Development and implementation of multi-breed genetic evaluation systems for the Australian beef industry

Abstract

The development of multi-breed genetic evaluations offers a number of potential benefits for Australian cattle breeders. Primarily, multi-breed evaluations offer a tool to optimise genetic gain through the provision of clear and readily-available comparisons to select genetics which best suit production environment, breeding objective and target markets. Development of multi-breed evaluations within the BREEDPLAN service would assist in maintaining a national evaluations system and common language and minimise the need for breeders to seek similar services overseas.

In this project the work has concentrated on the review of current client databases, including industry research databases, and investigated those with potential linkage to other breed databases and/or to other multi-breed, crossbred and/or composite breed databases. BREEDPLAN test analyses were conducted to determine overall data structure and connectedness in terms of progeny performance records.

In terms of genetic evaluation, the current BREEDPLAN software can accommodate multi-breed datasets. There is however a priority for research to enable the handling of genotypes from multiple breeds in a multi-breed Single-Step BREEDPLAN analysis.

Currently available data from commercial sources does not provide sufficient quality data to enable the development of multi-breed evaluations. Data limitations still exist for other than the four Tropical breeds involved in the Repronomics research project. There is a need for industry investment to create sound research datasets to allow for breed and trait comparisons, particularly for maternal traits. This needs to be followed by ongoing quality data collection to maintain linkage.

Executive summary

The development of multi-breed genetic evaluations offers a number of potential benefits for Australian cattle breeders. Primarily, multi-breed evaluations offer a tool to optimise genetic gain through the provision of clear and readily-available comparisons to select genetics which best suit production environment, breeding objective and target markets. Recent industry survey results show significant percentage of respondents want multi-breed Estimated Breeding Vales. Development of multi-breed evaluations within the BREEDPLAN service would therefore assist in maintaining a national evaluations system and common language and minimise the need for breeders to seek similar services overseas.

Previous research conducted by the Animal Genetics and Breeding Unit (AGBU) and database and system development work conducted by the Agricultural Business Research Institute (ABRI) has demonstrated proof-of concept and established the basic systems for conducting multi-breed (or across-breed) genetic evaluations for beef cattle. That work also identified that there are significant gaps in the data available for comparing animals from different breeds and crosses, meaning that not all breed combinations can be reliably compared, and only some traits can be analysed for comparison.

In this project, ABRI's work has concentrated on the review of current client databases, including industry research databases, and investigated those with potential linkage to other breed databases and/or to other multi-breed, crossbred and/or composite breed databases. BREEDPLAN test analyses were conducted to determine overall data structure and connectedness in terms of progeny performance records.

ABRI has a commercial process whereby multiple datasets can be sourced and used to create larger combined extracts, for use in research or in routine genetic evaluation using BREEDPLAN. As was demonstrated in this project, ABRI is currently able to create a range of data extracts in which different sources of breed data were combined, often with the inclusion of multi-breed research data.

In terms of genetic evaluation, the current BREEDPLAN software can accommodate multi-breed datasets. The expression of heterosis in multi-breed performance data can be accounted for and a sophisticated approach to the formation of genetic groups allows for breed differences in foundation animals to be modelled, including changes over time in each breed population. However, there are a number of technical issues that need to be addressed and each of these will require research and development input. In particular, it should be a research priority to enable the handling of multiple breed genotypes in a multi-breed Single-Step BREEDPLAN analysis.

The development of multi-breed evaluations relies on well-structured research data that provides the necessary head-on-head comparisons across a number of relevant traits. Currently available data from commercial sources does not provide sufficient quality data to enable the development of multi-breed evaluations. Data limitations still exist for other than the four Tropical breeds involved in the Repronomics research project. There is little or no linkage between other breeds and for traits other than growth traits. There is a need for industry investment to create sound research datasets to allow for breed and trait comparisons, particularly for maternal traits. This needs to be followed by ongoing quality data collection to maintain linkage.

The British and European breeds (or at least a sub-set of the significant breeds) require well-structured research projects to supply data for multi-breed evaluations. This would be in a similar manner to how the Repronomics project has facilitated the Tropical multi-breed analyses. The New

South Wales Department of Primary Industry's multi-breed project has the potential to supply the core of this information for some breeds.

The data collected as part of ongoing projects needs to be recorded (in BREEDPLAN-ready format) in database(s) that allow for access by multiple users. That is, the data should be stored in industry databases where access and usage is determined by technical criteria. The challenge will be to continue the collection of the necessary records beyond the initial research projects.

ABRI is transitioning clients to multi-breed analyses of increasing complexity as data becomes available. At completion of this project, a number of BREEDPLAN evaluations are using (or soon will be using) multi-breed data on a routine basis in the calculation of EBVs. These are the:
- Southern Limousin evaluation,
- Single-Step Brahman evaluation,
- Santa Gertrudis evaluation,
- Droughtmaster evaluation, and
- Belmont Red evaluation.

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1   Background

Previous research conducted by the Animal Genetics and Breeding Unit (AGBU) with MLA co-funding (project B.BFG.0050) and database and system development work conducted by the Agricultural Business Research Institute (ABRI) (including project BFGEN.006) has demonstrated proof-of concept and established the basic systems for conducting multi-breed (or across-breed) genetic evaluations for beef cattle. That work also identified that there are significant gaps in the data available for comparing animals from different breeds and crosses, meaning that not all breed combinations can be reliably compared, and only some traits can be analysed for comparison.

This project will identify all suitable datasets for multi-breed analysis, including both industry and research data, and conduct research into the extent to which use of existing pedigree and genomic data can enhance multi-breed evaluation. At the same time, it will identify the data gaps – both breed comparisons and traits – in the currently available data, to inform current and future investment into data collection. Finally, the project will provide updated information on multi-breed genetic evaluation, including both its strengths and limitations, to assist industry stakeholders in evaluating the benefits of using multi-breed evaluations as part of industry's ongoing genetic improvement program. This will include options for using international data within multi-breed evaluation in Australia, and identify the data-sharing arrangements that will be needed to allow this to proceed.

Three main outputs would require specific dissemination or commercialisation methods:
- Producing industry reports that outline the main results including estimates of breed differences for the traits that can be analysed reliably, and results outlining the potential extent and value of selection across breeds for individual traits and combinations of traits. The exact format of results relating to individual animals would be defined in consultation with the data providers, including breed societies. The reports could be both hard copy and on-line, including searchable lists. This information would be widely available to whole of industry.
- Industry information on how to optimise future or ongoing multi-breed evaluation, including how best to fill data gaps and how best to utilise commercial production data. This information would be primarily to help R&D investors and industry stakeholders plan forward investments in data collection.
- The system (databases and data processing pipeline) would be available as part of the overall BREEDPLAN system, and could therefore be accessible potentially to anyone who wished to submit appropriate data.

2   Project objectives

The project objectives were

a)   Identification of all datasets that are actually multi-breed within the current breed and research databases, and collation of a single dataset for research analysis

b)   Updated multi-breed evaluations for British, European and Tropical breeds, using all data currently held in breed and research databases. Approval for use of breed data will need to be sought, but it is not anticipated that it will be withheld for research analysis. The analysis will make use of genomic information where available within-breed and across-breed, to evaluate the extent to which this increases the accuracy of the across-breed evaluations.

c) From these evaluations, precise definition of the data gaps – what breed comparisons can and cannot be made reliably for what traits. This information can help prioritise future data collection in research and industry herds and projects.

d) Via consultation with commercial producers and processors, identify available datasets that include multi-breed data. Once identified, inclusion of that data into the multi-breed evaluations to determine the extent to which the commercial data improves the scope (breed and trait coverage) and power (accuracy) of the evaluations. These results will provide clear information to help breeds and other stakeholders make informed decisions about the value of contributing data to, and participating in, multi-breed evaluation, and provide industry with reliable information on the value of conducting regular or routine multi-breed evaluation.

e) Fully operational systems in place in ABRI to conduct routine multi-breed evaluations.

f) Via consultation with key industry stakeholders, including breeds, processors, commercial producers and MLA and R&D providers, a strategy for ongoing multi-breed evaluation – what breed and trait groups could be included, what datasets could be accessed for inclusion, formats and delivery systems for results.

g) A strategy for ongoing data collection to support reliable multi-breed genetic evaluation: what breed comparisons need to be conducted and/or continued, and what data to collect where and on what traits.

3 Methodology

3.1 Access and review of relevant cross-reference information

Subject to approval being provided, ABRI reviewed client databases and gained access to those with potential linkage to other breed databases and/or to other multi-breed, crossbred and/or composite breed databases. ABRI also manages two databases that are used to store pedigree and performance data that has been submitted for BREEDPLAN evaluation from a number of formal research projects. The objective of these databases is to enable data to be available for use by industry to support their genetic evaluations. One database relates to the northern or Tropical breeds (the Northern Multi-breed Research database) and the other contains data from British and European breeds (the Southern Multi-breed Research database).

All clients of ABRI have the ability in their current database (ILR2) software to store additional identifications for animals from outside their breed (i.e. store the original identifier of individuals from other country and/or breed societies). This information provides the cross-reference information needed if data extracts from different sources are to be combined. It is also the basis for determining genetic linkage across source / data extracts.

ABRI conducted a review of the cross-reference information held across all databases with potential for inclusion in larger multi-breed evaluations. Updating of the cross-reference information was conducted, where necessary.

3.2 Create multi-breed data extracts for routine BREEDPLAN evaluation

Pedigree and performance extracts were obtained for each ILR2 database identified as having cross-reference information available for potential combining with other breed or multi-breed data

extracts. Use was then made of ABRI cross-reference software and ABRI data merging software to create the larger "across-breed" or "multi-breed" extracts as required for routine BREEDPLAN evaluation.

This was undertaken for the British, European and Tropically-adapted breeds in Australia, making use of either the Northern or Southern Multi-breed Research databases where appropriate. Data extracts for the Simmental, Brahman and Simbra breeds in South Africa were also used to create a multi-breed extract for South Africa. Likewise, data extracts from South Africa, New Zealand and the USA were used to create multi-country multi-breed extracts.

3.3 Review contemporary group structures arising from test evaluations using current BREEDPLAN software

Assuming there is sufficient pedigree linkage between and within the extracts combined for multi-breed evaluation, a second key component is the extent to which there are head-on comparisons between each breed and trait combination. That is, head-to-head comparisons of animals of at least two "breeds" (i.e. can be pure breeds as well as composite and crossbred types) must be represented in the combined data extract, with pedigree links back to those breeds and with performance measurements recorded in the same management groups. Without such head-on comparisons, there will be limited capacity to rank all animals of differing breed type and content for genetic merit on the same scale.

ABRI conducted test evaluations using current BREEDPLAN software for each of the multi-breed extracts created in section 3.2, and reviewed the structure of the data in terms of multi-breed representation within contemporary groups by trait. Importantly, the EBVs calculated in these test evaluations were of no relevance to the current project, as they are subject to assumptions made regarding covariance components used in the test evaluations. The latter were determined by the primary breed represented in the test evaluation and are unlikely to be relevant for all other breeds and breed types represented.

3.4 Provide AGBU with access to multi-breed extracts and output files arising from test evaluations using current BREEDPLAN software

AGBU were notified of the availability of multi-breed extracts and given access to the output files arising from the test evaluations completed by ABRI.

3.5 Implementation of routine BREEDPLAN evaluations using multi-breed data

Subject to technical review by AGBU and approval from the relevant breed society or societies, multi-breed data will be included in the routine BREEDPLAN evaluation conducted by ABRI on behalf of the client.

3.6 Survey ABRI clients and stakeholders on priority for access to multi-breed EBVs

ABRI has conducted a survey of its Australian clients (i.e. breed societies) to ascertain attitudes and priorities regarding the development of across-breed BREEDPLAN evaluations. ABRI also conducted a separate survey of the attitudes and priorities of key industry stakeholders, targeting the attendees at the BREEDPLAN Champions workshop held in February 2019.

The surveys were created using SurveyMonkey and sent via email to survey recipients. The survey questions are shown in the Appendix – section 8.1.

4 Results

4.1 Multi-breed datasets in Australia

Table 1 provides a summary of the current situation with respect to multi-breed datasets and linkages for the major Australian breeds in the Tropical, British and European groups.

Table 1 Summary of multi-breed datasets in Australia

British breeds	Southern Multi-breed Research database - ABRI	Multiple research projects and sires from 3 British breeds represented
	Angus	Links to Red Angus and Murray Grey plus Multi-breed register - links to Brangus, Simmental, Shorthorn
	Hereford	Black Baldy BIN data
	Murray Grey	links to Angus
	Shorthorn	links to Performance Herds Australia and Beef Shorthorn
	Performance Herds Australia	identified links to Shorthorn, Wagyu, Senepol, Angus, Red Angus and Brahman
	Red Angus	links to Angus
European breeds	Southern Multi-breed Research database - ABRI	Multiple research projects and sires from 3 Euro breeds represented
	Limousin	BIN data in Southern Research database and links to Angus
	Charolais	BIN data
	Simmental	links to Angus
	Gelbvieh	links to Angus and Brahman
Tropical breeds	Northern Multi-breed Research database - ABRI	Repronomics and CRC data linking Brahman, Santa Gertrudis, Droughtmaster and tropical composites
	Tropical Composite	Belmont Red-based composites with links to Senepol and Brahman
	Belmont Red	Belmont Red and composites
	Brangus	links to Brahman and Angus
	Nindooinbah Ultrablacks	links to Brangus and Angus

In addition to the breed groups identified in the original project, the Wagyu breed currently has limited crossbred data on file. This data is predominantly from Angus cross animals with no identifiable links to Angus.

4.2 British and European breeds

ABRI's initial investigations indicated that linkage between current British breed society databases would be limited. For example, the Hereford database was, until recently, restricted to purebreds

only. ABRI has had discussions with society staff regarding the introduction of animals from the Black Baldy BIN project, where Hereford/Angus cross animals are represented. The Angus database includes a Multi-breed register and there is limited representation of other British breeds such as Murray Grey, Red Angus and Shorthorn. The duplication of animal and performance records for Murray Grey and Red Angus herds will potentially pose problems for combining datasets. The Angus database also has links with Tropical breeds through Brangus and Ultrablack animals recorded with performance.

The Performance Herds Australia database is predominantly Shorthorn based but does include other breeds from differing breed groups. The majority of the crossbred performance involves Angus and Red Angus animals. There are also links to tropical breeds through the use of Senepol genetics.

For the European breeds, the major linkages between the three significant breeds relate to common usage of Angus genetics (in Limousin and Simmental) and from the BIN data recorded for Charolais and Limousin (which included crossbred data).

The Southern Multi-breed Research database hosted by ABRI does contain data from both British and European breeds. There are a number of breeds represented across a number of research projects and over a number of years. Most of the data recorded is historic and does not represent current genetics. The research projects were undertaken in the late 1980s and 1990s, and included the Grafton project, the Struan cross bred trials, the Southern Crossbreeding Trial (SBEF.006) and the Regional Combinations project. The most recent data relates to the Limousin Beef Information Nucleus (BIN) project.

Sires in the database represent Angus, Brahman, Belgian Blue, Friesian, Hereford, Jersey, Limousin, South Devon, Simmental and Wagyu. Performance data covers birth, weights, ultra-sound scan and carcase traits. Table 2 summarises the total number of sire breeds represented and the total number of progeny records for 200-day weight and carcase weight on the Southern Research database.

Table 2 Sire breeds represented in Southern Multi-breed Research database

Breed of sire	No. of Sires	Total progeny records	
		200-day weight	Carcase weight
Angus	69	2,412	1,968
Limousin	65	1,435	938
Hereford	29	740	281
Simmental	22	599	171
Wagyu	27	486	465
Belgian Blue	20	224	210
South Devon	15	171	145
Charolais	13	53	49
Shorthorn	11	24	20
Other	16	232	168
Unknown	207	209	217
Total	**494**	**6,556**	**4,642**

Analysis of the Southern Research data using a BREEDPLAN crossbred model with pre-adjustment for heterosis permitted detailed investigation of within- contemporary group representation of multi-breed performance data. Table 3 summarises the 200-day weight and carcase weight data of progeny in such groups, indicating that Angus- and Hereford- crossbred progeny are the most well represented and sometimes in comparison with purebred progeny.

Table 3 Breed representation in Southern Multi-breed Research data - contemporary groups containing 2 or more breed

Breed of progeny	200-day weight	Carcase weight
Angus	790	636
Angus-X	2,813	2,038
Hereford	541	217
Hereford-X	1,916	1,191
Limousin-X	88	92
BelgBlue-X	214	190
Wagyu-X	65	75
Crossbred	54	54
Total	**6,481**	**4,493**

However, much of the Southern Research data represents historic sire usage since most progeny are born prior to 2005 (Table 4). The more recent data (calving years 2010-2011) relates primarily to the Limousin BIN herds, representing the Limousin breed and Angus crossbreds (including crosses with Limousin).

Table 4 Distribution of Southern Multi-breed Research data - breeds by year of birth

Year	Breed of progeny									
	AA	AA-X	HH	HH-X	LL	LL-X	BL-X	WY-X	Other	Total
1994		35	25	199			55			314
1995		58	42	189			43			332
1996		46	27	202			41			316
1997		26	25	172			46			269
1998	75	368	158	326						926
1999	96	591	253	509						1,449
2000	32	121	11	21				20		205
2001	52	278		117		16	2	17		482
2002	159	349		113		4		9	31	665
2003	237	390		68		34	27	19	6	781
2004	140	140							17	297
2010		200			20					220
2011		211			14					225
Total	**790**	**2,813**	**541**	**1,916**	**34**	**54**	**214**	**65**	**54**	**6,481**

The Southern Research data is currently used in the monthly Limousin BREEDPLAN production run combining Limousin data for Australia/New Zealand, South Africa and Namibia. The Southern Research data contributes to EBV calculations as well as improving the modelling of genetic group solutions for non-Limousin breed content represented in the analysis. More recently, ABRI extended this analysis to include the Simmental and Charolais breeds, in a test analysis of Australian European breeds. A BREEDPLAN crossbred model was used, allowing head-to-head comparisons between animals of different breed content within the same contemporary group. Pre-adjustments for heterosis and non-genetic effects (e.g. age at measurement; age of dam) were based on Limousin BREEDPLAN parameter files, irrespective of the actual breed of the individual animal. Each of the three breeds has progeny performance data recorded in their respective Australian breed database. However, as summarised in Table 5, Limousin is the only breed to benefit from additional progeny data in the Southern Multi-breed Research database. Only two of the Simmental sires represented on the research database could be matched to sires registered on the Australian Simmental

database, such that the research database records only contributed a further 48 performance progeny. While most of the Charolais sires on the research database were matched to sires registered on the Australian Charolais database, progeny records gained from the research database were minimal.

This suggests limited opportunity in using the Southern Multi-breed Research database to provide sufficient linkage for a combined European breed analysis. It also suggests little if any gains to be made in adding the research data to the BREEDPLAN evaluations for either Simmental or Charolais.

Table 5 Limousin, Simmental and Charolais sires registered with their respective Australian breed associations and represented in Southern Multi-breed Research progeny data

Sire Breed	No. sires	200-day weight progeny	
		Total recorded	via Research Database
Limousin	60	6,030	1,339
Simmental	2	147	48
Charolais	11	1,192	14

4.2.1 Hereford

Australian Hereford has two MLA Donor Company funded research projects. The Beef Information Nucleus (BIN) research project has involved the collection of data on purebred Herefords whilst the Black Baldy project is designed to build on the BIN project. The Black Baldy project is a structured Hereford x Angus cross breeding trial using Hereford and Angus sires over commercial Angus cows.

The Black Baldy trial has four primary objectives and each address limitations to current Hereford genetic evaluation. Significantly, a major objective is to generate data that will aid evaluation within and across breeds.

At present the Hereford BREEDPLAN evaluation includes data from Australia, New Zealand and Namibia and is restricted to analysing performance data from purebreds only. Both the BIN data and the Black Baldy data are recorded in the Hereford database but the current analysis only analyses performance data from purebreds. ABRI has been assisting Herefords Australia with the development of their Black Baldy data and potential inclusion in a crossbreed Hereford analysis. ABRI will be in a position to run a test analysis on the full crossbred data when HAL staff are confident of the correct recording of the Black Baldy animals. The Black Baldy data could provide valuable multi-breed data for inclusion in the Hereford analysis.

4.3 Tropical breeds

The Tropical breeds do not currently have direct major linkages between the breed society databases. They do however have the benefit of the multi-breed reference dataset in the Northern Multi-breed Research database. Data comes from both the Beef CRC and the MLA funded Repronomics™ Project (B.NBP.0759) and includes pedigree and phenotypes, some of which are new traits, and provide high quality records for multi-breed evaluations for the participating breeds – Brahman, Santa Gertrudis, Droughtmaster and tropical composites. This data has been used in combination with the relevant breed society databases to conduct multi-breed BREEDPLAN evaluation, initially for research purposes, but ultimately as regular production services.

In addition to the breeds included in the Repronomics™ Project, ABRI investigated the potential for combining data from other databases hosted by ABRI. These include data from NAPCO (tropical composites), Nindooinbah (Ultrablacks and tropical composites), Belmont Red (tropical composites)

and individual herds from ABRI's Tropical Composite database (which is a service provided to breeders outside of any company or breed society structure).

ABRI's work in this project concentrated on the preparation and analysis of multi-breed data for the Tropical breeds. This work on Tropical breeds was identified as a priority to AGBU's work plan but also as an industry priority. These developments have led to the introduction of two Tropical multi-breed BREEDPLAN analyses into production during 2018 (Brahman) and early 2019 (Santa Gertrudis). A third multi-breed evaluation (Droughtmaster) is scheduled for production in early 2020 whilst development work is continuing for the Belmont Red and Tropical Composite databases.

Initially, work for the Tropical breeds focused on combining the Northern Multi-breed Research data with that of the Brahman breed. This involved utilising ABRI's existing cross-referencing system to include the animal identifiers for the animals from the Repronomics project with the identifiers of animals in common with the Australian Brahman database. ABRI then provided combined datasets to AGBU for testing of data structure. In August 2018, ABRI launched into production a Brahman multi-breed analysis which included the Northern Multi-breed Research dataset. This analysis includes Brahman genotypes and is analysed using Single-Step BREEDPLAN software.

A similar approach was followed to complete the work of combining the Northern Multi-breed Research data with that of the Santa Gertrudis breed in Australia. ABRI's cross-referencing software was used to include the animal identifiers for the animals from the Repronomics project with the identifiers of common animals in the society database. These details were then provided to AGBU for checking. A combined Santa Gertrudis/Multi-breed dataset was subsequently provided to AGBU for testing. In February 2019, ABRI launched into production a Santa Gertrudis multi-breed analysis, utilising the Northern Multi-breed Research data. Although the job stream has been configured to use genomics (when available), a Single-Step BREEDPLAN analysis has yet to be completed. This development requires further input from AGBU.

ABRI has also completed the work of combining the Northern Multi-breed Research data with that of the Droughtmaster breed in Australia. Data files of a combined dataset were provided to AGBU and further developments are pending.

In addition to the high priority work to develop multi-breed analyses for the Australian breeds, ABRI has completed additional test analyses. In January 2019 ABRI supplied AGBU with the results of two major multi-breed test analyses, one relating to Australian datasets and the second including data from additional countries.

The first test analysis combined Australian Brahman, Santa Gertrudis and Droughtmaster data with the Northern Multi-breed Research data, to create a "Northern Tropical Breed" extract. The analysis was configured as per the current Brahman Single-Step BREEDPLAN analysis, including Brahman-specific parameter files and a G-matrix comprising Brahman genotypes only. The aims of this test analysis were:
  (i)   to develop a more practical and dynamic pathway for combining a number of "breed specific" and multi-breed data extracts;
  (ii)   to provide AGBU with a larger combined dataset for review of data structure; and
  (iii) to determine if convergence could be achieved in this analysis.

Given that aims (i) and (iii) were achieved, a second test was conducted to expand the range of data sources involved. This test analysis combined the Northern Multi-breed Research data with data from Australian Brahman, Australian Santa Gertrudis, Australian Droughtmaster, American Brahman, South African Brahman and Namibian Brahman, to create a multi-breed and multi-country

"International Tropical Breed" data extract. This test was also configured as per the Brahman Single Step analysis, with some revision to ensure the correct identification of animals and their records. This analysis was undertaken with a goal to fostering further discussion between AGBU and ABRI as to what can and can't be achieved in terms of multi-source (country and breed) Single-Step analyses given the current BREEDPLAN software. Such discussions have not as yet been held, given the limited availability of relevant AGBU staff in 2019.

In the Tropical breeds, ABRI has been assisting individual breeders who are currently breeding crossbreds or composites cattle and who operate outside of a breed society. ABRI is providing such a service through the Tropical Composite database. Initial enquiries have been from breeders with Belmont Red and Brahman-based breeding operations. ABRI will be investigating combining this database with the Northern Multi-breed Research database to enable valid multi-breed comparisons. Outcomes from this research may then provide opportunities for individual breeders of Belmont Red and Brahman-based breeding operations to have their data included in a future "Northern Tropical Breed" BREEDPLAN evaluation. This would constitute an important step in the research and development of multi-breed genetic evaluations for the northern Australian beef industry.

ABRI has undertaken developments to re-include the Northern Multi-breed data into the Belmont Red analysis. These datasets were originally combined in 2014 but the Belmont Red Association subsequently requested the removal of the research dataset due to concerns over the genetic trends that were reported from the analysis, particularly following the addition of significant additional research data. ABRI has now developed processes to report genetic trends on a "breed database" level, rather than reporting genetic trends on the basis of the entire population of animals represented in the analysis of combined databases. This approach has already been implemented in the Brahman and Santa Gertrudis BREEDPLAN evaluations, such that each breed only reports the genetic trends based on animals of relevance to their respective databases. ABRI is expecting to report to the Belmont Red Association with a recommendation to recommence the combined analysis. This will allow Belmont Reds to take full advantage of the additional traits and breeds represented in the research database, while also having their genetic trends reported on the basis of Belmont Red animals only.

4.4 Using composite breed databases

As a further exercise in combining separate, though potentially linked, databases, ABRI reviewed the South African Simbra database to identify possible linkages to the Simmentaler and Brahman breed databases in South Africa. This involved populating an ABRI cross-referencing system to include the identifiers of sires and dams of the two pure breeds as recorded on the Simbra database, along with their identifiers as recorded with their respective Breed Associations. The cross-reference file was then used to combine the three separate breed databases and a combined test (RSA Multi-breed) analysis was conducted using the configuration of the South African Simbra BREEDPLAN analysis. The latter uses a crossbred model with pre-adjustment for heterosis and other non-genetic sources of variation such that head-to-head comparisons can occur between animals of different breed content within the same contemporary group.

A total of 7,461 Simmentaler sires and 5,528 Brahman sires were represented by performance progeny in the RSA Multi-breed test analysis. However, only 169 Simmentaler and 95 Brahman sires gained additional performance progeny from the Simbra database (Table 6). Approximately 80% of Simmentaler and Brahman sires were of historic relevance in the analysis, with their last calf being born prior to 2010. Furthermore, the overall lower rates of performance recording in the Brahman breed is limiting for linkage as defined by progeny recorded with performance in more than one database.

Table 6 Simmentaler and Brahman sires registered with their respective South African breed association and represented In the South African Simbra progeny data

Sire Breed	No. sires	200-day weight progeny	
		Total recorded	via Simbra
Simmentaler	169	10,332	1,956
Brahman	95	3,014	1,495

The potential for including two other breeds - South African Brangus and Braford – were explored, but identifiable linkage to the Brahman database was only marginal.

4.5   New Zealand

The ABRI negotiated access to multi-breed progeny test data collected by Beef and Lamb New Zealand (BLNZ) as part of two current research projects.

The first is their *Beef Progeny Test* where bulls are compared under New Zealand commercial farming conditions. This progeny test involves about 2,200 cows and heifers (predominantly Angus but some Hereford) on five properties across New Zealand, with a mix of both internationally-sourced and New Zealand semen being used. Steers and cull heifers were assessed on their carcase traits, while replacement heifers were to be tracked for their maternal characteristics.

The second trial is the New Zealand Dairy-Beef Progeny Test aims to calculate the additional value that can be added by using high-genetic-merit beef bulls, versus the unrecorded bulls traditionally used as "follow-on bulls" in most New Zealand dairy systems. The multi-breed progeny test was opened up to all breeds. Sires selected include Angus, Hereford, Simmental, Shorthorn, Murray Grey, Stabiliser and Limousin, and involve leading studs supplying genetics to beef and/or dairy farmers. Bulls were selected with strong percentile EBVs across gestation length, birth weight, calving ease (direct and daughters), 400-day weight, 600-day weight, eye muscle area (EMA) and intramuscular fat percentage (IMF).

Discussions were held on options for storing and submitting the New Zealand research data. These options include the use of ABRI's standard database software (as used by breed society clients) or the storing of data in third-party databases and extracting the relevant data for BREEDPLAN evaluation. It was agreed that BLNZ would store their research data and initially submit a test extract to ABRI, prior to any longer term database solutions being considered.

Beef and Lamb New Zealand (BLNZ) submitted a test extract of their progeny test data to ABRI, in preparation for developing a pipeline for introducing externally-sourced multi-breed data. In March 2018 ABRI was provided with a multi-breed extract of BLNZ data, comprising growth and carcase (ultra-sound scan and slaughter) trait data on heifer and steer progeny born in 2015. ABRI completed an analysis of the BLNZ multi-breed data (i.e. without inclusion of any other data source) using a crossbred BREEDPLAN model with pre-adjustment for heterosis and allowance for head-to-head comparisons across breed types within the same contemporary group. The goal of this analysis was to determine the relative potential for this multi-breed data to be of use within a BREEDPLAN context.   Review of 200-day weight contemporary groups showed that in addition to those comprising only purebred Angus or Hereford progeny, a considerable number of contemporary groups also represented 2 or more breeds: (I) progeny of Angus, Simmental, Stabiliser and Hereford sires over Angus cows; (ii) progeny of Hereford, Angus, Simmental, Stabiliser and Charolais sires over Hereford cows. However, multi-breed representation within the slaughter trait contemporary

groups was markedly reduced and limited mostly to Angus with Angus-cross progeny as fewer of the Hereford-based cohorts had slaughter traits recorded (Table 7).

Table 7 Breed representation in BLNZ contemporary groups containing 2 or more breeds

Breed of sire	No. of Sires	Breed of dam	200-day weight	Carcase weight
Angus	79	Angus	675	222
		Hereford	40	13
Hereford	23	Hereford	202	40
		Angus	51	22
Simmental	8	Angus	82	42
Stabiliser	5	Angus	67	37
Charolais	2	Hereford	8	4
Total	**117**		**1125**	**380**

Given that some BLNZ data recording protocols differ from those promoted by BREEDPLAN, an investigation of the quality of this data is warranted before recommendations can be made as to if/when/how this BLNZ multi-breed data may be incorporated into existing BREEDPLAN analyses. Investigations of "data integrity" as they relate to use in BREEDPLAN remain beyond the scope of the current project, requiring engagement with the owners of the BREEDPLAN technology. ABRI is currently reviewing the impact of BLNZ Angus data on the Estimated Breeding Values (EBVs) of the New Zealand and Australian Angus sires represented, when including this data in a conventional Trans-Tasman Angus BREEDPLAN analysis. Preliminary comparative reports have been provided to both New Zealand and Australian Angus, as well as to BLNZ, but discussions have been suspended subject to additional BLNZ Angus cohort data being provided for inclusion. Subject to approval from all parties, the Trans-Tasman Angus BREEDPLAN analysis could be extended to include the Angus crossbred data as well.

Opportunities for utilising the BLNZ Hereford data are more limited, given the current Hereford BREEDPLAN evaluation is restricted to purebred performance data only (from Australia, New Zealand and Namibia). However, the Herefords Australia (HAL) Black Baldy trial has a major objective of generating data that will aid evaluation within and across breeds.

In late December 2019, BLNZ delivered an updated extract of their multi-breed progeny test data, including additional carcase data.

5 Discussion

5.1 Technical considerations

The undertakings by ABRI in this project highlighted a number of technical considerations for the development of multi-breed BREEDPLAN analyses.

Firstly, the current suite of BREEDPLAN software allows for phenotypic data to be adjusted using breed- and country- specific parameter files. For those analyses where data sources correspond to different breed and/or country and can be readily identified as such within a combined analysis – as in the Northern Tropical breed and RSA Multi-breed test analyses – it is possible to apply a different set of adjustment factors to each source of data. However, for those multi-breed data extracts originating from a single source (e.g. the BLNZ, Southern Multi-breed Research and Northern Multi-breed Research databases), it is not currently possible to apply breed-specific adjustment factors to the different breeds and breed combinations represented within the data extract and subsequent contemporary groups. In the case of production runs using the Northern Multi-breed data extracts,

the data adjustments used vary according to the main breed for which this data is used. Thus Brahman adjustment factors are applied to the multi-breed data in the Brahman analysis, and Santa Gertrudis adjustment factors are applied to the same data when used in the Santa Gertrudis analysis, meaning that EBVs in each analysis are based on different adjusted phenotypes for the multi-breed data source. Progressing development of a Northern Tropical Breed production analysis which uses the Northern Multi-breed research data would therefore require decisions as to how phenotypes are to be pre-adjusted in ways that maintain the breed-specificity evident in the data.

Related to the previous point is the choice of (co)variance components to be used in multi-breed analyses that include different breed data extracts linked via a common data set. Currently, BREEDPLAN analyses use a single (co)variance parameter file which is specific for the breed (and country) represented, such that the Australian Brahman and Santa Gertrudis breeds assume different genetic parameters in their respective analyses. In the Northern Tropical Breed test analysis, for example, only one set of genetic parameters could be used – and the Brahman set was assumed. In a production run, however, the suitability of these genetic parameters for use with the Santa Gertrudis and Droughtmaster breeds would need further investigation.

In relation to multi-breed Single-Step analyses, the Australian Brahman analysis is the only one in which genomic information is currently used. Importantly, genotypes are restricted to pure Brahman animals only, as the current Single-Step BREEDPLAN software cannot accommodate breed diversity within the construction of the G matrix. Because the breed purity criterion is currently set at such a high level, it results in genotypes on "largely Brahman" animals being excluded. A recent example involves a number of commercial Brahman breeders where genotyped animals failed to meet the current breed criterion for inclusion. The current requirements of the Single-Step analysis are therefore an impediment to the inclusion of genotypes from Brahman-cross and/or Brahman-derived individuals.

Finally, linkage as reported here has been restricted primarily to 200-day weight, the most well-recorded of all phenotypic traits across the breeds reviewed. Linkage in terms of the less common or more difficult to record traits (e.g. days to calving) has not been considered.

5.2 Data Sharing

There needs to be long term ongoing agreement of clients to run their data in a multi-breed analysis. There has been long-term and strong support for international evaluations.

In 2004 the Australian Registered Cattle Breeders' Association (ARCBA) ran a Strategic Planning Workshop with one session allocated to 'Sharing Data Between Breeds'. Although no formal vote was taken, there was general support from participants for more data sharing but it was identified that there was a need for a shift in policy for some societies.

There are currently a number of formal and informal data sharing arrangements between breed societies and breeders. Most of these arrangements are for long term data sharing and require a copy of data to be retained even if a particular client chooses to discontinue their participation. To date these arrangements have been primarily for multi-country evaluation with a small number involving multi-breed analyses. There are also agreements for the sharing of EBVs between analyses.

In the future, industry research data, ie research data that is industry funded and will potentially benefit more than one breed, should be loaded into research datasets that are made available for relevant genetic evaluations. If such data is loaded into a breed society database, then there is increased inefficiencies in making that data available for other breeds.

5.3   Survey of ABRI clients and stakeholders

ABRI conducted a small survey of its Australian breed society clients to ascertain attitudes and priorities regarding the development of across-breed BREEDPLAN evaluations. ABRI also conducted a separate survey of the attitudes and priorities of key industry stakeholders, targeting the attendees at the BREEDPLAN Champions workshop held in February 2019. Survey requests were sent to 25 breed associations and to 127 other industry stakeholders. Responses were received from 15 breed associations (5 from smaller sized associations and 10 from larger associations) and 30 stakeholders.

In general, breed associations were supportive of the development of multi-breed evaluations but considered them to be a lower priority than within breed and international evaluations. A comment from one of the associations summarised this point - "With limited R&D resources for BREEDPLAN analytical software, our breed association would prefer priority is given to ensuring BREEDPLAN delivers world leading within breed, across country genetic evaluation software, rather than re-directing resources to the development of multibreed genetic evaluation. This will ensure our breed can deliver higher rates of genetic improvement and contribute to the industry goal of doubling the rate of genetic progress."

There were 45 respondents representing breed associations and industry stakeholders. In summary:

- Each group identified development of multi-breed BREEDPLAN evaluations as a priority. It was less of a priority for the larger breeds.
- Each group identified benchmarking EBVs internationally as highly important.
- The larger breeds identified a lower priority for benchmarking breeds against other breeds.
- Each group identified that the selection of genetics within a breed was the highest importance for commercial breeders. Both breed association groups (small and large) ranked selection from multiple breeds as the lowest importance for commercial breeders, with international selection more important.

For the breed associations:

- The majority of respondents agreed that 'benefit to commercial producers' was a reason why breed associations should participate in multi-breed evaluations.
- No breed associations identified that they would not be willing to provide data for multi-breed research. Half of the respondents were positive about providing research data.
- No breed associations identified that they would not be willing to provide data for routine multi-breed evaluations. Less than half were positive about provide routine data.

With respect to reasons why breed associations might not participate in a multi-breed evaluation:

- The smaller breeds group identified potential cost and data security as the primary reasons.
- For the larger breeds, 'other' was identified as the primary reason for not participating. This was followed by 'no reason' and 'potential for additional cost'.
- Industry stakeholders identified that the primary reasons for breed association's to not participate would be firstly, the outcome of benchmarking of their breed against other breeds and secondly, the impact on market share.

There was uncertainty as to the preferred method of reporting results from multi-breed evaluations. Although industry stakeholders were strongly in favour of reporting collectively (ie combined results), the breed associations were generally unsure.

A full summary of the survey results are presented in the Appendix.

5.4 Objectives

In relation to the extent to which the project objectives were met, these objectives were:

a) Identification of all datasets that are actually multi-breed within the current breed and research databases, and collation of a single dataset for research analysis

ABRI's work has concentrated on the collation of multi-breed data and the conducting of BREEDPLAN test analyses to determine overall data structure and connectedness in terms of progeny performance records.

ABRI's initial investigations indicated that linkage between current British breed society databases will be limited due to limited representation of multi-breed performance data on these databases. For example, the Hereford database has been restricted to purebreds only, until recently. ABRI held discussions with Hereford society staff regarding the addition of animals and performance data from the Black Baldy BIN project, where Hereford/Angus cross animals are represented. Similarly, the Angus database includes a Multi-breed register but only has limited representation of other British breeds such as Murray Grey, Red Angus and Shorthorn. The duplication of animal and performance records for Murray Grey and Red Angus herds will potentially pose problems for combining these datasets with Angus. The Angus database also has links with Tropical breeds - through Brangus and Ultrablack animals recorded with performance – and with Simmental.

ABRI also created a single dataset comprising the Australian European breeds – Limousin, Simmental and Charolais - by way of each breed's linkage to the Southern Multi-breed Research database.

A major part of ABRI's work has focused on combining multi-breed data that relates to the Australian Tropical breeds. This involved utilising ABRI's existing cross-referencing system to include animal identifiers for individuals recorded on the Northern Multi-breed Research database with their identifiers as recorded on the corresponding society database. To date, cross-referencing of the multi-breed data to each of the Brahman, Santa Gertrudis, Droughtmaster and Belmont Red breed databases has been completed. Extracts for each breed, with the multi-breed data included, were created and provided to AGBU. This work was identified as a priority to both AGBU's work plan and as an industry priority, as identified by the National Livestock Genetics Consortium. A "Northern Tropical" extract combining all 4 breeds with the multi-breed data included was also created and provided to AGBU. This extract was subsequently expanded to an "International Tropical" extract via the inclusion of Brahman extracts from the USA and Southern Africa.

b) Updated multi-breed evaluations for British, European and Tropical breeds, using all data currently held in breed and research databases. Approval for use of breed data will need to be sought, but it is not anticipated that it will be withheld for research analysis. The analysis will make use of genomic information where available within-breed and across-breed, to evaluate the extent to which this increases the accuracy of the across-breed evaluations.

During the period covered in this project, ABRI completed BREEDPLAN analyses using data extracts that combined multiple sources of breeds and countries, including the Northern and Southern Multi-breed Research data where appropriate. A standard multi-breed BREEDPLAN model was used,

which involved pre-adjustment of heterosis (direct and maternal) and allowing head-on comparisons between animals of varying breed content within contemporary groups. Results of these analyses have been investigated, largely in terms of data structure for head-to-head comparisons across breed types and the potential for combining separately-recorded breed-specific databases. This research demonstrated limited opportunity for the British and European breeds in Australia, but considerably more opportunity for the Tropically-adapted breeds.

These outcomes led to two Tropical multi-breed BREEDPLAN analyses being transitioned into commercial production: one for the Brahman breed and one for the Santa Gertrudis breed. The Droughtmaster evaluation is likely to transition to inclusion of the multi-breed data in 2020, while inclusion of the multi-breed data in a test evaluation for Belmont Red has also been completed and documented for the society.

Genomic information was already included in the Brahman BREEDPLAN evaluation before the Northern Multi-breed Research data was included. While this evaluation can be described as a multi-breed analysis using genomics, the genotypes included are restricted to pure Brahman animals only. The current Single-Step BREEDPLAN software does not allow for a mixture of breeds in the construction of the Genomic Relationship Matrix.

c) From these evaluations, precise definition of the data gaps – what breed comparisons can and cannot be made reliably for what traits. This information can help prioritise future data collection in research and industry herds and projects.

The Tropically-adapted breeds are best positioned to benefit from the availability of multi-breed data that is comprehensive (in terms of quantity, quality and range of traits recorded), current and with appropriate linkage to the each of the Brahman, Santa Gertrudis, Droughtmaster and Belmont Red databases.

With the exception of Angus and Hereford, the remaining British breeds have limited opportunity for having their data combined within a multi-breed (or across-breed) extract and routine BREEDPLAN evaluation. The representation of Angus and Hereford genetics in research databases and in other progeny test datasets (e.g. Black Baldy Project; BLNZ extract) may provide some opportunities for these breeds, but will be limited potentially by the quantity and quality of multi-breed trait data recorded.

The Australian European breeds are most limited in capacity to benefit from the multi-breed data that is currently available. Linkage between the three main breeds remains historic and limited, such that a BREEDPLAN evaluation combining the European breeds remains unlikely.

d) Via consultation with commercial producers and processors, identify available datasets that include multi-breed data. Once identified, inclusion of that data into the multi-breed evaluations to determine the extent to which the commercial data improves the scope (breed and trait coverage) and power (accuracy) of the evaluations. These results will provide clear information to help breeds and other stakeholders make informed decisions about the value of contributing data to, and participating in, multi-breed evaluation, and provide industry with reliable information on the value of conducting regular or routine multi-breed evaluation.

Given the lack of quality data in the seedstock sector (i.e. data with linkage across herds and traits), ABRI's development work concentrated on the data available from large scale and well-constructed research projects.

e) Fully operational systems in place in ABRI to conduct routine multi-breed evaluations.

One of the main requirements in combining data extracts from different breed sources is the ability to identify animals in common across those sources. This process, known as "matching", is a core task that has been undertaken by ABRI for a considerable number of years. It is a commercially-feasible process made possible by ABRI's cross-referencing system, which interrogates the relevant ILR2 database fields to identify animals in common. It can be, however, a time-consuming process and is not an exact science due to the idiosyncrasies in data recording over years and databases. The best approach to matching is to cover the most significant animals in the databases first (probably around 70-80% of the total matches) then followed by a more exhaustive (and much more time consuming) matching protocol which becomes a largely manual exercise. During the period covered in this project, ABRI reviewed and updated the cross-referencing system for those breeds represented in the various multi-breed databases, in order to facilitate the preparation and availability of combined / multi-breed extracts as required for research and development.

There are also seed-stock herds that maintain more than one registered breed, yet each breed has its pedigree and performance records submitted to its respective breed society. Even if the breeds are run together, the method of data submission essentially "pulls apart" the contemporary groups that could provide head-on breed comparison information. This represents another challenge for the combining of breed extracts: the matching of **herds in common** across different databases. This is a new area of development and is absolutely essential if, for example, some breeds such as Murray Grey and Angus are to be evaluated together. From ABRI's experience, this matching of herds cannot be automated, one reason being that automation cannot determine if the breeds are run "as one" or if each breed is "run separately" but owned by the same breeder.

There is also likely to be duplicated performance data across these databases, but the performance information for a particular animal may not be entirely duplicated on both databases. For various reasons, it is likely that not all animals in a herd/year cohort have been added to both databases. Therefore, ABRI will also be required to match herds across databases as well – something that has not been required to date. An alternative strategy would involve identifying herds that do maintain more than one breed as part of the one herd and have them submit their performance data combined.

Assuming that across-breed and multi-breed extracts can be created, with effective head-on comparison across breed types within contemporary groups, transitioning towards routine multi-breed evaluations remains constrained by the requirements of the current BREEDPLAN software. These requirements include:
- Use of a single covariance matrix: no potential to allow for breed specificity when 2 or more (diverse) breeds are represented;
- Adjustment factor files are assigned on the basis of data "source" – but different adjustment factors cannot be applied to different breed types <u>within</u> a data source;
- Construction of the G matrix: Single-Step BREEDPLAN analyses can include multi-breed performance data, but only those genotypes representing the dominant pure breed can be used in constructing the G matrix;

f) Via consultation with key industry stakeholders, including breeds, processors, commercial producers and MLA and R&D providers, a strategy for ongoing multi-breed evaluation – what breed and trait groups could be included, what datasets could be accessed for inclusion, formats and delivery systems for results.

It became clear during this project that the development of multi-breed evaluations rely on well-structured research data that provides the necessary head-on-head comparisons across a number of relevant traits. Currently available data from commercial sources does not provide sufficient quality data to enable the development of multi-breed evaluations. This data may however play an important role once the developments are complete and production runs are in place. This will be true for both single breed and multi-breed analyses.

ABRI has defined systems for receiving data for genetic evaluation and for delivering results of these evaluations. These processes are in place for both customers of ABRI and for those who use third-party service providers.

The results of ABRI's survey of key stakeholders indicate that breed associations would at least consider the contribution of data to routine multi-breed BREEDPLAN evaluations. They are more willing to provide data access for multi-breed research.

A business strategy needs to be developed in consultation with MLA. This strategy will need to consider the protocols for obtaining permission to share or use data as well as delivery of results and any commercial arrangements that may be required to ensure multi-breed production runs. Feedback from ABRI's survey indicated that some larger breed associations were concerned about evaluations that might compete with their existing evaluations and whether there would be consideration for the associations in commercialisation models.

g) A strategy for ongoing data collection to support reliable multi-breed genetic evaluation: what breed comparisons need to be conducted and/or continued, and what data to collect where and on what traits.

The British and European breeds (or at least a sub-set of the significant breeds) require well-structured research projects to supply data for multi-breed evaluations. This would be in a similar manner to how the Repronomics project has facilitated the Tropical multi-breed analyses. The NSW DPI multi-breed project has the potential to supply the core of this information.

The data collected as part of ongoing projects needs to be recorded (in BREEDPLAN-ready format) in database(s) that allow for access by multiple users. That is, the data should be stored in industry databases where access and usage is determined by technical criteria.

The challenge will be to continue the collection of the necessary records beyond the initial research projects.

6 Conclusions/recommendations

The development of multi-breed genetic evaluations offers the following benefits for Australian cattle breeders:
- As a means for optimising genetic gain: clear and readily-available comparisons to select genetics which best suit production environment, breeding objective and target markets;
- Recent industry survey results show significant percentage of respondents want multi-breed EBVs, i.e. there is a demand for these results;
- It would reinforce Australia and BREEDPLAN as the leading international beef analysis technology;
- Assist in maintaining a national evaluations system and common language and minimise the need for breeders to seek similar services overseas;

ABRI has a commercial process whereby multiple datasets can be sourced and used to create larger combined extracts, for use in research or in routine genetic evaluation using BREEDPLAN. This process utilises:

(i)   the capacity of client (ILR2) databases to record the identifier or registration details of animals sourced from "outside" the population, whether that be from other countries or other breed databases,

(ii)   ABRI's cross referencing software to match animals in common across data sources, and

(iii)   ABRI's data merging software.

As was demonstrated in this project, ABRI is currently able to create a range of data extracts in which different sources of breed data were combined, often with the inclusion of multi-breed research data. However, data limitations still exist:

- other than the four Tropical breeds involved in the Repronomics project, there is little or no linkage between other breeds and for traits other than growth traits;
- Genetic linkage within the British and European breeds represented in research datasets is limited, historic and does not represent current genetics;
- Current genetic linkage within the British and European breeds is predominantly based upon crossbred progeny ie purebred sires used within another breed. Genuine multi-breed data is required which provides head to head comparisons of animals of at least two pure breeds which have performance recorded in the same management groups;
- The Repronomics project has provided well-structured data to enable integration of the research data into existing genetic evaluations for Brahman, Santa Gertrudis and Droughtmaster;
- There is a need for industry investment to create sound research datasets to allow for breed and trait comparisons, particularly for maternal traits. This needs to be followed by ongoing quality data collection to maintain linkage;

As the commercialiser of BREEDPLAN genetic evaluations, ABRI will need agreement from its clients before the respective data can be made available for inclusion in one or more multi-breed analyses. While there has been long-term and strong support among ABRI's client for inclusion of data in international evaluations involving their respective breeds, support and/or interest in participation in multi-breed evaluations among clients remains unclear. There are existing data sharing and evaluation agreements in place between ABRI and its clients, and these would need to be re-drafted to accommodate the requirements of multi-breed evaluations. The availability of such multi-breed evaluations does, however, provide ABRI with possible options for commercial (non-breed society) clients to participate in BREEDPLAN, as currently happens with the Tropical Composite database.

In terms of genetic evaluation, the current BREEDPLAN software can accommodate multi-breed datasets – but not comprehensively so. The expression of heterosis in multi-breed performance data can be accounted for and a sophisticated approach to the formation of genetic groups allows for breed differences in foundation animals to be modelled, including changes over time in each breed population.

However, there are a number of technical issues that need to be addressed and each of these will require the input of AGBU:

- Ability to include genomic data from multiple breeds and/or crossbred animals in Single-Step BREEDPLAN of multi-breed data;
- Ability to adjust performance data based on breed of the individual animal rather than "database source" of the animal's data. This could be handled by ABRI via pre-adjustment of phenotypes in the preparation of the data extracts, rather than adjustments being made by the BREEDPLAN software;

- Accurate identification and merging of herds recorded in different databases;
- Data to accurately link all traits across breeds;
- Decisions on reporting, base etc for the multi-breed analysis;
- Ability to handle breed-specificity in genetic parameters, when multiple (and diverse) breeds are combined for evaluation;
- Parallel developments to BreedObject software;

At completion of this project, the following BREEDPLAN evaluations are using (or will soon be using) multi-breed data on a routine basis in the calculation of EBVs:

- The Southern Limousin BREEDPLAN evaluation: combines Limousin data from Australia, New Zealand, South Africa and Namibia, and includes the Southern Multi-breed Research data (which includes the more recent Limousin BIN data);
- The Single-Step Brahman BREEDPLAN evaluation: combines the Australian Brahman data and the Northern Multi-breed Research data, using genomic information on pure Brahman animals;
- The Santa Gertrudis BREEDPLAN evaluation: combines the Australian Santa Gertrudis data and the Northern Multi-breed Research data;
- The Droughtmaster BREEDPLAN evaluation: combines the Australian Droughtmaster data and the Northern Multi-breed Research data;
- The Belmont Red BREEDPLAN evaluation: combines the Australian Belmont Red data and the Northern Multi-breed Research data;

As is evident in this summary, the role of the Northern Multi-breed Research database remains critical in the on-going development and provision of routine BREEDPLAN evaluations for the Tropically-adapted breeds. One additional client of ABRI – Tropical Composites – may also benefit from linkage to the northern multi-breed database but this has not as yet been investigated. Likewise, it might be feasible to move each of the Tropical breed analyses to a combined "Northern Tropical" BREEDPLAN evaluation with the Northern Multi-breed Research database playing a pivotal role. Of course, such a development would also require technical enhancements to the BREEDPLAN evaluation software (e.g. inclusion of multi-breed genotypes) as well as agreements between the participating breeds.

It should be a research priority to enable the handling of multiple breed genotypes in a multi-breed Single-Step BREEDPLAN analysis.

7   Key messages

ABRI has a commercial process whereby multiple datasets can be sourced and used to create larger combined extracts, for use in research and/or in routine BREEDPLAN genetic evaluation. ABRI is currently able to create a range of data extracts in which different sources of breed data can be combined, often with the inclusion of multi-breed research data residing on separate databases.

ABRI is transitioning clients to multi-breed analyses of increasing complexity as data becomes available. This effort has largely focused on the Tropically-adapted breeds, and the Angus and Hereford breeds to a lesser extent.

The Tropically-adapted breeds in Australia are best positioned to utilise multi-breed data in their respective BREEDPLAN evaluations. There is further potential for all such breeds to combine for a single "Northern Tropical" BREEDPLAN evaluation, subject to technical enhancements becoming available (such as multiple breed genotypes being used in Single-Step BREEDPLAN) and data sharing agreements.

The need for ongoing research projects to provide high quality and up-to-date data on breed and trait combinations is readily apparent. With the exception of the Northern Multi-breed Research data, there are few if any comprehensive and current multi-breed datasets that could assist in development of multi-breed BREEDPLAN evaluations, especially of relevance to the British and European breeds in Australia.

The development of commercial services for providing multi-source BREEDPLAN evaluations needs to be prioritised so as to balance the priority of international evaluations among ABRI client breeds (ie. seed-stock populations) and the priority of multi-breed evaluations for the commercial beef sector.

The development of a more sophisticated yet flexible suite of BREEDPLAN software for completing multi-breed evaluations remains essential. This is particularly relevant for the inclusion of genomic information representing multiple breeds in the evaluation and for ensuring that BREEDPLAN can remain as a competitive product in the global market of genetic evaluation services.

8 Appendix

8.1 Survey Questions

8.1.1 Breed Society Survey Questions

1. Indicate the predominant geographic distribution of members in your society
   - ☐ Southern (Temperate)
   - ☐ Northern (Tropical)
   - ☐ Both

2. How would you describe your breed?
   - ☐ British
   - ☐ European
   - ☐ Composite
   - ☐ Indicus/Indicus Derived
   - ☐ Other

3. Do you have crossbred or multibreed data on your database?
   - ☐ Yes
   - ☐ No
   - ☐ Unsure

4. Rate the importance (1-10) of benchmarking your breed against other breeds based on EBV.

1	2	3	4	5	6	7	8	9	10
Not important									Extremely important

5. How important (1-10) is it for commercial bull buyers to compare bulls <u>across</u> breeds?

1	2	3	4	5	6	7	8	9	10
Not important									Extremely important

6. Rate the importance (1-10) of benchmarking your breed internationally.

1	2	3	4	5	6	7	8	9	10
Not important									Extremely important

7. Rank the importance (1-3) to your breed of the following:
   - ☐ Selection of genetics within your breed
   - ☐ Selection of genetics from multiple breeds
   - ☐ Selection of genetics from multiple countries

8. What priority should be given to developing a multibreed BREEDPLAN evaluation?

1	2	3	4	5	6	7	8	9	10
No priority									High priority

9. Would your breed association be willing to provide data access for multibreed research projects?

☐ Yes

☐ No

☐ Maybe

10. Would your breed association contribute data to a routine multibreed BREEDPLAN evaluation?

☐ Yes

☐ No

☐ Maybe

11. Choose reasons why your breed <u>would</u> participate in a multibreed evaluation. (Multiple reasons can be selected)

☐ Benefit to seedstock producers

☐ Benefit to commercial producers

☐ Benchmark breed against other breeds

☐ Access to new markets

☐ Other reason _____

☐ None - would not participate

12. Choose reasons why your breed <u>might not</u> participate in a multibreed evaluation. (Multiple reasons can be selected)

☐ Outcome of benchmarking breed against other breeds

☐ Potential for additional cost

☐ Impact on market share

☐ Data security

☐ Other reason _____

☐ No reason

13. If a multibreed evaluation was available would you prefer to see results reported:

☐ Separately (within breed)

☐ Collectively (combined breeds)

☐ Unsure

14. Additional comments on multibreed analyses

8.1.2 Stakeholder Survey Questions

1. Indicate your industry background
   - ☐ Extension / education
   - ☐ Livestock Producer
   - ☐ Breed association staff member
   - ☐ Service Provider (e.g Scanner, Genotyping etc)
   - ☐ Software Company
   - ☐ Researcher
   - ☐ Peak industry body
   - ☐ Other _____

2. Rate the importance (1-10) of benchmarking breeds against other breeds based on EBV.

1	2	3	4	5	6	7	8	9	10

Not important   Extremely important

3. How important (1-10) is it for commercial bull buyers to compare bulls across breeds?

1	2	3	4	5	6	7	8	9	10

Not important   Extremely important

4. Rate the importance (1-10) of Australian breeds being able to benchmark on EBV against other international beef populations.

1	2	3	4	5	6	7	8	9	10

Not important   Extremely important

5. Rank the importance (1-3) to commercial breeders of the following:
   - ☐ Selection of genetics within a breed
   - ☐ Selection of genetics from multiple breeds
   - ☐ Selection of genetics from multiple countries

6. What priority (1-10) should be given to developing a multibreed BREEDPLAN evaluation?

1	2	3	4	5	6	7	8	9	10

No priority   High priority

7. Choose reasons why you believe breed associations should participate in a multibreed evaluation. (Multiple reasons can be selected)
   - ☐ Benefit to seedstock producers
   - ☐ Benefit to commercial producers
   - ☐ Benchmark breed against other breeds
   - ☐ Access to new markets
   - ☐ Other reason _____
   - ☐ None - I would not participate

8. Choose reasons why you believe breed associations <u>might not</u> participate in a multibreed evaluation. (Multiple reasons can be selected)
   - ☐ Outcome of benchmarking breed against other breeds
   - ☐ Perceived additional cost
   - ☐ Impact on market share
   - ☐ Data security
   - ☐ Other reason _____
   - ☐ No reason

9. If a multibreed evaluation was available would you prefer to see results reported:
   - ☐ Separately (within breed)
   - ☐ Collectively (combined breeds)
   - ☐ Unsure

10. Additional comments on multibreed analyses