is capable of exploiting multiple CPUs (parallel processing) and is based on the pre-conditioned conjugate gradient (PCG) algorithm. The PCG algorithm is more efficient than that currently used in BREEDPLAN, namely successive over relaxation. The PCG algorithm is so called because a pre-conditioner is used to expedite the solving process. Different pre-conditioners can increase the rate of convergence. The new solver will greatly reduce the solving time for all BREEDPLAN runs and will significantly increase the feasibility of running more complex models such as those required for multi-breed analyses in the future.

1. Acknowledgements

BFGEN.100 project has involved the work of several scientists, research assistants, support staff and students at AGBU. Principal investigators were H-U Graser, D. Johnston, B. Tier, K. Meyer, S. Barwick. Other AGBU staff who contributed to the research, or data management, included: W. Upton, C. Girard, T. Henzell, K. Moore, D. Robinson, A. McCann, M. Kadel and T. Reverter. Research undertaken often involved collaboration with several other institutions, seedstock breeders, research herds and Breed Societies. Their involvement is gratefully acknowledged. Finally, and most importantly, the financial support of the MLA and the parent organisations of AGBU (NSW DPI and the University of New England) are acknowledged.

2. Background/Description

The Animal Genetics and Breeding Unit (AGBU) has consistently and methodically developed genetic evaluation systems for Australian beef cattle for nearly 20 years. Funding for this work has come from R&D funds provided by MLA and its predecessor organisations. Considerable input into the development of these genetic evaluation systems has also been made by the two joint venture partners in AGBU; the University of New England (UNE) and NSW Department of Agriculture (NSW Ag). Consequently the Intellectual Property Ownership of the genetic evaluation system and associated software rests with the MLA, NSW Ag and UNE as described in the Analytical Software Ownership Agreement (1992). The genetic evaluation system termed BREEDPLAN and GROUP BREEDPLAN has been commercialised by the Agricultural Business Research Institute (ABRI) with an exclusive licence since 1992. This exclusive licence has recently been renewed with modified clauses relating to the distribution of the royalties, which are now directly paid to the owners.

The currently used BREEDPLAN Version 4.1 is one of the best beef cattle genetic evaluations systems available. AGBU will continue its beef genetics R&D program, further fine tuning the breeding objective for different market production systems (MPS) for Australian beef cattle through new knowledge on economically important traits. This will lead to new selection criteria, which will be added to the genetic evaluation system BREEDPLAN. Development of new or upgraded statistical procedures and models for some performance data, including the use of DNA marker information is also planned. AGBU will contribute to the MLA extension efforts and to breeder education in the application of genetic principles. This application outlines the planned research and development for 2001/02 until 2003/04.

Potential Industry Benefit

Benefits for the industry will come from genetically improved beef cattle, which will have higher weaning rates, increased carcass and meat quality combined with higher efficiency of feed utilisation.

Increased accuracy of Estimated Breeding Values (EBVs) through improved analytical methods and increased quality of performance recording, combined with greater focus within the seedstock sector towards quantifiable breeding objectives and higher selection intensities will increase the rate of genetic gain. The analysis of historical beef cattle performance data from 1980 to 2000 clearly shows genetic trends for breeding objectives derived for a number of market-production systems in those breeds which took performance recording and genetic evaluation seriously. Increases in the annual rate of genetic improvement can be directly linked to increased performance recording and to improvements in the genetic evaluation system BREEDPLAN which were developed in previous MLA funded projects.

Consistent use of breeding objectives and an increase in selection intensity combined with more accurate selection will more than double the genetic trends in seedstock herds in the next decade compared to the previous decade. The increased accuracy of selection will make mating tools like TGRMTM even more valuable.

The increased genetic performance in the seedstock sector will be transmitted through the traditional sale of genetic material, performance recorded bulls, semen and few females into the commercial sector. An increased participation in performance recording in BREEDPLAN, specifically by northern pastoral companies, will increase the number of performance recorded animals. This will have a direct effect on the selection intensity and accuracy of selection of commercial bulls allowing the commercial sector to narrow the gap with the seedstock herds. Advances in reproduction technology, which might be achieved in other projects will become even more valuable with an increase in the accuracy of selection.

Increased genetic value of Australian seedstock cattle combined with a best practice genetic evaluation system will make them internationally more competitive. This will increase the demand for Australian beef cattle genetics worldwide and will increase export of Australian genetics as semen, embryos and live animals. The direct beneficiaries of the increased demand will be Australian seedstock producers, and in case of live animals also commercial cattle producers.

Finally, continued development of BREEDPLAN analytical software will enhance the competitiveness of the BREEDPLAN International system. This will assist the licensee (ABRI) to maintain, and even increase, its share of animal performance recorded and evaluated with the BREEDPLAN system. BREEDPLAN owners will receive additional royalties from increased numbers of overseas recorded and evaluated animals.

3. Objectives

- Research and develop industry breeding objectives, including expanded development of BreedObject software and services in parallel with BREEDPLAN developments.

- Maintain the operational integrity of BREEDPLAN Analytical software (Version 4.1) and facilitate all new analyses required as outlined in the Analytical Software License Agreement.

- Evaluate and include additional traits into BREEDPLAN by September each year (Version 4.2-4.3).

- Facilitate and support multi-breed genetic evaluations from existing databases and develop recommendations for the future.

- Develop genetic audit methodology and software that will document by breed and herd key population indicators that influence genetic progress.

- Undertake basic research in the key areas of random regression analysis and inclusion of DNA marker information into Genetic Evaluation Software (new BREEDPLAN (V5.0) or BREEDPLAN like products).

- Develop new analytical code that takes advantage of the more commonly used multi-processor computers and different approaches to solving huge linear equation systems in BREEDPLAN or new Genetic Evaluation Software.

- Support MLA's genetics extension objectives on an ongoing basis as requested by MLA and communicate the research findings of this project to the industry at large and to national and international peers. Further information about these objectives is set out below.

4. Approach/Methodology

AGBU will maintain a core group of highly qualified scientists that are dedicated to the Australian beef industry. The approaches/methodology for the different objectives are described below. Each objective is subsequently divided into separate tasks.

1) Research and development for industry breeding objectives, including expanded development of BreedObject software and services in parallel with BREEDPLAN developments

AGBU will expand the capacity of the BreedObject software in parallel with BREEDPLAN developments. These include new traits, new EBVs, new estimates of genetic parameters, across breed EBVs, genetic markers and index accuracies. Also included in this area of work will be development of selection indexes that facilitate more effective importation of genetics; and breeding objectives and indexes that will aid export of Australian genetics. The theoretical work is lead by Dr Stephen Barwick a NSW Ag scientist working at AGBU to support this work, MLA has budgeted 25% of the cost of a programmer.

In association with industry and MLA the Research Organisation will modify and further develop breeding objectives for use in monitoring industry rate of genetic gain. The Research Organisation must also provide monitoring in line with Objective 5 (genetic auditing). Industry use of selection indexes will be incurred by the Research Organisation by providing enhanced BreedObject delivery via the Internet.

2) Maintain the operational integrity of BREEDPLAN Version 4.1 and facilitate all new analyses required

The Research Organisation will engage a Junior Scientist to provide support to ABRI in using the BREEDPLAN Analytical Software. (As MLA is 51% owner of analytical software this responsibility should be funded jointly by MLA and RO and not only by RO)

AGBU scientists will implement (implement means prepare parameter and control file for each new breed/PC which uses the system for the first time) the BREEDPLAN system for additional breeds and large pastoral companies not previously analysed with GROUP BREEDPLAN. In addition the type of analysis for existing GROUP BREEDPLAN breeds (eg. activate correct crossbred data option if required) will be upgraded to include new traits, and revised imported data (Overseas EBVs). Routine updating of new or re-estimated variance components and adjustment factors will be required, as more data in a breed or trait(s) becomes available.

3) Evaluate and include additional traits into BREEDPLAN each year

By September each year new traits that have been assessed to be beneficial for example (cost effective recording, heritable and correlated with traits in the breeding objective) will be added to the BREEDPLAN analytical software. To include a new trait into BREEDPLAN suitable analytical models have to be developed, genetic and environmental parameters and adjustment factors will be estimated and the software code will be modified to handle the new trait. Subsequently the results have to be extended to the participation breeds.

From time to time it will be necessary for the Research Organisation to investigate models and adjustment procedures for selection criteria traits already included in the analysis as a larger quantity of data becomes available and breeders question the correctness of the EBVs. Such work will inevitably lead to modifications to models and variance component estimates, which have to be included into the BREEDPLAN analytical software and its control parameter files.

4) Facilitate and support multi-breed genetic evaluation from existing databases and develop recommendations for the future

The Research Organisation must, if required, modify BREEDPLAN software to deliver the Industry across-breed EBVs. The Research Organisation will consult with the owners of the data (eg breed societies) and key industry players during 2002. Recommendations to Industry will be developed by the Research Organisation to ensure accurate comparisons across breeds are being made and therefore maximising the benefits to beef producers. This will require an intensive discussion with the representatives of the different breeds which will be affected by an across breed evaluation. Test results from multi-breed runs will be available by December 2001.

5) Develop genetic audit methodology and software, which will document by breed and herd, key population indicators that influence genetic progress

This will involve the development of software to quantify key indicators and to determine, on a breed and on an individual herd level, the performance against these key population parameters that influence genetic progress. The work will require identification of key performance indicators by a ‘breeding program effectiveness team' as outlined MLA Genetic Business plan attached and marked C. A first version of this "BreedAudit" software will be operational by June 2002 with test results provided to MLA by December 2001 after the specifications have been outlined by the by the Research Organisation by September 2001. In addition, by December 2001 the Research Organisation will have developed recommendations to perform data quality audits (for a breed or breeder) for determining deficiencies in performance recording. These recommendations will subsequently have to be translated into software programs by the Research Organisation.

6) Undertake basic research in the key areas of random regression analysis and inclusion of DNA marker information into BREEDPLAN or new Genetic Evaluation Software

Random regression (RR) models have been advocated to model ‘traits’, which are measured repeatedly on individuals and which change gradually and continually with time. A simulation study will be undertaken by the Research Organisation on the potential benefits and problems associated with a genetic evaluation for growth of beef cattle under a RR model.

The Research Organisation will undertake by June 2002 a review and simulation studies, which will consider different combinations of assumed gene action, gene frequency, amount of information and pleiotrophic effects to find the best use of genetic markers information, if at all, in the genetic evaluation system BREEDPLAN. This work will be done in consultation with Prof Mike Goddard (at the University of Melbourne)

Following the review and simulation studies the Research Organisation will investigate the incorporation of molecular data into genetic evaluations. This will require development of new methodology and computer algorithms currently not available in BREEDPLAN. It will be a key requirement for such software that it can analyse genotypic and phenotypic data jointly on a routine basis and in a timely and affordable way.

The Research Organisation will investigate the possibility of screening beef cattle performance and pedigree data using segregation analysis, for the presence of Quantitative Trait Loci (QTL) and develop strategies and incorporating the effect into BREEDPLAN and BreedObject, or other new software. Such work will have to be repeated, as data on new traits becomes available.

7) Develop new BREEDPLAN analytical code that takes advantage of the more commonly used multi-processor computers and new approaches to solving huge linear equation systems

Solving large linear models from animal breeding data with possible 100s of millions of equations require considerable computing resources. Several strategies exist that will be researched by the Research Organisation, and, if useful or as determined by MLA, implemented to help ensure shorter solving times and the possibility to offer Industry better models of analysis (eg random regression).

8) At a high level, support MLA’s strategic genetics extension objectives on an ongoing basis and communicate the research findings of this Project to the industry at large and to national and international peers

The Research Organisation will contribute substantially to the genetic extension objectives of MLA's beef genetics business plan and will primarily play a coordination role with the technical expertise to run ‘train the trainer’ workshops, develop extension material (in conjunction with the MLA EGDE network as directed by MLA from time to time) and develop a genetics awareness strategy for all sectors of the beef industry. The Research Organisation will have separate 2-3 day workshops with invited elite breeders to introduce them to the latest developments in the area of genetic evaluation, development of breeding objectives, TGRM and molecular genetics during 2002.

The key dissemination of the Project outcomes and objectives will be the delivery of updated software on an annual basis to ABRI for use in the large GROUP BREEDPLAN runs undertaken in December and January each year. Upgrades of software will be delivered by the end of September each year.

5. Results and Discussion

The project has successfully achieved the majority of its original milestones and several additional ones that developed during the course of the project. Achievements against each milestone are described below and supporting material, including publications are contained in a series of annexes and reports [R1-R2]. Annex P contains publications [P1-P35], Annex C contains AGBU internal (confidential) research reports [C1-C25] and Annex A contains associated publications [A1-A12].

5.1 BreedObject

5.1.1 BreedObject R&D

The nominated project tasks in breeding objectives and indexing research and development were well achieved, these all occurring in parallel with developments in BREEDPLAN. The principal achievements included:

1) **Expanded development of software in parallel with BREEDPLAN developments**

- development of a new Version (4.2) of the BreedObject software, encompassing improved methodology, especially for evaluating calving ease impacts in $Indexes [A11]; and new knowledge of genetic parameters arising from BREEDPLAN and Beef CRC research. The new genetic parameters were incorporated in revised genetic parameter matrices for Angus, Brahman, Charolais, Hereford & Poll Hereford, Murray Grey, Limousin, Santa Gertrudis, Shorthorn and Simmental.
- release of corresponding Version 4.2 software adapted for application on ABRI Vax machines. The Vax version of the software is for use in calculating $Indexes for breed databases.
- inclusion of a facility for outputting trends in breeding objective traits for use in industry monitoring of genetic gains.

Inclusion of new traits and EBVs

- A key area of breeding objectives research has been in the area of modelling and costing feed. Ramifications of different approaches to costing feed were considered and presented in a World Congress review paper [P2]. Studies were also carried out of alternative recording and breeding schemes for including net feed intake in selection [A1, A7]. These studies demonstrated how industry feed intake measurement costs could be reduced. As few as 5% of bulls need to be tested for feed intake if those for testing are first screened using criteria that include a measurement of serum IGF-I level.

Non-linear Index development, and towards the inclusion of across breed EBVs and genetic markers

- Methods were developed for evaluating trait economic impacts at the level of individual animals for use when trait value varies non-linearly over the trait range. The economic impact assessment is based on the expected performance level of progeny. The method is relevant for valuing carcase trait improvements, for example, for individual or mate selection. It will also be an important feature of procedures for including across breed EBVs and DNA markers in $Indexes. The procedure was presented to the 2003 AAABG Conference [P1].

$Index accuracies

- A procedure was developed, jointly with ABRI and the BREEDPLAN Technical Liaison Group, for controlling the reportability of $Indexes, and their displayability on web sites, so that low accuracy $Indexes are not reported or displayed. The procedure uses reference to the accuracy of the EBVs that contribute to the Index. Individual breeds are responsible for formulating accuracy reportability/displayability cut-offs. These cut-offs also apply to user-customised $Indexes.

- Significant progress was also made towards deriving $Index accuracies algebraically. Upper limits of $Index accuracies were presented to an MLA 'Proof of Profit' Workshop for example cases. A method was developed for approximating key elements of multiple-trait Index accuracy that previously could not be quantified. The procedure is presented in a paper by Tier and Meyer [P29].

Development of indexes to facilitate export of Australian genetics and more effective importation

- The number of breed, market x production system cases addressed by 'standard' $Indexes (i.e. $Indexes that have been adopted by breeds and made routinely available on all animals of the breed) was increased to 24, representing approximately 70% of Australian industry production situations. This was achieved in close consultation with industry and included development of new Indexes for Hereford/Poll Hereford, Charolais and Australian Agriculture Co., and revised $Indexes for a number of breeds. Standard $Indexes (one for Angus and three for Hereford) were also developed and adopted for use in New Zealand; and a further $Index was developed and adopted for use in Angus in Argentina. The ready availability of these $Indexes on web sites goes a substantial way towards facilitating more effective importation and genetics exports. A remaining step to be achieved is for countries & breeds with $Indexes to agree to reciprocate in making available each other's $Indexes for animals of their databases.

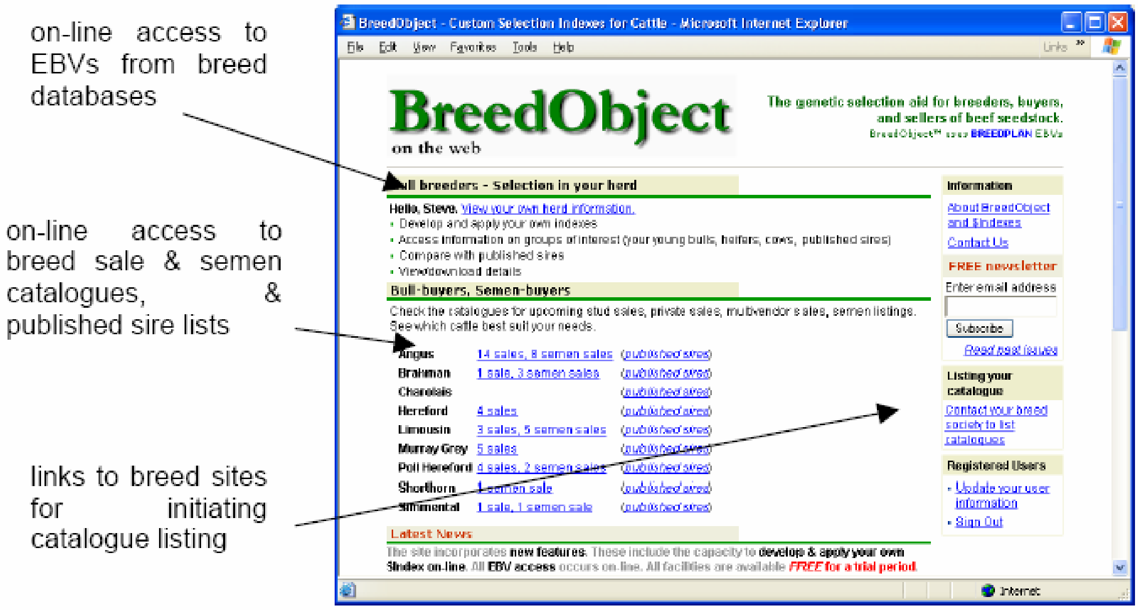
5.1.2 Customised Indexes

Renewed Commonwealth 'Information Technology On-Line' (ITOL) funding for work on 'BreedObject on the web' was successfully obtained and commenced in mid 2002, with MLA, other industry and commercialiser support. Substantial R & D to enhance delivery of BreedObject via the Internet was completed in association with this project and is detailed in a 76-page report [R1]. It included:

- extension of the 'BreedObject on the web' site to include new features and to be functionally integrated with breed EBV databases and listings of sale and semen catalogues available on breed web sites.
- providing breeders and buyers with the ability to customise their own $Indexes on-line, for immediate use. The process requires users to complete a 20 multiple-choice questionnaire (cut down version of the full questionnaire underlying BreedObject). The resulting $Index can then be applied to a given set of animals e.g. from a user's own herd, a sale or semen catalogue, or a published sire list.
- extending web facilities to include the full BreedObject questionnaire, effectively also enabling the web site to become the primary front-end software for all uses of BreedObject.

The BreedObject web site is considered to have been an important catalyst for significant industry change, spurring the more general availability of EBVs to industry and contributing significantly to enhancing rates of genetic gain [A12]. The BreedObject web site (see Figure 1) and its underlying technology were also the bases of an invited keynote paper presented to the 'ITadvances in Agriculture' Conference in 2002 [A9].

Figure 1. BreedObject web site 'Home' page



on-line access to EBVs from breed databases

on-line access to breed sale & semen catalogues, & published sire lists

links to breed sites for initiating catalogue listing

BreedObject
on the web

The genetic selection aid for breeders, buyers, and sellers of beef seedstock.
BreedObject™ uses **BREEDPLAN** EBVs

Bull breeders - Selection in your herd

Hello, Steve. View your own herd information.

- Develop and apply your own indexes
- Access information on groups of interest (your young bulls, heifers, cows, published sires)
- Compare with published sires
- View/download details

Bull-buyers, Semen-buyers

Check the catalogues for upcoming stud sales, private sales, multivendor sales, semen listings. See which cattle best suit your needs.

Angus	14 sales, 8 semen sales	(published sires)
Brahman	1 sale, 3 semen sales	(published sires)
Charolais		(published sires)
Hereford	4 sales	(published sires)
Limousin	3 sales, 5 semen sales	(published sires)
Murray Grey	5 sales	(published sires)
Poll Hereford	4 sales, 2 semen sales	(published sires)
Shorthorn	1 semen sale	(published sires)
Simmental	1 sale, 1 semen sale	(published sires)

Latest News

The site incorporates **new features**. These include the capacity to **develop & apply your own $Index on-line**. All **EBV access** occurs on-line. All facilities are available ***FREE* for a trial period.**

Information

About BreedObject and $Indexes

Contact Us

FREE newsletter

Enter email address

Read past issues

Listing your catalogue

Contact your breed society to list catalogues

Registered Users

- Update your user information
- Sign Out

5.1.3 Monitoring genetic progress

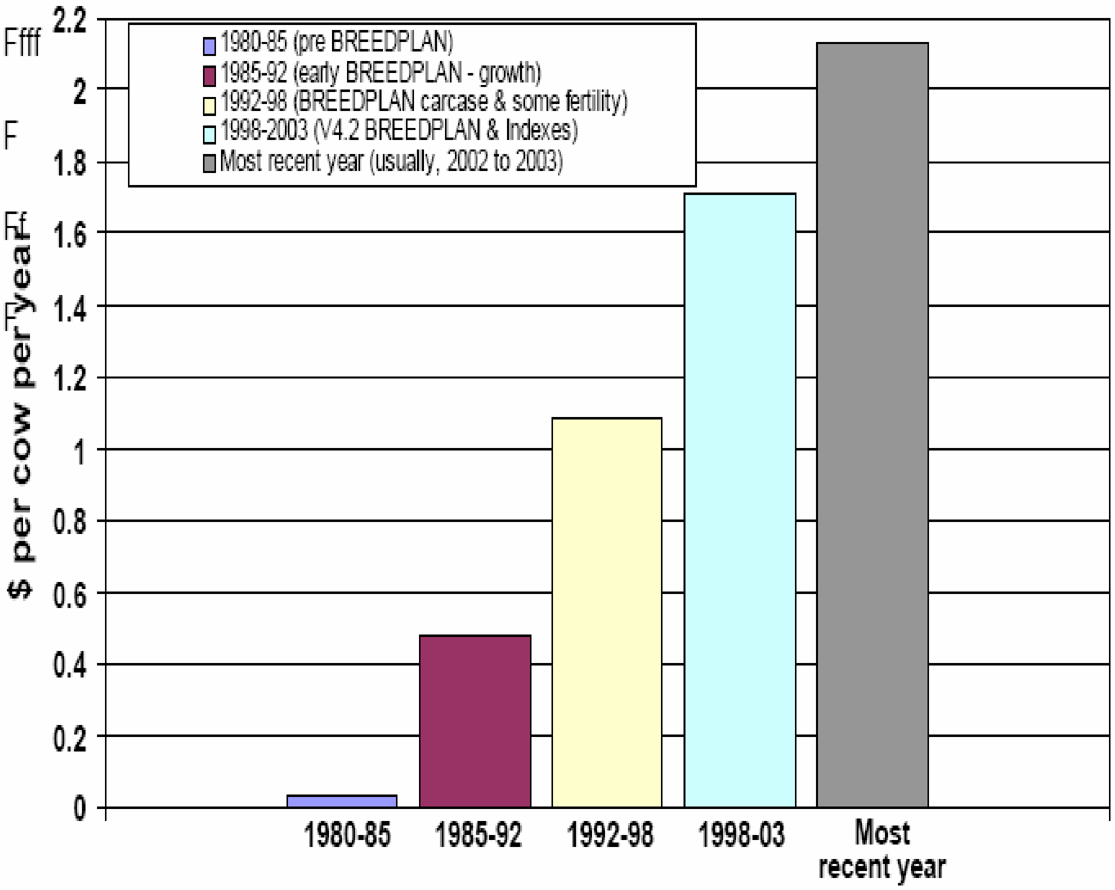
BreedObject $Indexes can be used to compute genetic trends for all animals within a breed over time by averaging the $Index EBV for all animals of the breed born in a given year (eg. all 1980 drop, all 1981 drop, all 1982 drop to all 2003 drop). These trends reflect the genetic change occurring in the industry market production system profit addressed by the $Index. The slopes of the trends, for given time intervals, can be accumulated to give figures representative of the entire beef industry by summing the gains occurring across all of the available standard market production system $Indexes. To arrive at the sum, each market production system is weighted by its estimated contribution to the total beef industry.

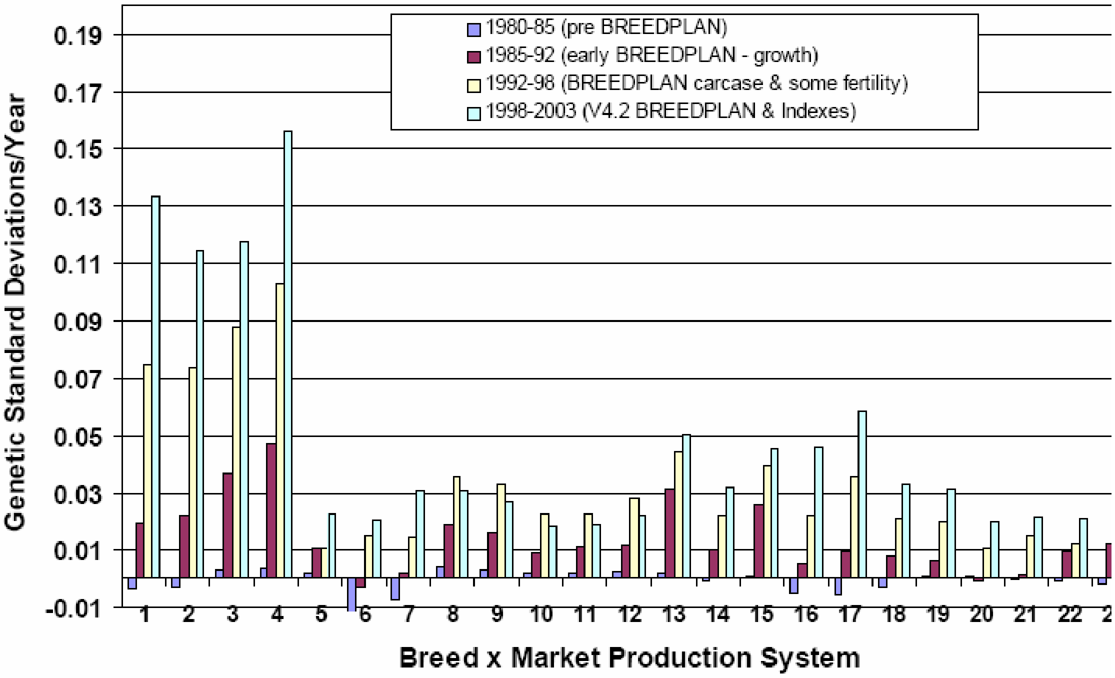
Figure 2 shows the most recent estimate (August 2004) of industry rates of genetic gain in market production system profit over time, assessed from the weighted sum of the rates of genetic gain in 23 industry breed x market production systems. The rate of gain in animals born over the period 1998-2003 is 1.58 times that of animals born over the period 1992-1998. Figure 2 also gives an early estimate of the rate of genetic gain in animals born over the most recent year (i.e. 2002-2003). The rate of gain in this most recent year is 1.97 times that of animals born over the period 1992-1998. Note that this figure is already close to the nominated MLA Beef Business Plan target of doubling (i.e. 2.0 times) the industry rate of genetic gain by 2006.

Figure 3 shows the rates of genetic gain, over time, for each of the 23 industry breed x market production systems encompassed in Figure 2. Clearly, Angus shows impressive increases in rates of genetic gain but several other breeds are now making solid progress as well. These encouraging results for increase in the rate of genetic gain for Australian beef production profitability are potentially of immense value and can substantially be attributed to the research, development and implementation achieved through this project.

Genetic trends were also earlier assessed for individual breeding objective traits and $Indexes for representative breed x market production systems. This was performed as part of an evaluation of the returns from beef cattle genetics R & D in Australia conducted for MLA by Farquharson, Griffith and Barwick and was published in a conference proceeding [A10]. This study, conducted in association with other providers, showed industry gains occurring to 2000 from genetic selection to have a net value of the order of $500 million. About one third of this benefit was expected to be captured by beef producers and about one half by domestic Australian consumers. These results further emphasise the expected value to industry of the increasing rates of genetic gain that are summarised in Figure 2.

Figure 2: **RATES OF GENETIC GAIN IN AUSTRALIAN BEEF INDUSTRY MARKET PRODUCTION SYSTEM PROFIT, OVER TIME**





[1]weighted estimates, based on the rates of genetic gain in 23 industry breed x market production systems

[2]includes account of expected feed costs

Figure 3: Rates of Genetic Gain for Industry Breed x Market production sys profitability

KEY - Breed x market production systems shown are those addressed by the following widely ava BreedObject $Indexes. See separate list for more details of each system:

1. Angus B3
2. Angus CAAB
3. Angus Supermarket
4. Angus Terminal North
5. Brahman Jap Ox
6. Charolais Domestic Supermarket
7. Charolais Export
8. Hereford & Poll Hereford Supermarket
9. Hereford & Poll Hereford Hereford Prime
10. Hereford & Poll Hereford Short-Fed (100-150 Days)
11. Hereford & Poll Hereford Long Fed Export
12. Hereford & Poll Hereford EU Index
13. Limousin Domestic (Terminal) Index
14. Limousin Steer (Self Rep) Index
15. Limousin Steer (Terminal) Index
16. Murray Grey Long-Fed Export
17. Murray Grey Supermarket
18. Shorthorn Domestic Supermarket
19. Shorthorn Domestic Restaurant
20. Shorthorn Export B3
21. Shorthorn Export B3M
22. Simmental Self-Rep Supermarket Index
23. Simmental Japan (Terminal) Index

5.2 Maintained Operational Integrity of BREEDPLAN

Throughout the project AGBU researchers have ensured the operational integrity of BREEDPLAN by altering or correcting the analytical code, enhancing analytical models, implementing new variance component estimates and modifying the configuration of analyses of several breeds (e.g. to incorporate overseas breeding values or to configure their analysis to use crossbred data). This was an important component of the project to ensure the research and development (i.e. new software) was implemented correctly and used effectively by the beef industry. However at the start of the project we underestimated the time required to undertake the necessary research to accommodate all the breeds in BREEDPLAN. This caused delays in some areas of R&D planned in the project. Listed is a brief description of some of the major enhancements made over the past three years:

5.2.1 Variance component estimation

• BREEDPLAN Version 4.2 was implemented at ABRI at the end of 2001. The main enhancement was the implementation of new variance components files for abattoir traits estimated from the final analyses of the 7,500 animals from the Beef CRC1 straightbred project [A2-A5]. Incorporation of these variances and covariances has greatly enhanced the BREEDPLAN and BreedObject analyses, particularly for carcase traits.

• Significant variance component work was undertaken throughout the project. The first major work involved the estimation of variance components for all 22 traits in the Hereford breed using series of bi-variate REML analyses (N=231) and a six-variate analysis. Results were combined, using a weighted summation of partial, expanded covariance matrices and required the development of new statistical procedures for producing positive definite matrices [P3]. The new parameter estimates were implemented into Hereford/Poll Hereford BREEDPLAN and the research was presented at a conference [P4] and a full journal paper [P5] that was released at the World Hereford Conference in Armidale in March 2004.

• Research was undertaken to investigate the effect of data structure on the estimation of variances due to sire x herd interation (sxh) effects. BREEDPLAN Version 4.1 introduced the additional random effect for sxh and required an estimate of the size of the effect be known for each trait. This research showed that large numbers of sires used across many herds is required to avoid biased estimates of the sxh and additive variances [P6].

5.2.2 Software and trait enhancements

• December 2001 saw the implementation of Trial BREEDPLAN Net Feed Intake (NFI) EBVs for Angus and Herefords [C1]. The EBVs used feed intake data collected from Industry and research herds. This was an extremely important development in the evolution of the BREEDPLAN system. Australian beef producers now have the first tool that allows them to genetically improve a trait directly associated with one of the largest cost of production i.e. feed (see section 3.1).

• Research into the improved modelling and analysis of cow weight data occurred for the tropically adapted breeds. In brief, problems with correct recording of contemporary groups and relatively small numbers of records created similar problems identified previously with the temperate breed analyses. Therefore the changes made to the BREEDPLAN runs for temperate breeds were used as a starting point for the tropically adapted breeds.

Unfortunately the numbers of cow weight records were much fewer (Santa = 5974, Brahman = 4807 and Belmont Red = 1898). Also due to the recent recording of this trait in these breeds the majority of cows had no previous entries so variables such as previous weight information, lactation status, age at first calving, or foetus age could not be modelled. The outcomes of the research were a new definition for contemporary group for cow weight records and new age adjustment factors specific for tropically adapted breeds [C23]. The BREEDPLAN code was altered and now requires the breed to be nominated as either temperate or tropical in initial controller files. This enables different subroutines to be used to build contemporary groups and process data files. The new procedure and adjustment factors were tested on Santas and Brahmans and implemented at ABRI.

• Inconsistencies in BREEDPLAN results with respect to the treatment of Multiple Sire groups were identified by ABRI and investigated with a high priority, particularly for northern breeds. The causes of the problem were identified and fixed. Following some preliminary analyses to ensure that the software was operating correctly, the impact of the method on the EBVs of the sires in those groups, and their mates, was investigated. Data from a breed up to the end of 2000 with all multiple sire group data deleted was analysed to provide a reference. The 2001 data, complete with multiple sire group information, were added to this set that was also analysed. The EBVs from a number of subclasses of these analyses were compared. These included all sires used only as singles in each set of data, sires in the multiple sire groups and the mates of this group of sires. Results showed the new code significantly improved the EBVs of animals from multiple sire groups. The new code was implemented at ABRI for all breeds using the multi-sire group option.

• Calving ease diagnostics software was written and implemented at ABRI. The software allows AGBU and ABRI staff to quickly, and timely, assess enquiries regarding a calving ease EBV on an individual, offspring, parents or contemporary group [C2].

• A very thorough investigation of the ultrasound scan IMF% data (SIMF) was undertaken given the importance of the trait to some sectors of the industry. The problem was identified when ABRI started producing outlier reports and it showed large numbers of very low values, in high frequency. This prompted a detailed look at the raw data and subsequently full variance component analyses to research the extent of the problem and more importantly, the impact it was having on the computation of BREEDPLAN IMF% EBVs. The research showed large differences between scanners in their additive variances for SIMF, although their heritabilities were similar and the genetic correlation between scanners was close to one [C24]. This highlighted differences between machines and the SIMF reading of animals with very low SIMF (i.e. machine defaults). As a result AGBU ran a small industry trial with several senior ultrasound technicians. The results showed high correlations between scanners for SIMF however large differences existed in their means and standard deviations. The differences were being influenced by machine/operator “default” readings of very lean animals. All technicians were informed of the results and one clear outcome was that they were discouraged from scanning lean animals, particularly young bulls where the default value was most common. SIMF data from the latest scanning accreditation clinic (Aug 2004) will be analysed to further assess the machine/operator differences.

• Version 4.1 of BREEDPLAN released in 1999, included the facility to include overseas EBVs of imported animals as starting values for their BREEDPLAN EBVs. However after a couple of years of V4.1 being used, feedback from industry (particularly Angus breeders) suggested that too much emphasis was being placed on the overseas information. Research was undertaken to examine the procedure used and the structure of the imported data. The outcome of this work was that the procedure was modified, the code altered and tested, the results discussed and the procedure further refined [C3, C4]. The modified procedure included requirements for changes to the structure of the data received, as well as reducing the emphasis on the overseas data (differentially across traits). The new code has been tested at ABRI and will be implemented as part of Version 4.3 BREEDPLAN for all breeds.

5.2.3 Breed specific BREEDPLAN enhancements

• Research and development was undertaken to investigate the suitability of Shorthorn calving ease data (N=28,000) to develop CE EBVs for the Shorthorn breed [C5]. The threshold model was used (as used for other breeds e.g. Angus, Hereford, Simmental) in a multiple trait model with gestation length and birth weight. The Shorthorn technical committee accepted the outcomes and recommendations from this research and calving ease was implemented into Shorthorn BREEDPLAN. Shorthorn BreedObject Index cases were also modified to include calving ease information and the availability of the CE EBV.

• Research was undertaken to develop the female fertility trait days to calving for two large tropically adapted BREEDPLAN breeds the Belmont Red and Santa Gertrudis. Over 17,000 joining records were available for both breeds but unfortunately in both cases the recommendations from the research [C6, C7] were not to implement this EBV due to limitations in data structure. The main problems were the absence of whole herd inventory recording in these breeds and the low level of genetic linkage across herds. It was recommended that ABRI investigate assisting these breeds through their northern development officer.

• Preliminary work was undertaken for the large pastoral company, NAPCo., to investigate developing BREEDPLAN evaluations for their Alexandria Composite, Kynuna Composite and Tuli herds. This involved extensive examination of the data in terms of numbers, traits, structure, pedigrees, and fixed effects. Work was also undertaken quantifying the effect of linked markers on 14 of the NAPCo nucleus sires. The final stage was the production of test EBVs. This work was presented to the NAPCO technical committee however the decision was made to go with another genetics service provider.

• AGBU was requested to provide technical advice on the most suitable evaluation for the inclusion of Murray Grey data into Angus BREEDPLAN [C8]. However due to political and legal intervention the incorporation of the data did not occur and the Angus BREEDPLAN analysis was not altered.

• The Limousin genetic grouping structure was examined following large changes observed in the genetic group solutions between successive BREEDPLAN runs. The research showed that changes in the pedigrees and country of origin flags in the data of several imported sires had occurred and therefore required changes to the configuration of their genetic groups. The changes were made to allow the formation of new groups and was tested and implemented in the following Limousin BREEDPLAN [C9].

• New Brahman age of dam adjustments were developed after feedback from industry that the performance of calves from 2 year old dams appeared to be under adjusted. Research was undertaken using the most recent Brahman extract. Summary statistics showed it contained sufficient data from young cows (N=2368) to allow estimation of new regressions (previously too few data existed). The research showed a significant improvement in the adjustment of records for age of dam using the new regression estimates and an adjustment procedure that gives additional adjustment to two year olds. The Brahman technical committee endorsed the results and they were implemented in the July 2004 Brahman BREEDPLAN [C10].

5.3 New Traits

Several new traits were developed and evaluated throughout the project.

5.3.1 Net feed intake (NFI) and IGF-1

The project saw the implementation of single trait Net Feed Intake EBVs and subsequently the incorporation of IGF-1 data into the bivariate prediction of NFI EBV [C11, C12, C13]. The development of the BREEDPLAN NFI EBV required the establishment of data recording protocols (developed in conjunction with ABRI). Adjustment factors and preliminary variance components from NSW Agriculture Trangie (MRC DAN.75 project) and the Beef CRC research were used to develop the initial models and EBVs. However as more NFI data became available (from Industry and research herds), and IGF-1 results from the BFGEN100a were available, the computation of NFI EBV was enhanced using this latest information and the IGF-I data from industry herds. Protocols for the inclusion of these traits into BREEDPLAN Version 5.0 have been written outlining the development process required for the implementation of NFI and IGF-I into the full multi-trait BREEDPLAN evaluation [C14]. Several scientific and industry publications have been written from this work [P8, P9, P10, A6].

Currently, Angus and Herefords compute NFI EBVs at each BREEDPLAN evaluation and it is expected with the uptake of IGF-I testing by industry that other breeds will develop NFI EBVs in the next 12 months. Prior to the inclusion of the IGF-I data Angus had published 8,422 animals with NFI EBVs with accuracies greater than 30%. When the IGF-I data was included in June 2004 (N=7,497) the number of published animals increased to 17,223, greatly increasing the ability of breeders in this breed to improve feed efficiency.

5.3.2 Flight time

Preliminary work was undertaken on the development of industry recording of flight time as an objective measure of temperament. This was prompted following the results from the Beef CRC1 that showed, for the tropically adapted breeds, that FT was a heritable measure and was correlated to meat tenderness (e.g. shear force) and eating quality (e.g. MSA MQ4 score). However the device used in the CRC was only an experimental prototype so AGBU initiated talks with the Ruddweigh Company, Guyra, to develop and market a new flight time recording machine. AGBU subsequently purchase 4 machines to be used in various projects (e.g. Durham, Trangie Angus, Beef CRC and Breed Societies). Northern seedstock breeders have been encouraged to purchase the device and record flight time on all animals at weaning and submit the data to their BREEDPLAN databases.

A small collaborative study was also undertaken in the Angus breed [P11] where weaner bulls in four BREEDPLAN recorded herds were measured for flight time and visual crush score. The results showed both flight time and crush score were repeatable both within, and across, measurement time and the heritability estimate (approx. 500 records) suggested the existence of genetic variation for the trait. Flight time data from the first year intake of sires into the Durham Shorthorn project also indicate considerable sire differences for progeny flight time.

This preliminary research on flight time will provide the basis of developing a tenderness EBV in the future using phenotypic and molecular data.

5.3.3 Days to calving EBVs from AI records

Research was undertaken to investigate the use of AI joining records in the prediction of days to calving EBVs. The research showed a suitable trait could be developed from the existing database of AI joining data that was heritable and well correlated to the existing measure of natural service days to calving [P12]. The BREEDPLAN code was altered to accommodate the new trait, as per the recommendations developed [C15]. Data recording, storage and extraction procedures are currently being considered at ABRI and the new procedure will be released as part of BREEDPLAN Version 5.0. The new procedure has the potential to add thousands of records to the genetic analysis of female fertility each year and will greatly enhance the days to calving EBV and the BreedObject Indexes, particularly for those breeds using large levels of artificial insemination.

5.3.4 Structural soundness EBVs

AGBU staff assisted industry in developing guidelines for the structural soundness scoring of beef cattle suitable for genetic evaluation. Results from a pilot accreditation test [C25] were used to assess the suitability of each trait and minimum levels of proficiency were determined. The Performance Beef Breeders' Association have now accredited several technicians and software, databases and costing for receiving the data have been finalised at ABRI. Data is now accumulating slowly on those databases and AGBU will develop structural soundness EBV as part of future work when sufficient records are available to warrant the start of this work.

5.4 Multibreed EBVs

The project delivered to industry the first BREEDPLAN across breed EBVs. This was achieved via the publication of a simple conversion table (Table 1) that allowed the EBVs of four breeds to be directly compared for the full range of growth traits. The adjustment factors were computed by firstly establishing the breed differences for a given trait (e.g. 200 day weight) using the breed comparison data. The average EBV (e.g. 200d wt EBV) of the sires used from each breed from the own breeds BREEDPLAN run was compute. The adjustments were computed as the amount that would need to be added (or subtracted) from the mean EBV (i.e. adjusting for base difference) of the breed to reflect the observed differences. Presented in Table 1 is the amount that needs to be added to an existing EBV, in each breed, to make them comparable.

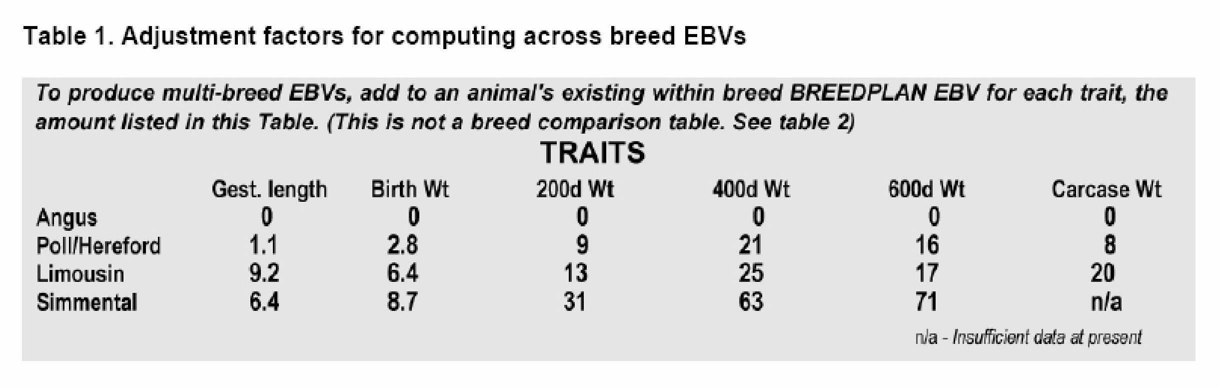


Table 1. Adjustment factors for computing across breed EBVs

To produce multi-breed EBVs, add to an animal's existing within breed BREEDPLAN EBV for each trait, the amount listed in this Table. (This is not a breed comparison table. See table 2)

	TRAITS					
	Gest. length	Birth Wt	200d Wt	400d Wt	600d Wt	Carcase Wt
Angus	0	0	0	0	0	0
Poll/Hereford	1.1	2.8	9	21	16	8
Limousin	9.2	6.4	13	25	17	20
Simmental	6.4	8.7	31	63	71	n/a

n/a - Insufficient data at present

The conversions were computed from data collected in the Victorian multibreed EBV Project and the Beef CRCI northern crossbreeding project. Several publications have accompanied this research and its implementation to industry [P13, C16, A8]. Research was also undertaken for other breeds but not released to Industry due to insufficient accuracies on the breed comparisons. As soon as additional data becomes available (e.g. Durham Shorthorn, Angus, Northern CRC2.3 project) these tables will be updated.

Alternative models of analyses and delivery were also examined as part of this research. A preliminary analysis of the combined Victorian data, utilising the facility to import the EBVs of the sires from the 4 breeds, was configured and run to give EBV for the four breeds simultaneously. Combining of breed databases into a single analysis produces EBVs that are comparable across breeds and has the added benefit of accommodating data from crossbred/composite animals. The complexities of running this experimental dataset provided valuable insight into alternative delivery methods of multibreed EBVs for the future.

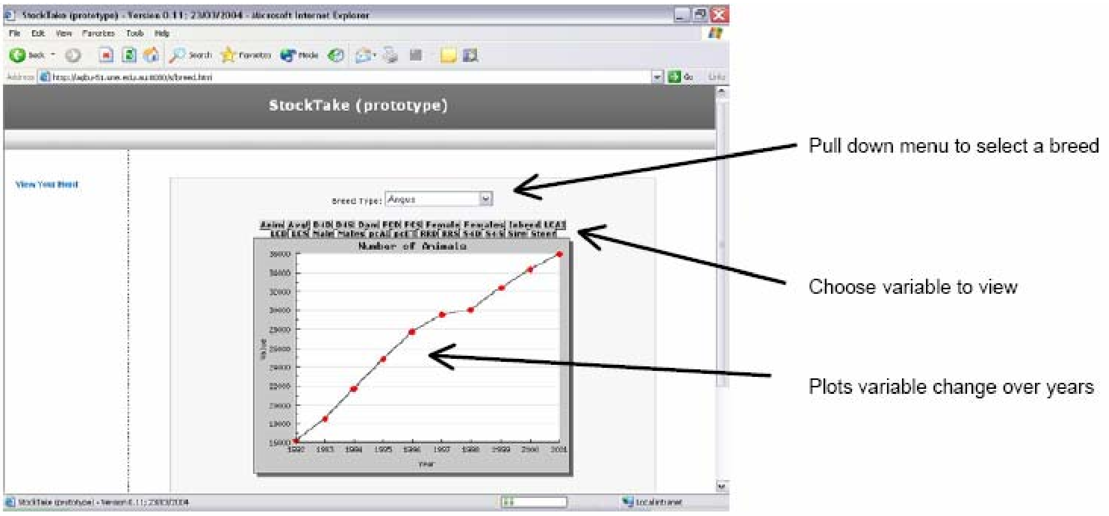
Although the research described above focussed on developing multibreed EBVs, several breeds (e.g. Limousin, Belmont Reds) have had their BREEDPLAN analyses configured to use the crossbred data analysis facilities of BREEDPLAN Version 4.2. This allows them to analyses straightbred and crossbred data simultaneously however it is currently a sub-optimal option. It is hoped the outcomes of this project and further data collection and sharing will lead to these breeds, and others, being able to greatly enhance their evaluations by using information (performance and pedigree) from combined breed databases (or adjustment tables).

5.5 Audit Software

StockTake software was developed during the project and has been designed to be run at the completion of a breed's BREEDPLAN run using existing input and output files. The software computes changes over time (e.g. last 15 years) for an individual breed for several important variables associated with the genetic profile of a breed. StockTake can also be used as genetic benchmarking tool to identify key performance indicators (KPI) of genetic progress across herds [R2]. The software computes numerous variables at the herd level over a defined period (e.g. 1995-2000). A stepwise regression procedure is used to identify those variables that explain differences between herd for genetic progress against a given $Index (or individual EBV). The significant variables are called key performance indicators (KPI) for genetic progress. Herds are then ranked against these KPI.

The software has been tested on all BREEDPLAN breeds and requires breed specific parameters (via an input controller file) to ensure consistent results. Some herds cannot be included in a StockTake analysis because they are too small or infrequent recorders.

To aid in the delivery and interpretation of results, both for a breed or individual herd, a web interface prototype has been developed at AGBU. Examples of the web interface for presentation of results are presented in Figures 4-6.

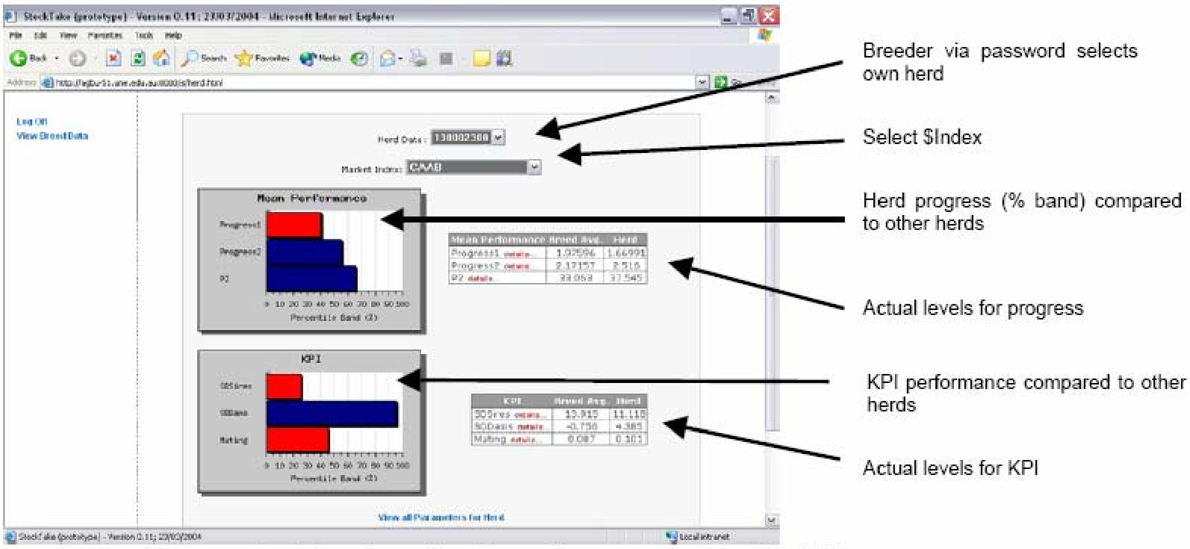


Pull down menu to select a breed

Choose variable to view

Plots variable change over years

Figure 4: StockTake output showing changes in a breed over time



Herd Data: 130002300

Market Index: CAAB

Mean Performance	Breed Avg.	Herd
Progress1 details...	1.07596	1.66991
Progress2 details...	2.17157	2.516
P2 details...	33.053	37.545

KPI	Breed Avg.	Herd
30Sires details...	13.915	11.116
90Dams details...	-0.756	4.385
Mating details...	0.087	0.101

Breeder via password selects own herd

Select $Index

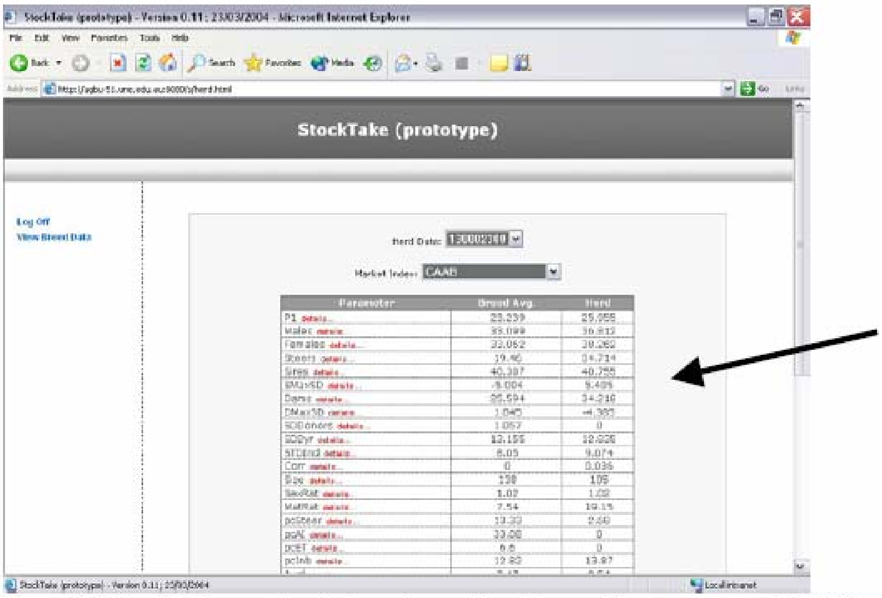
Herd progress (% band) compared to other herds

Actual levels for progress

KPI performance compared to other herds

Actual levels for KPI

Figure 5. StockTake output showing a herd's performance against the KPI



Herd Data: [illegible]

Market Index: CAAB

Parameter	Breed Avg.	Herd
P1 details...	23.239	25.055
Males details...	33.099	36.812
Females details...	33.062	38.262
Steers details...	19.46	14.734
Sires details...	40.387	40.755
SMaxSD details...	-5.004	5.405
Dams details...	35.594	34.216
DMaxSD details...	1.045	-4.305
SCDonors details...	1.057	0
SDDyr details...	12.155	12.026
STDInd details...	8.05	9.074
Corr details...	0	0.036
Size details...	138	105
SexRat details...	1.02	1.02
MatRat details...	7.54	10.15
pcSteer details...	13.32	2.60
pcAI details...	33.00	0
pcET details...	6.5	0
pcInb details...	12.92	13.87

Actual levels for non-KPI variables

Figure 6. StockTake output showing a herd's performance against the non-KPI variables

StockTake has currently been released to industry on a limited trial basis and the web prototype is under development (as shown above). Release to industry has been via StockTake reports containing tables of results and simple discussion of results [C17]. Feedback from industry indicated more graphical presentation would aid the interpretation of the results. Some breeders requested help in understanding the various genetic concepts presented, particularly as they relate to making changes to their breeding programs. Therefore additional diagnostics and simpler presentation of results from StockTake could be developed to assist with its adoption and use by breeders. It is planned that StockTake will be an integral part of the upcoming "BreedLeader" courses being developed by the National Beef Genetic Extension Team.

5.6 Strategic Research

5.6.1 Random regressions

The majority of time during the last three years was spent on research related to the application of random regression models to the analysis of growth data from beef cattle. This was supplemented by some theoretical work and program developments.

Analyses of beef cattle data
Following initial work which considered records from the Wokalup selection experiment, analyses concentrated on field data. Analyses can be divided into those considering "early" growth from birth to close to 2 years of age, and those including "mature" cow weight records.

An initial analysis of a large set of field data considered close to 368,000 records from birth to 820 days of age for just over 130,000 Hereford cattle. The model of analysis fitted a cubic regression on orthogonal polynomials of age at recording for direct and maternal, genetic and permanent environmental effects, and a step function for measurement error variances with 20 classes, resulting in 60 covariance components to be estimated. Results were presented at the Seventh World Congress on Genetics Applied to Livestock Production [P14].

In common with other analyses, estimates for the Hereford data were subject to “end-of-range” problems. A second study for the same range of ages considered data for Angus cattle, selecting only herds with a high proportion of animals with 3 or more weights recorded. This yielded a smaller data set with a better data structure (84,533 records on 20,731 animals), and allowed eleven combinations of orders of polynomial fit for the random effects fitted to be examined. Results showed consistent estimates for ages with many records, but that the form of the regression equation dominated estimates of covariances and genetic parameters for ages with few records, i.e. after birth to about 4 months of age and from about 650 days onwards. The previously favoured cubic regression model performed worst in terms of generating implausibly high estimates of variances for the highest ages. Results emphasized that there is limited scope to fit detailed random regression models for field data in beef cattle at the current data structure, and suggested that a model fitting a quadratic regression for direct genetic and both genetic and permanent environmental maternal effects together with a quartic regression to model changes in animals' permanent environmental effects was a reasonable compromise between detailedness of the model and data structure. This work has been presented at the 54-th annual meeting of the European Association of Animal Production [P15], and a full journal paper recently has been submitted for publication [P16].

Further analyses of this data set fitted a number of random regression models using the basis functions of B-splines as covariables. Using piece-wise, low degree polynomials rather than higher degree polynomials as in previous analyses was expected to be less affected by numerical problems. Results indicate that such models are a suitable alternative to orthogonal polynomials, which are more robust to “end-of-range” problems. A manuscript summarising this work is awaiting approval for publication [P17].

Sufficient mature cow weight records to attempt estimation of “lifetime” covariance functions are only available for Angus cattle. An initial analysis, including records up to 3000 days of age, was based on data available up to July 2002 and considered a single model of analysis only. On the whole, results [P18] agreed with expectations, showing genetic correlations of essentially unity among all ages from about 1200 days onwards, but were plagued by erratic estimates of variances at the highest ages. Further analyses, using data up to November 2003 and employing more stringent edits to ensure a higher average number of records per animal, are in process. These involve regressions on orthogonal polynomials of age as well as on basis functions of B-splines.

Evaluation of potential genetic gain

A simulation study was carried out to evaluate the potential, additional genetic progress which could be made if genetic evaluation considering birth, 200-, 400- and 600-day weights as separate traits were to be replaced by a random regression analysis for weights from birth to about 2 years of age. Results showed that, at the current data structure, gains in accuracy of genetic evaluation were modest and predominantly due to more appropriate modelling of covariances and genetic parameters. If the numbers of records were doubled, however, accuracies of genetic could be increased by about 5% across all animals. This emphasized that introduction of a random regression model for genetic evaluation would need to be accompanied by a recording scheme allowing for numerous weights to be worthwhile.

Results were presented as an invited paper in a symposium on “Application of Random regression Models in Animal Breeding" at the 2002 meeting of the American Society of Animal Science [P19], and have been published as a journal paper [P20].

Review
An invited paper on random regression models has been presented at the 54th session of the International Statistical Institute (ISI) [P21]. This has been expanded to a full review [P22] and submitted to ISI Review, but been considered unsuitable for that journal.

Methodological developments
Analyses of large sets of field data via restricted maximum likelihood proved computationally infeasible. Hence software ("RRGIBBS") to estimate covariance components for random regression models through Bayesian analysis, employing a Gibbs sampling algorithm has been developed. This is available to the animal breeding community for downloading from the AGBU website (http://agbu.une.edu.au/~kmeyer/rrgibbs.html), and has been demonstrated at the Seventh World Congress on Genetics Applied to Livestock Production [P23].

On the theoretical side, joint work with Mark Kirkpatrick from the University of Texas has addressed the use of principal component analysis within mixed model analyses, and the direct estimation of genetic principal components using restricted maximum likelihood (REML), both for random regression and standard multivariate analyses. This has been presented at the recent International Biometrics Conference [P24], and manuscripts describing the principles involved [P25] and the estimation via average information REML [P26] have been accepted for publication.

Prediction error covariances
Attempting to approximate accuracies of genetic evaluation from a random regression model yielded a general procedure to approximate prediction error covariances from the coefficient matrix in the mixed model equations, suitable for random regression analyses and multi-trait selection indexes. This work has resulted in two conference contributions [P27, P28] and a journal paper [P29].

5.6.2 Miscellaneous software development

"ITSUMCOV" software
A program, "ITSUMCOV" has been written to facilitate the pooling of results from individual analyses, each involving a subset of the traits of interest, to an overall, non-negative definite covariance matrix. "ITSUMCOV" carries out a weighted, iterative summation of partial, expanded covariance matrices, and is part of the "PDMATRIX" package available from the AGBU web site (http://agbu.une.edu.au/~kmeyer/pdmatrix.html). It has been presented at the Seventh World Congress on Genetics Applied to Livestock Production [P3].

"SECATEURS" program
Animals which do not have a record themselves and only have a single link to another animal in the pedigree, are uninformative for variance component estimation, and thus can be eliminated from the analysis. This is referred to as pruning of pedigrees, and can reduce the number of equations in the analysis substantially, in particular, if genetic maternal effects can be pruned separately. Whilst this is included in RRGIBBS, it is not available in most other software used to estimate genetic parameters. A program "SECATEURS" has been made available (http://agbu.une.edu.au/~kmeyer/prune.html) which allows this pruning step to be carried out independently. "SECATEURS" not only produces pruned lists of pedigrees, but can also set up the corresponding inverse numerator relationship matrices very quickly, and gives various characteristics of the pedigree and data structure. This software is now used to by AGBU scientists to reduce the number of animals in estimation runs thus reducing total computing time.

5.6.3 Incorporation of DNA information

Modifying BREEDPLAN EBVs

A number of direct markers or quantitative trait loci (QTL) for beef quality traits are now commercially available. This type of genotypic information can now contribute to the EBVs and Indexes produced by BREEDPLAN and BreedObject. The BREEDPLAN suite of analytical software has been enhanced with programs that adjust EBVs and hence Indexes after routine analyses. The process used to incorporate genotypic information into the EBVs is called 'de-regression'. At the end of the routine BREEDPLAN evaluation part of any genotyped locus's effect is included in the EBVs as shown in equation 1.

$$EBV^{*} = EBV + (1-acc2)*(F(g)-F(m)), \qquad (1)$$

where, EBV* is the modified EBV, EBV is the original EBV, acc is the accuracy of the original EBV, (F(g)-F(m)) is the difference between the effect of genotype (g) and the mean effect (m) of the locus in the population.

Therefore the proportion of the QTL effect that is included in the modified EBV depends upon the accuracy of the EBV. EBVs of genotyped individuals are adjusted to include that part of the locus's effect that has been omitted. The accuracy of the modified EBV is also adjusted to reflect the increase in accuracy resulting from the genotypic information as shown in equation 2.

$$acc^{*}=acc +(1-acc)*Vq \qquad (2)$$

where, acc* is the modified accuracy, acc is the original accuracy and Vq is the proportion of the genetic variance due to the QTL. The full procedure has been outlined in the internal discussion papers [C18, C19]. Other work reviewing and exploring possible methods of including QTL effects have also been published [P30, P31].

Given the present industry position of relatively few markers and relatively small proportions of our beef populations being genotyped, this method of 'de-regressing' EBVs has also recently been proposed by leading US scientists (e.g. Thallman, BIF, 2004). The results of a series of simulation studies illustrating the efficacy of de-regression were presented in a paper to the AAABG conference in Melbourne in 2003 [P32]. Besides knowing individual animals' genotypes, it is essential for this process that the effect each genotype for each locus has on each trait in the evaluation be known. A protocol for ratifying this type of information is under development with Genetic Solutions, the leading provider of gene tests for QTL for beef cattle carcase quality traits. It is proposed that an independent committee be established to ratify the information provided by organisations involved with genotypic testing for use in BREEDPLAN analyses. This will reduce the time from experimentation to implementation as results can be used before they are published. Once sufficient genotypic records are available in the BREEDPLAN database(s) the effect for any marker will be estimated for all traits in the evaluation. Many Breed Societies have prepared their databases to accept genotypic information and there are now a few thousand records for all markers in these databases. However, these markers are for traits that are not commonly recorded e.g. marbling in long-fed cattle, and tenderness.

Programs have also been written that use recorded genotypic information and the pedigree to infer the genotypes of unrecorded individuals where possible. This will assist industry to extend the value in their databases from genotyping. Results of basic research have been published on the effect of founder allele frequencies on the accuracy of estimating genotype probabilities [P33, P34, P35]. This research has been important for developing strategies for the inclusion of QTL data given that initially large numbers of animals in breed will not have genotypic data.

TG5 effects on BREEDPLAN traits

Research was undertaken to establish the size of effect of allelic variations in the thyroglobulin gene (TG5), known commercially as GeneSTAR marbling on existing BREEDPLAN traits. The analysis used all animals genotyped for TG5 recorded on the Angus BREEDPLAN database (N=901) and Angus animals evaluated in the Beef CRC straightbreeding project (N=698). The size of effect of TG5 was determined for a range of BREEDPLAN growth and carcase traits using various models. The results showed few statistically significant outcomes, with the exception that 2* animals were generally leaner than 0* animals. TG5 was not associated with any measures of intramuscular fat however some evidence existed for an effect on AusMeat marble score. The CRC Angus data are being further analysed by Genetic Solutions in combined meta-analysis of several experiments to help determine the most suitable estimate of the size of effect. Full results are presented in [C20, C21]. More conclusive results on the size of effect will be available when all the CRC1 animals have been genotyped and analysed. These data will also allow the estimation of the size of effect under grain versus pasture finishing and that different carcase weight endpoints (domestic and export).

CAST effect on meat quality traits

Calpastatin (CAST3) genotypes from the Beef CRC from 2861 and 2458 tropically adapted and temperate breeds, respectively from a sub-set of animals measured in the straightbreeding project were used to determine the size of effect on several key meat quality traits, in particular measures of meat tenderness. Estimates of gene frequencies, allelic contrasts and the variance due to the QTL were computed separately for the tropically adapted and temperate breeds [C22]. Results showed a consistent effect of the 2* genotype compared to the 0* genotype for tenderness traits e.g. -0.18 to -0.27 kg for shear force (SF). The proportion of phenotypic variance explained by CAST for other traits studied was generally very small, for SF the proportion explained was 1.2% for both temperate and tropically adapted breeds. On a small sub sample the effect of the different CAST genotypes on MSA tenderness was negligible, particularly for the temperate breeds. These results, and the genotypes, will form the basis of the development of a tenderness EBV using phenotypic and molecular data in the future.

5.7 Computing

5.7.1 Parallel processing solver

A new solver capable of exploiting multiple CPUs has been developed and is based on the pre-conditioned conjugate gradient (PCG) algorithm. The PCG algorithm is more efficient than that currently used in BREEDPLAN, namely successive over relaxation. The PCG algorithm is so called because a pre-conditioner is used to expedite the solving process. Different pre-conditioners can increase the rate of convergence.

In single processor mode, the new algorithm is significantly faster than the previous one but its advantage depends upon the nature of the problem and tends to increase with the complexity (numbers of animals and traits) of the problem.

The new solver has been designed to exploit the use of clustered CPUs rather than single computers that have more than one processor. However, it can be used on single and multi-processor computers. The algorithm was developed after a detailed analysis of the equations that are solved in BREEDPLAN was undertaken. This was done to ascertain alternative ways that the problem can be partitioned among a number of processors, and choose on a theoretical basis that which minimises the total elapsed time. Further testing continues of all BREEDPLAN features, different pre-conditioners and alternative methods of partitioning equations among processors. The new solver will greatly reduce the solving time for all BREEDPLAN runs and will significantly increase the feasibility of running more complex models, including the possibility of large multi-breed analyses in the future.

5.8 Communication and Dissemination

5.8.1 Dissemination

The project was very focused on the dissemination of research outcomes and provided support and leadership to the industry to encourage adoption of the technologies. The most significant vehicle for the delivery of research to industry was through continual implementation of outcomes into BREEDPLAN and BreedObject and the close interaction with industry through the BREEDPLAN Technical Liaison Group that met 4 times per year. In addition, outcomes were disseminated to both the scientific community and the beef industry by many means including: presentations at numerous conferences and breed Society Board meetings, workshops and seminars, field days, industry and producer newsletters, commercial media, web pages and farm visits. All these mechanisms were aimed at increasing the use of improved genetics in beef cattle enterprises and therefore increasing the rate of genetic gain in seedstock herds and making commercial breeders more profitable.

Industry liaison to develop BreedObject indexes continued to be a major extension activity for the AGBU beef team. During the project the number of standardised breed indexes has grown to 24 (see section 1.1). Standard indexes include breed society sponsored indexes as well as indexes developed for major pastoral companies. Publication of BreedObject indexes has forged closer ties between AGBU and the seedstock industry. BreedObject is one of the major subject areas for extension but has often proved to be a conduit into more detailed BREEDPLAN extension i.e. questions on BreedObject often lead into broader BREEDPLAN discussions. This is a growing area that will need to be serviced in future.

Listed below is a sample of the types of communication activities involving all members of the AGBU beef team throughout this project.

Presentations to conferences and workshops

- World Congress on Genetics Applied to Livestock Production • International Biometrics Conference
- International Statistics Institute meeting
- AAABG conferences • Annual INTERBULL conference
- European Association of Animal Production conference
- American Association of Animal Science annual meeting
- Aust. Vet. Assoc. annual conference
- NSW Ag Annual Beef Conference
- US Beef Improvement Federation Annual Conference
- Armidale Feeder Steer schools
- NT Cattlemen’s Assoc. Annual Conference
- AGBU workshop
- MLA “Proof of Profit” Workshop

- Lectures and practical for UNE Feedlot Management Course
- NZ Hereford BREEDPLAN workshop
- Visiting NSW Minister for Agriculture
- World Hereford Congress
- WA Effective Breeding Workshop
- MLA Genetic Horizon Conferences
- Advanced Genetic Solutions Workshop

Field days

- MLA Meat Profit Days
- Durham R&D project field day
- Hereford Society breeding field day
- Victorian Beef Week presentation
- Singleton Beef and Land Management Association
- “Te Mania” annual team day
- “Rangers Valley” field day
- Reiland Angus Client breeding forum

Presentations to Boards and groups

- MLA Board • MLA Beef Genetics Consultative Group
- Montana State University students
- Iowa State University Extension team
- BREEDPLAN technical liaison group (BTLG) quarterly meetings
- BREEDPLAN Lecture series WA Animal Science
- South Devon meeting
- Australian Hereford Board
- Durham R&D Board
- Shorthorn Board
- Wesfarmer State managers
- Genetic Solutions

Written material and articles

- Numerous scientific publications (see Annex R, P, C, A)
- BreedObject Newsletter
- Genetics material for MLA’s “More Beef from Pastures”
- Articles written for each annual edition of BREEDPLAN news
- Articles for Feedback magazine
- Article for Prograzier magazine
- Articles for Breed Society and breeder publications
- BREEDPLAN fact sheets
- Press releases

5.8.2. National genetics extension team

During the project the MLA national genetics extension team (NBGET) was formed and gained separate MLA funding. This group was an initiative of the MLA Strategic Plan for Beef Genetics. An integral part of this plan was to develop national extension strategies for beef genetics. Due to the close association of members of the AGBU beef genetics team with the industry, we were invited to convene a National Beef Genetics Extension Team with objectives to:

1. Define constraints to adoption of beef breeding technology

2. Develop a National Beef Genetics Extension plan to achieve the goals of the MLA Strategic Plan.

MLA accepted the proposed plan and the resulting project submission was funded for a one year period from January 2004. The National Plan for Beef Genetics included extension of all sources of genetic improvement e.g. crossbreeding, gene markers as well as the products from the AGBU project. BREEDPLAN related projects constituted the largest component of the extension effort and the AGBU beef team have made significant contributions to the extension project over the last twelve months with the extension project supplying the vehicle and the AGBU team supplying much of the information. A new extension project submission is currently being prepared and it is expected the new AGBU project with MLA will be required to assist in servicing the extension plan.

Activities of the NBGET, involving participation of the AGBU beef team include:

- “Proof of Profit” Workshop

- Writing of MLA “Tips and Tools”

- Armidale, Hamilton and Rockhampton MLA Beef Genetics Horizons Workshops
- Production of educational CD Rom

6. SUCCESS IN ACHIEVING OBJECTIVES

The project has clearly met its objectives and several others that developed through the project.

- The BREEDPLAN and BreedObject genetic technologies have been greatly improved for all users and the benefits of these improvements will be realised through increased accuracies of EBVs, greater ability to meet market specifications, more focused breeding objectives and faster rates of genetic progress.

- Through the use of the BreedObject software, we have been able to monitor and report genetic trends for profitability across all breed, production x market systems.

- New traits have been introduced into the BREEDPLAN system including, net feed intake and IGF-I along with important developments in the use of AI joining data for days to calving EBVs and flight time data as a measure of temperament and tenderness.

- Multi-breed EBVs are available through individual breed BREEDPLAN analyses and across breed EBVs via the publication of an adjustment table for Angus, Hereford, Limousin and Simmental breeds.

- StockTake software was developed and allows genetic benchmarking of breeds and individual breeders within breeds for key performance indicators associated with genetic progress against BreedObject $Indexes.

- Extensive evaluation of random regression techniques for the beef industry lead to the development of new and novel procedures for estimating variance components and accuracies for random regression models and provides clear directions for changes to recording practices and computer requirements necessary to capture the benefits.

- Procedures to incorporate direct DNA markers into BREEDPLAN have been developed and are ready for testing and subsequent implementation.

- A new procedure to take advantage of multi-processor computers has been written and offers substantial increases in computing speed and power.

- Implementation and communication of the research outputs and knowledge have occurred throughout the project.

Areas of planned research that require further work or implementation are:

- Implementation of Version 5.0
    - ◊ Inclusion of NFI and IGF-I into the full multi-trait system
    - ◊ Develop structural soundness EBV module
    - ◊ New solver

- Full Industry release of StockTake

- Development of “data audit” software

- Industry implementation of the new procedure for using direct DNA markers