Final report

Investigating and implementing international multi-trait genetic evaluations for beef cattle

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Abstract

International genetic evaluations for beef breeds can accelerate rates of genetic gain in the Australian beef population by providing a more objective basis on which selection decisions are made regarding foreign genetics. International evaluations also have potential to enhance Australia's high-value genetic export opportunities, by demonstrating how Australian genetics compare to other genetics available internationally for a range of production traits and scenarios. The development of international genetic evaluations was shown to be of very high priority to many of the beef breeds surveyed, both domestically and internationally.

This project focused on developing a commercial pipeline that would allow international evaluations to be conducted routinely, using BREEDPLAN technology in the calculation of Estimated Breeding Values (EBVs). Alternative pipelines and analytical services available for international beef evaluations were reviewed.

International multi-trait BREEDPLAN evaluations were completed for three breeds represented in Australia, demonstrating that each could transition into commercial production using existing database and applications software and provided as a routine service. Specific breed populations were identified as necessary in creating genetic linkage and reinforced the importance of collaboration between countries to ensure key populations are represented in such international evaluations.

The recommendation is for routine international BREEDPLAN evaluations to supplement on-going national evaluations, rather than being a replacement of them. Opportunities for the on-going development of international BREEDPLAN evaluations will depend on strategic collaborations between breed associations and service providers and the continued enhancement of BREEDPLAN to better service the requirements of the international market.

Executive Summary

The provision of commercial services for the genetic evaluation of beef cattle represents a rapidly changing context. With advancements in computational speed and analytical approaches as well as the increasing needs of beef seed-stock breeders for genetic gains in production efficiency and sustainability, the demand has grown for developments in more complex and more frequent genetic evaluations capable of accessing more globally-distributed sources of data. Where national breed-specific evaluations were once common place, there is now growing interest and opportunity for countries to combine their pedigree, performance and genomic data into larger-scale international genetic evaluations. The participation of Australian beef breeds in such international evaluations has potential to assist seedstock breeders select genetics from “beyond the national border" that are appropriate for their production environment, breeding objective and target market. International evaluations can therefore accelerate rates of genetic gain in the Australian beef population by providing a more objective basis by which selection decisions are made regarding the international gene pool available. International evaluations also have potential to enhance Australia’s high-value genetic export opportunities, by demonstrating in a directly comparable system how Australian genetics compare to other genetics available internationally for a range of production traits and scenarios. This project identified the development of international genetic evaluations as being of very high priority to many of the beef breeds surveyed, both domestically and internationally. For seedstock breeders and for those involved in the international marketing of semen and embryos, access to large-scale international evaluations for a given breed was ranked as being of higher priority than access to multi-breed evaluations. The latter was considered of higher importance for commercial breeders.

This project concentrated primarily on developing a commercial pipeline of processes that would allow international genetic evaluations to be conducted routinely, using BREEDPLAN technology as the analytical process for the calculation of Estimated Breeding Values (EBVs). This pipeline was developed by the Agricultural Business Research Institute (ABRI) and implemented as test case scenarios for the Hereford, Brahman and South Devon breeds. An alternative pipeline was evaluated for the Charolais and Limousin breeds. A wider review of other pipelines and analytical services available for international evaluation highlighted the ABRI to be well-positioned as a commercial provider of the products and services necessary for international beef evaluations.

This project reports country-specific estimates of variance components for 200-day weight in five beef breeds, where each breed represented a number of countries including Australia. Estimates of across-country correlations for 200-day weight are also reported for the Hereford, Brahman and South Devon breeds and are taken as indicative of potential genetic linkage between countries for each breed, at least on the basis of 200-day weight. This work highlighted the key role of specific populations within each breed in creating the linkage on which international genetic evaluations depend and the importance of collaboration between countries to ensure these key populations are represented in the international data. For each of the Hereford, Brahman and South Devon breeds, an international genetic parameter matrix was defined and then implemented for the range of production traits selected for inclusion in each international BREEDPLAN evaluation. The largest of these was for the Hereford breed, with 7 countries included and almost 7.8M performance records for a subset of growth, scan and scrotal traits combined within the one multi-trait analysis. With an analytical run time of approximately 9 hours for the largest evaluation, this project demonstrated these international BREEDPLAN evaluations could be transitioned into commercial production using ABRI’s existing database and applications software, and provided as a routine service.

It is the recommendation of this project that routine international evaluations be used as a supplement to current national evaluations, rather than as a replacement of them. This will help avoid the challenge associated with maintaining a “one size fits all” model, especially as new traits are developed, and accommodates the potential for across-country correlations being significantly less than 1.0 for traits other than growth. However, none of the international BREEDPLAN evaluations considered in this project have transitioned beyond a commercial feasibility study and data-sharing agreements beyond the scope of this project have not yet been formalised.

This project also fostered collaborative relationships with the Interbeef Working Group and a number of European beef breed associations, the goal being to strengthen the basis on which European genetics imported to Australia are evaluated and to review the potential for the marketing of Australian genetics into the European market. This provided opportunities for BREEDPLAN and the services of ABRI to be promoted to European-based beef breeds as well as exposing ABRI to alternative approaches being used in the conduct and validation of multi-country evaluations.

The undertaking of this project did highlight an increasingly competitive market in the provision of international genetic evaluation services. The marketing strength and speed of delivery of other organisations does mean the priority given to developing international evaluations requires careful consideration of the models and methods available. The growing interest in these other service providers becoming evident within Australian breed associations should not be taken lightly, given their capacity to facilitate multi-country evaluations. In this regard, the need for validation of outcomes from international models of evaluation will remain ever critical.

This project demonstrated that ABRI as a commercial service provider and BREEDPLAN as the genetic evaluation service are each held in very high regard internationally. Opportunities for the on-going development of international BREEDPLAN evaluations will be dependent on the international reputation of each being reinforced through strategic collaborations involving ABRI and continual enhancement of the BREEDPLAN technology to better service the requirements of the international market.

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1 Background

1.1 Moving towards international genetic evaluations

1.1.1 Introduction

The provision of commercial services for the genetic evaluation of beef cattle represents a rapidly changing context. With advancements in computational speed and analytical approaches as well as the increasing needs of beef seed-stock breeders for gains in production efficiency and sustainability, we are seeing the development of more complex, more frequent and globally-focused initiatives as service providers. Where national breed-specific evaluations were once common place, there is now a growing interest and opportunity for countries to combine their pedigree, performance and genomic data into larger-scale multi-country genetic evaluations. This allows individual animals to be compared directly on Estimated Breeding Value (EBV) across countries, allowing breeders to take a more informed approach to the selection of possible genetics from "beyond the borders". This also means that superior local genetics can be more accurately identified when benchmarked within the wider international gene pool.

1.1.2 ABRI and BREEDPLAN

The Agricultural Business Research Institute (ABRI) is a commercial company founded in 1970 at the University of New England, Armidale Australia. The primary business of ABRI is to provide both domestic and international livestock industries with a wide range of multi-species agribusiness information services, including: integrated pedigree and performance database systems (ILR2), genetic analyses, breed registry services and extension services. One of ABRI's flagship products is BREEDPLAN®, a comprehensive suite of multi-trait genetic evaluation technologies developed by the Animal Genetics & Breeding Unit (AGBU)[1] for the beef cattle industry. ABRI provides the BREEDPLAN service to both Australian and international clients under a commercialisation licence from the owners of the BREEDPLAN technology.[2] At present, approximately 63 separate BREEDPLAN genetic evaluations have been developed, with most conducted either monthly or fortnightly. This represents over 14 million animals, almost 40 beef cattle breeds and at least 100 breed associations distributed across 14 countries, with most BREEDPLAN clients accessing 12-24 genetic evaluations per year, subject to the needs of their members. This makes BREEDPLAN the most widely used genetic evaluation service for beef cattle internationally.

1.1.3 Multi-country BREEDPLAN evaluations

ABRI has facilitated multi-country BREEDPLAN evaluations for over 20 years (e.g. Australia with New Zealand; South Africa with Namibia) and a number of larger scale evaluations for the last 10 years (e.g. Pan American Hereford evaluation: joint analysis of the USA, Canada, Uruguay and Argentina). However, the changing commercial context of beef cattle genetic evaluation means we are moving towards significantly larger and more complex evaluations, combining pedigree, phenotypic and genomic information from an increasing number of participating countries. This latter development warrants investigation of options by which Australian beef breeds might progress towards participation in International evaluations.

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[1] AGBU is a joint venture of the University of New England (UNE) and NSW Department of Primary Industries (NSW DPI), with support from Meat & Livestock Australia (MLA)

[2] The owners of the BREEDPLAN technology are MLA, UNE and NSW DPI.

1.1.4 The perceived benefits of international evaluations for Australian beef breeds

As the international trade in beef cattle genetics increases, so too does the exchange of information that allows for developments in the provision of commercial services for international beef genetic evaluations. The participation of Australian beef breeds in such evaluations has potential to provide the following benefits:

- Helping seedstock breeders to identify and select the most suitable genetics internationally, thus accelerating genetic progress given Australian environments and production systems;
- Enhancing Australia's high-value genetic export opportunities, by demonstrating in a directly comparable system how Australian genetics compares to other genetics available internationally, for a range of production traits and scenarios;
- Improving the viability of BREEDPLAN and its ability to withstand competition from other internationally-based providers of genetic evaluation technology that base their models on data that does not adequately reflect Australia's environments, production systems and performance outcomes;

The benefits of the proposed developments in international evaluations will come mainly after the life of the project as the new systems go into production. However, the components of the benefits are measurable and can be used to estimate the value of these evaluations to Australia's beef industry.

2 Project objectives

The objectives as given originally in the agreed project schedule are outlined in points 2.1.1 to 2.1.5 below. For the purposes of this report and to reflect more coherently the course of the project, these objectives have been partitioned into two main objectives: **Scope of Data Availability** and **Commercial Implementation of International Evaluations**. These are outlined in points 2.2 and 2.3 below.

2.1.1 Multi-country genetic parameters

Estimates of multi-country genetic parameters (heritabilities, genetic correlations) which are essential to running international evaluations and which will inform the development of shared reference populations.

2.1.2 Multi-country estimates of genetic relationships between beef populations

Estimates of genetic relationships between populations for each breed which are essential for defining the scope for international reference populations to underpin genomic selection.

2.1.3 Multi-country multi-trait genetic evaluations

Multi-country multi-trait genetic evaluations developed, tested and implemented for five major beef cattle breeds, nominally Angus, Hereford, Brahman, Charolais, Limousin and Wagyu. In addition the Director of AGBU (Dr Rob Banks) and MD of ABRI (Hugh Nivison) will continue to liaise with the ICAR InterBeef working group to ensure that BREEDPLAN technology is strongly advocated internationally.

2.1.4 Multi-country datasets

A review of multi-country datasets to identify the phenotypes and genotypes available to underpin genomic selection in collaborating countries.

2.2 Scope of data availability

2.2.1 Genetic linkage

This project will evaluate genetic linkage between databases maintained by ABRI on behalf of domestic and international beef breed clients, as required for undertaking larger-scale international genetic evaluation. Genetic linkage between ABRI client breeds and other populations outside the commercial business of ABRI will also be reviewed.

2.2.2 Multi-source data extracts

This project will gain permission from ABRI clients to access pedigree and performance data for use in developing international genetic evaluations for beef breeds. The objective is the create multi-source (international) data extracts for a range of beef breeds. For those breed populations where genotypes are available, these international extracts will inform the development of shared reference populations.

2.2.3 Genetic parameters

This project will provide estimates of genetic parameters (heritabilities and genetic correlations) of relevance to international genetic evaluations. Estimates of across-country genetic correlations will also inform the degree of linkage between populations and the decisions made about appropriate models for evaluation.

2.2.4 International collaboration

This project will foster collaborative relationships with European beef breed associations as well as with Interbeef. The objective is to strengthen the basis on which European genetics imported to Australia are evaluated and to review the potential for the marketing of Australian genetics into the European market.

2.3 Commercial implementation of international evaluations

2.3.1 Pipeline processes

This project will define the commercial pipeline of processes necessary to undertake international genetic evaluations for beef breeds on a routine basis. This pipeline will also facilitate the inclusion of genomic data in international evaluations. If this commercial pipeline proves feasible for running large-scale international evaluations, it will mean that Australian breeders will have EBVs available on overseas animals comparable to EBVs reported on Australian animals. Breeders will then be able to target a wider range of genetics to meet their breeding objectives and production goals. Similarly, breeders in other countries will be able to evaluate and identify Australian genetics for consideration in their own breeding programs. The outcomes will be disseminated via local breeders and breed societies, and local extension programs. Depending on what is learned in the project, both Australian and other country analyses could move to multi-country, multi-trait on a routine basis.

2.3.2 Models of evaluation

This project will review and develop a range of models for the international evaluation of Australian beef breeds where international genetics are accessed for increasing rates of genetic gain and breed improvement. Appropriate models will be implemented, where possible.

2.3.3 Data reporting

This project will develop and demonstrate systems for use in the reporting of international EBVs.

2.3.4 Data sharing agreements

This project will formalise data sharing agreements required for the development and commercial undertaking of international genetic evaluations for beef breeds.

3 Methodology

3.1 International BREEDPLAN evaluations

3.1.1 A review of beef breeds for collaboration

A review was conducted of the distribution of beef breed populations represented among the international clients of ABRI, where “client” was defined as a breed association that utilised at least one of the following three commercial services provided by ABRI:

- BREEDPLAN genetic evaluation service
- ILR2 breed registry database
- ABRI data management processes

Focus was given to those beef breeds where pedigree and performance data was available from international clients (ie. in addition to Australian clients) and for which there was some degree of genetic linkage between the respective populations beyond that which existed between Australia and New Zealand (ie. populations beyond those represented in current Trans-Tasman BREEDPLAN evaluations). These breeds represented opportunities for developing international BREEDPLAN genetic evaluations, especially for those breeds with an Australian-based population.

3.1.2 Permission to access client data

For each of the breeds identified for consideration in developing an international genetic evaluation, permission was sought from clients to access the relevant pedigree, performance and cross-reference data for this research.

3.1.3 Construction of international cross-reference files

Clients that use ABRI’s ILR2 breed registry software also use the database to store details on foreign animals, such as country of origin, overseas registration number (or animal identifier) and the overseas Association that assigned the registration number. A foreign animal can be a direct import from the country of origin (birth country) or it can be an animal from one country that appears in the pedigree of an animals imported from a different country, meaning that some animals are represented on more than one breed association database. Foreign animals can therefore have multiple identifiers and registration numbers globally, and ABRI clients store the details available to them within the cross-reference table of their ILR2 database. ABRI has software and processes in place to extract this cross-reference information from relevant ILR2 databases for use in combining (ie. merging) data extracts that share linkage via common animals.

ABRI reviewed, compared and updated the cross-reference information available in ILR2 databases for a range of breeds. This information was used to create an international cross-reference extract for those breeds and clients where permission was given.

3.1.4 Creating data extracts for International BREEDPLAN evaluations

ABRI created international pedigree and performance extracts using individual country extracts, an international cross-reference extract and ABRI Merging Software. Priority was given to the Hereford, Brahman and South Devon breeds.

3.1.5 Estimation of genetic parameters for 200-day weight

International extracts were used to estimate variance components for 200-day weight for each country population and for the international population using WOMBAT (Meyer, 2006). Models included direct and maternal genetic effects and an additional random effect for dam permanent environment. The 200-day weight contemporary group defined by Graser *et al* (2005) was fitted as a fixed effect and three covariates as described by Graser et al (2005) were included (a linear effect of age within sex, a quadratic effect of age of dam, and an additional linear effect of age of dam for dams less than 3.2 years in age). Data was restricted to single- and natural- born animals only, with single-calf and single-sire contemporary groups excluded.

The international pedigree extract was used to create the required pedigree file, with three generations included for performance animals.

3.1.6 Estimation of across-country genetic correlations for 200-day weight

Pair-wise across-country genetic correlations were estimated for 200-day weight using the data extracts and models described in 3.1.5. Residual correlations and the correlation between dam permanent environment effects were assumed to be zero.

3.1.7 International multi-trait covariance matrix

For the Brahman breed, the international data extract was used to estimate the variance components for a subset of traits in the international evaluation: birth weight, 200-day weight, 400-day weight, 600-day weight, mature cow weight, scrotal circumference, ultrasound scan traits (eye muscle area and rib fat). All other variance components and correlations for the full range of traits in the international evaluation were as per the covariance matrix currently used in the Australian Brahman BREEDPLAN evaluation. These additional traits included: gestation length, days-to-calving, age at puberty (heifers), lactational anoestrus, percent normal sperm, flight time and a range of carcase traits (carcase weight, eye muscle area, rib and rump fat, retail beef yield, intramuscular fat, shear force).

For the Hereford and South Devon breeds, the international data extracts were used to estimate variance components and correlations for the following traits in the international evaluations: birth weight, 200-day weight, 400-day weight, 600-day weight, mature cow weight, scrotal circumference, ultrasound scan traits (eye muscle area, rib fat, intramuscular fat). Models as described in 3.1.5 (univariate analysis) and 3.1.6 (bivariate analysis) were used. Note that these traits represented a subset of the full range of traits that can be included in BREEDPLAN evaluations.

3.1.8 Test evaluations

An international BREEDPLAN evaluation was completed for each of the Hereford, Brahman and South Devon breeds using version 6.2 of the BREEDPLAN analytical software. A conventional BLUP multi-trait model was used, with either a complete set of BREEDPLAN traits (Brahman) or a subset of traits (Hereford and South Devon) included as outlined in 3.1.7. Country-specific data adjustment factors for age of animal at measurement and age of dam effects as derived from the univariate analyses (3.1.7) were applied in the pre-BLUP job stream.

As per the standard multi-trait BREEDPLAN model, two records per animal were included for 200-, 400- and 600-day weight traits and four records per animal for mature cow weight. Sex-specific expression of the ultrasound scan traits was also modelled. In the Brahman evaluation, up to six records per animal for the days-to-calving trait were included. Genetic groups representing breed, country and birth year combinations were included for the modelling of base animals. The interaction of sire and herd was included as an additional random effect for weight traits, accounting for approximately 2% of the corresponding phenotypic variance. Heterogeneity of variance was modelled for all traits.

These models assumed the across-country correlations to be close to 1.0 for each of the traits included.

All job streams and parameter files were configured for compliance with Single-Step BREEDPLAN version 6.2, yet with null parameters relating to the Genomic Relationship Matrix (switching it to a conventional BLUP analysis). A Single-Step model was therefore available subject to permission for access to genomic data for inclusion in the relevant international BREEDPLAN evaluation. This job stream made use of an enhanced solver algorithm with capacity to solve more than 450 million equations in less than 24 hours, thus facilitating the implementation of single-step GBPLUP procedures into routine BREEDPLAN evaluations (Johnston *et al*, 2018) and reducing the time to convergence for larger international evaluations.

3.1.9 Reporting procedures

ABRI developed a web-based system for each of the Brahman and Hereford evaluations, allowing international BREEDPLAN EBVs to be reported and allowing for a wide range of selection criteria to be applied.

3.1.10 Data sharing agreements

ABRI sought formal data sharing agreements from the relevant clients who chose to participate in the research phase. Transitioning to routine international runs required further formal agreement as to data sharing, frequency of runs, reporting, fees etc. That is, the agreements could not be determined prior to clients being presented with outcomes of the relevant research. The development of formal agreements was part of the normal commercialisation process that ABRI would undertake if analyses were to progress to multi-partner production runs.

3.1.11 Documenting the process pipeline

ABRI documented the procedures required from start to finish of the process pipeline required for the implementation of international BREEDPLAN evaluations.

3.2 Assessing the priority of ABRI clients for international evaluations

3.2.1 A survey of ABRI clients perspectives

The finalising of data-sharing agreements for routine international evaluations, or at least progressing towards that goal, presumed that participation in such evaluations remained a vision shared across multiple countries representing the same breed. A survey of ABRI beef clients was therefore conducted to gauge thoughts and level of interest regarding participation in international genetic evaluations for beef cattle.

A copy of the survey is given in Appendix A.

3.2.2 Review of survey responses

Australian and international client breeds were surveyed separately to allow comparison between domestic and international client priorities for the development of international BREEDPLAN evaluations. International responses were clustered according to breed societies representing:

(i) Europe and the United Kingdom,
(ii) Southern Africa,
(iii) the USA and Canada, and
(iv) New Zealand

3.3 Collaboration between ABRI and Interbeef

The International Committee for Animal Recording (ICAR) is a body composed of 115 members from 57 countries and strives to be the leading global provider of guidelines, standards and certification for animal identification, animal recording and animal evaluation.

The Interbeef Working Group is one part of ICAR's Working Group structure and has an objective to develop, provide and promote a system for routine international genetic evaluations of beef breeds. The Interbeef Working Group (Interbeef) conducts across-country single trait (weaning weight) analyses primarily for European-based breeds such as Limousin, Charolais and Beef Simmental. These analyses have been considered by Australian breeds as being largely irrelevant, especially given the significant costs to participate. However, this project provided ABRI with opportunity to collaborate with ICAR and to actually identify the processes, costs and potential benefits from participating in their analyses. Preliminary discussions between ICAR, ABRI and AGBU indicated some potential for mutual sharing of pedigree and performance data between the Interbeef evaluations based in Upsala, Sweden, and the BREEDPLAN evaluations based in ABRI, Australia. There is considerable potential for benefits to accrue from collaborative Research and Development.

3.3.1 ICAR Membership

Under the auspices of this project, ABRI applied to become a full member of ICAR and to gain access to the Interbeef Technical and Working Groups. This provided opportunities for ABRI to submit suitable data extracts to the relevant Interbeef breed evaluations, allowing a benchmarking of the BREEDPLAN and Interbeef approaches to beef breed evaluations. It also provided opportunity for the BREEDPLAN technology to remain strongly advocated internationally, creating opportunities for BREEDPLAN in Europe (i.e. either via data received from Interbeef under reciprocal arrangements or directly from European-based breed associations).

3.3.2 Collaboration with Interbeef: Australian Charolais and Limousin

ABRI gained permission from Australian Charolais and Australian Limousin to undertake the database processes required to create data extracts for inclusion in the Interbeef analysis of 200-day weight data. These extracts contained the pre-adjusted 200-day weight and corresponding slice group associated with the nominated BREEDPLAN analysis. ABRI estimated variance components relevant to each Interbeef data extract using WOMBAT (Meyer, 2011). These estimates were provided to Interbeef for use in their analysis of weaning weight for the Charolais and Limousin breeds.

As members of ICAR and Interbeef ABRI received access to the InterBeef test database. Access to file formats and data checking software installed at ABRI facilitated the provision of the relevant files of identification numbers and pedigree details. ABRI engaged with the Irish Cattle Breeding Federation (ICBF) to ensure the correct identification of animals recorded on the Australian Charolais database, given the ICBF database records the current Interbeef identifiers.

ABRI participated with Interbeef as the supplier of data files for the Charolais and Limousin breeds in Australia. No other Australian-based breeds were considered.

3.3.3 ABRI engagement on technical and operations working groups

ABRI gained representation at each of the ICAR Working Groups of relevance to Interbeef, these being the Technical Group and the Working Group.

3.3.4 Reciprocal arrangement for Hereford and Angus breeds

ABRI sought to gain access to the Interbeef data extracts available for the Hereford breed in Europe, for inclusion in developing an international Hereford BREEDPLAN evaluation. Consideration was also given to gaining access to the Interbeef data extracts for the Angus breed, for possible use in other Angus BREEDPLAN evaluations conducted in the northern hemisphere (e.g. Aberdeen Angus in the UK and Portugal).

4 Results

4.1 International BREEDPLAN evaluations

Table 1 provides a summary of beef breeds for which ABRI provides a commercial service and where permission was gained for accessing the data necessary for developing an international BREEDPLAN evaluation for the breed. A more detailed account of each breed follows.

Table 1. Example of beef breeds available for International BREEDPLAN evaluation

Breed	Countries[1]	Evaluations[2]	Total animals[3]	Total 200-wt[4]
Hereford	7	3	5,596,974	2,223,585
Simmental	4	3	1,502,138	530,802
Charolais	4	3	905,210	326,798
South Devon	4	3	411,034	200,801
Brahman	4	2	1,361,692	546,069
Limousin	3	1	467,618	142,931
European Angus	2	2	447,722	129,944

[1] Separate databases

[2] Separate BREEDPLAN genetic evaluations, with each evaluation conducted monthly or fortnightly

[3] Total animals across BREEDPLAN multi-trait evaluations (including 2 generations of pedigree)

[3] Total count of animals with at least one 200-day weight included in a BREEDPLAN evaluation

4.1.1 Hereford

ABRI received support from seven clients representing the Hereford breed: Hereford Australia Ltd, New Zealand Hereford Association, the Canadian Hereford Association, Hereford Cattle Society (in the United Kingdom), Hereford Cattle Breeders Society of Namibia, Hereford Association of Uruguay and the Hereford Association of Argentina. However, it took a considerable length of time for clients to provide permission for ABRI to access data for this project, with some Associations needing to take the matter to their respective Boards. While most clients gave permission in early 2019, the last permission granted was in early 2020 and corresponded to a Hereford population of significance to Australia.

Five Hereford Associations use the ILR2 breed registry product developed by ABRI, making for straightforward access to data extracts for analysis. In contrast, the two South American associations each use a domestic registry product but engage ABRI to receive their data and create extracts as required for inclusion in the Pan American Hereford evaluation. This evaluation combines data from America, Canada, Uruguay and Argentina and was historically provided by ABRI using BREEDPLAN software. However, since early 2019, this 4-country analysis has been provided by Theta Solutions using BOLT software. Importantly for the current project, permission to use data was given by each Association in Canada, Uruguay and Argentina. The American Association declined to contribute data directly to the current project but remains represented by way of progeny born to American genetics in the participating countries.

Table 2 summarises the total number of Hereford animals with 200-day weight records available in each country and used for parameter estimation. Variance component estimates are also provided for each country as well as those estimated using the international extract. Namibia has been omitted from this table as the number of 200-day weight records was too small for variance component estimation (n=2,722).

Table 2. Estimates of variance components and heritabilities[1] for 200-day weight, for each Hereford population and for the international Hereford population

	AUS	NZ	CAN	URY	ARG	UK	INT
Records	338,853	296,768	413,039	259,461	75,752	26,221	1,410,094
V_A	96.34	98.73	117.04	57.79	53.62	89.46	93.39
V_M	53.81	71.37	74.50	52.28	32.80	61.47	62.30
V_C	143.50	163.61	129.94	94.99	95.78	141.17	132.23
V_E	343.57	289.83	307.71	320.56	363.22	348.35	318.67
V_P	637.22	623.54	629.20	525.61	545.41	640.45	606.58
h^2_A	0.145	0.152	0.179	0.106	0.09	0.134	0.148
h^2_M	0.081	0.11	0.114	0.095	0.06	0.092	0.099

[1]Additive genetic variance (V_A), maternal genetic variance (V_M), dam PEV (V_C), residual variance (V_E) and total phenotypic variance (V_P); direct heritability (h^2_A) and maternal genetic heritability (h^2_M)

Estimates of across-country correlations for 200-day weight are given in Table 3. Estimates above the diagonal are for the correlations between direct genetic effects while those below the diagonal are for maternal genetic effects. Estimates involving the UK were generally close to unity and with very high standard errors.

Table 3. Estimates of across-country genetic correlations for 200-day weight in Hereford cattle. Direct genetic correlations above the diagonal; maternal genetic correlations below the diagonal

	CAN	AUS	NZ	URY	ARG
Canada	-	0.81 + 0.07	0.92 + 0.07	0.76 + 0.10	0.84 + 0.16
Australia	0.84 + 0.09	-	0.91 + 0.04	0.96 + 0.09	0.91 + 0.20
New Zealand	0.71 + 0.16	0.92 + 0.06	-	0.89 + 0.13	0.89 + 0.22
Uruguay	0.87 + 0.09	0.76 + 0.14	0.77 + 0.20	-	1.00 + 0.64
Argentina	0.73 + 0.21	0.24 + 0.33	1.00 + 0.28	0.99 + 0.62	-

The international Hereford cross-reference file contained 28,126 equivalences. The primary source of this information and the secondary countries in which these genetics are represented is given in Table 4. Note that this table summarises the total number of matches between countries and does not indicate how many of these matches are shared in common across secondary countries.

Table 4. Total number of Hereford animals in common between each primary and secondary source database

Primary	Secondary source						
	AUS	NZ	URY	ARG	UK	NAM	Total
Canada	11,042	3,127	1,756	2,377	4,503	9	22,814
Australia	-	3,268	19	28	0	26	3,341
New Zealand	1,241	-	27	0	0	2	1,270
Uruguay	0	0	-	368	0	0	368
Argentina	0	0	333	-	0	0	333

Table 5 indicates the number of animals (by primary source) in the cross-reference file that are represented in 2 or more other Hereford databases. For example, there are 2,602 animals that have Canada as the primary source of information in the international Hereford cross-reference file, with 2 other countries providing a secondary source of information on these animals. In other words, these animals are recorded on THREE databases. Likewise, there are 1,458 animals with Canada as a primary source of information, recorded on FOUR databases in total. Approximately 98% of all primary cross-reference information for animals recorded on THREE or more databases is derived from Canada.

Table 5. Number of Hereford animals by primary source in the cross-reference file that are represented in 2 or more other Hereford databases

Primary	Secondary sources				
	2	3	4	5	Total
Canada	2,602	1,458	370	138	4,568
Australia	41	5	2	0	49
New Zealand	27	0	0	0	27
Total	2,670	1,463	372	138	4,644

4.1.2 South Devon

ABRI gained support from four clients representing the South Devon breed: South Devon Cattle Society of Australia (2020), South Devon Cattle Society of New Zealand (2020), South Devon Herd Book Society in the United Kingdom (2019) and American South Devon Association (2020). While all four clients currently use ABRI's ILR2 breed registry product, the American Association does not use BREEDPLAN for their genetic evaluation.

Table 6 summarises the total number of South Devon animals with 200-day weight records available in each country. Variance component estimates are given for each country as well as those estimated using the international extract.

Estimates of across-country correlations for 200-day weight are given in Table 7. Estimates above the diagonal are for correlations between direct genetic effects while those below the diagonal are for maternal genetic effects. The international South Devon cross-reference file contained 1,877 equivalences. The primary source of information on these genetics and the secondary countries in which these genetics are represented is given in Table 8.

Table 6. Estimates of variance components and heritabilities[1] for 200-day weight, for each South Devon population and for the international South Devon population

	UK	USA	NZ+AU	INT
Records	40,723	52,568	45,133	138,525
V_A	130.76	108.86	133.56	112.35
V_M	60.80	43.92	67.07	54.41
V_C	137.87	97.70	137.63	111.34
V_E	547.38	358.45	385.53	401.15
V_P	876.81	608.93	723.79	679.25
h^2_A	0.149	0.179	0.185	0.165
h^2_M	0.069	0.072	0.093	0.080

[1] Additive genetic variance (V_A), maternal genetic variance (V_M), dam PEV (V_C), residual variance (V_E) and total phenotypic variance (V_P); direct heritability (h^2_A) and maternal genetic heritability (h^2_M)

Table 7. Estimates of across-country genetic correlations for 200-day weight in South Devon cattle. Direct genetic correlations above the diagonal; maternal genetic correlations below the diagonal

	UK	USA	NZ+AUS
UK	-	n.e.	0.96 ± 0.11
USA	n.e.	-	1.00 ± 0.12
NZ+AUS	0.04 ± 0.37	0.65 ± 0.38	-

Table 8. Total number of South Devon animals in common between each primary and secondary source database

Primary	Secondary source				
	UK	AUS	NZ	USA	Total
UK	-	495	292	167	954
Australia	-	-	369	3	372
New Zealand	27	211	-	62	300

USA	-	169	82	-	251

Table 9 indicates the number of animals (by primary source) in the cross-reference file that are represented in 2 or more other South Devon databases.

4.1.3 Simmental

ABRI gained support from four clients representing the Simmental breed: Simmental Australia, Simmental New Zealand, Simmentaler Cattle Breeder's Society of South Africa and the British Simmental Cattle Society. All four clients currently use ABRI's ILR2 breed registry product and the BREEDPLAN genetic evaluation service.

Table 9. Number of South Devon animals by primary source in the cross-reference file that are represented in 2 or more other South Devon databases

Primary	Secondary sources		
	2	3	Total
UK	204	30	234
Australia	3	0	3
New Zealand	35	13	48
USA	45	0	45
Total	287	43	330

Table 10 summarises the total number of Simmental animals with 200-day weight records available in each country. Variance component estimates are also provided for each country. Variance components representing an international extract were not estimated.

Table 10. Estimates of variance components and heritabilities[1] for 200-day weight, for each Simmental population

	AUS	NZ	RSA	UK
Records	37,300	77,178	102,966	22,797
V_A	162.80	102.28	85.65	120.29
V_M	58.15	53.67	34.08	23.38
V_C	64.51	67.17	53.16	66.59
V_E	393.50	340.64	323.20	483.78
V_P	678.95	563.75	496.09	694.04
h^2_A	0.240	0.181	0.173	0.173
h^2_M	0.086	0.095	0.069	0.034

[1] Additive genetic variance (V_A), maternal genetic variance (V_M), dam PEV (V_C), residual variance (V_E) and total phenotypic variance (V_P); direct heritability (h^2_A) and maternal genetic heritability (h^2_M)

The international Simmental cross-reference file contained 4,304 equivalences. The primary source of information on these genetics and the secondary countries in which these genetics are represented is given in Table 11.

Table 11. Total number of Simmental animals in common between each primary and secondary source database

Primary	Secondary source				
	AUS	NZ	RSA	UK	Total
Australia	-	1,213	12	4	1,229
New Zealand	645	-	1	21	667
South Africa	917	184	-	16	1,117
UK	1,258	321	2	-	1,291

Table 12 indicates the number of animals (by primary source) in the cross-reference file that are represented in 2 or more other Simmental databases.

Table 12. Number of Simmental animals by primary source in the cross-reference file that are represented in 2 or more other Simmental databases

Primary	Secondary sources		
	2	3	Total
Australia	4	0	4
New Zealand	13	0	13
South Africa	140	7	147
UK	265	2	267
Total	422	9	431

ABRI completed a review of the overseas identifiers recorded for American and Canadian Simmental imports on the Australian database, updating these where necessary. There are currently 3,947 American identifiers and 2,376 Canadian identifiers in the Australian Simmental cross-reference table.

4.1.4 Charolais

ABRI gained support from three clients representing the Charolais breed: Charolais Society of Australia, the British Charolais Cattle Society and the National Association of Hungarian Charolais Cattle Breeders. Each of these clients currently uses ABRI's ILR2 breed registry product and the BREEDPLAN genetic evaluation service. Given positive relationships between the Australian society and each of the associations in Canada and Mexico, ABRI contacted each association and provided an overview of the project, including an invitation to participate. The Canadian Charolais Association declined the invitation and a reply from the Mexican Association was not received.

Table 13 summarises the total number of Charolais animals with 200-day weight records available in each country and the variance components estimated for each country. However, an international Charolais cross-reference file was deemed premature and as such, an international extract was not created nor were international variances components estimated.

Table 13. Estimates of variance components and heritabilities[1] for 200-day weight, for each Charolais population

	AUS	UK	HUN
Records	75,589	85,544	23,101
V_A	163.11	98.40	434.37
V_M	64.57	44.79	196.77

V_C	107.06	96.64	43.14
V_E	407.49	574.94	769.22
V_P	742.22	814.79	1443.50
h^2_A	0.220	0.121	0.301
h^2_M	0.087	0.055	0.136

[1]Additive genetic variance (V_A), maternal genetic variance (V_M), dam PEV (V_C), residual variance (V_E) and total phenotypic variance (V_P); direct heritability (h^2_A) and maternal genetic heritability (h^2_M)

ABRI completed a review of the overseas identifiers recorded for American and Canadian Charolais imports on the Australian database, updating these where necessary. There are currently 456 American identifiers and 763 Canadian identifiers in the Australian Charolais cross-reference table.

4.1.5 Brahman

Following the International Brahman Technical Committee meeting in Rockhampton (2016), an agreement was made to progress the development and commercial delivery of an international Brahman BREEDPLAN evaluation. This collaboration represented the American Brahman Breeders Association, the Australian Brahman Breeders Association, the Brahman Cattle Breeders Association of South Africa and the Brahman Cattle Breeders Association of Namibia. Each of these were clients of ABRI, users of the ILR2 breed registry system and users of the BREEDPLAN genetic evaluation service at the time of formalising this collaboration. In early 2018, however, the American Brahman Breeders Association terminated their service agreement with ABRI, with their November 2017 extracts being the final data left available for use in the current international project.

Table 14 summarises the total number of Brahman animals with 200-day weight records available in each country as of January 2018. Variance component estimates relevant to these data extracts are also provided for each country as well as those estimated using the international extract available at January 2018.

Table 14. Estimates of variance components and heritabilities[1] for 200-day weight, for each Brahman population and for the international Brahman population

	AUS	RSA	NA	USA	INT
Records	140,466	85,048	27,370	77,652	306,120
V_A	95.44	63.75	78.99	93.94	84.01
V_M	29.99	41.75	25.71	27.78	30.76
V_C	38.40	43.14	47.64	42.42	40.79
V_E	323.71	330.10	289.47	323.59	319.88
V_P	487.54	478.74	441.81	487.74	475.42
h^2_A	0.196	0.133	0.179	0.193	0.172
h^2_M	0.062	0.087	0.058	0.057	0.065

[1]Additive genetic variance (V_A), maternal genetic variance (V_M), dam PEV (V_C), residual variance (V_E) and total phenotypic variance (V_P); direct heritability (h^2_A) and maternal genetic heritability (h^2_M)

Estimates of across-country correlations for 200-day weight are given in Table 15. Estimates above the diagonal are for correlations between direct genetic effects while those below the diagonal are for maternal genetic effects.

Table 15. Estimates of across-country genetic correlations for 200-day weight in Brahman cattle. Direct genetic correlations above the diagonal; maternal genetic correlations below the diagonal

	USA	AUS	RSA	NAM
USA	-	0.83 ± 0.06	0.91 ± 0.09	0.96 ± 0.16
Australia	0.83 ± 0.17	-	1.00 ± 0.11	0.80 ± 0.21
South Africa	0.75 ± 0.20	0.67 ± 0.29	-	0.57 ± 0.12
Namibia	0.08 ± 0.55	-0.06 ± 0.64	0.56 ± 0.21	-

Table 16. Total number of Brahman animals in common between each primary and secondary source database

Primary	Secondary source				
	USA	AUS	RSA	NAM	Total
USA	-	5,285	6,162	1,074	12,521
Australia	0	-	90	68	158
South Africa	0	1,325	-	37,544	38,869
Namibia	0	-	10,125	-	10,125

The international Brahman cross-reference file contained 50,403 equivalences. The primary source of information on these genetics and the secondary countries in which these genetics are represented is given in Table 16. Approximately 97% of these equivalences represent the considerable commonality of genetics between South Africa and Namibia. Table 17 indicates the number of animals (by primary source) in the cross-reference file that are represented in 2 or more other Brahman databases.

Table 17. Number of Brahman animals by primary source in the cross-reference file that are represented in 2 or more other Brahman databases

Primary	Secondary sources		
	2	3	Total
USA	1,586	724	2,310
Australia	68	0	68
South Africa	775	0	775
Total	2,429	724	3,153

4.1.6 Limousin

ABRI currently combines the pedigree and performance data for joint evaluation of the Limousin breed as recorded on the Australian, South African and Namibian ILR2 servers. In the absence of access to other Limousin populations and data extracts, no further developments were considered for this breed.

ABRI completed a review of the overseas identifiers recorded for American and Canadian Limousin imports on the Australian database, updating these where necessary. There are currently 3,145 American identifiers and 441 Canadian identifiers in the Australian Limousin cross-reference table.

4.1.7 Angus

ABRI sought permission and initiated work on two Angus databases in Europe: Aberdeen-Angus Cattle Society in the United Kingdom and Aberdeen Angus Portugal. While separate BREEDPLAN evaluations were in place for each country, potential linkage between the two populations was investigated. This resulted in release of a joint BREEDPLAN evaluation of Aberdeen Angus in February 2018 and is now run as a standard monthly BREEDPLAN production run.

The combined analysis includes approximately 21,500 sires and 118,000 dams. At this stage data from Portugal is limited to growth traits with approximately 5,000 weaning weights analysed compared to 150,000 for the UK.

In addition to this work, ABRI identified considerable potential linkage to the Danish Angus population given the representation of Danish genetics on both the UK and Portuguese databases. Angus genetics originating from other member associations of Interbeef were also represented in the combined pedigree extract. This may facilitate future expansion into other European countries and/or incorporation into Interbeef.

Since June 2019, ABRI has received expressions of interest from other European Angus Associations, including those based in the Czech Republic, Romania and Hungary. In May 2020, ABRI was supplied with an extract of pedigree and performance records from the Czech Republic in order to conduct a trial BREEDPLAN analysis for this population. This trial analysis included a total of 55,574 animals of which 39,114 had at least one 200-day weight record analysed. More importantly, imported genetics were identified in the pedigree extract based on country of origin, with each having the animal identifier in the country of origin provided. This provides another potential database for combining in the joint evaluation of the Angus breed in Europe.

4.1.8 International genetic parameter matrix

Table 19 summarises the final heritabilities and correlations assumed for the International Hereford covariance matrix. Direct heritabilities are given on the diagonal, with genetic and residual correlations given above and below the diagonal, respectively. A correlation of 0.25 was assumed between the maternal genetic components of birth weight and 200-day weight, but no direct-maternal correlations were modelled. The correlation between dam PEV for birth weight and 200-day weight was 0.32.

Table 19. International Hereford covariance matrix: direct heritabilities on the diagonal, genetic correlations above diagonal; residual correlations below diagonal

	BW	200	400	600	MCW	SC	EMA	RIB	IMF
BW	**0.36**	0.70	0.55	0.60	0.45	0.10	0.10	-0.05	0.0
200	0.34	**0.15**	0.75	0.70	0.40	0.10	0.20	-0.05	0.0
400	0.23	0.60	**0.37**	0.85	0.60	0.15	0.35	-0.10	0.0
600	0.16	0.50	0.67	**0.35**	0.70	0.15	0.35	-0.10	0.0
MCW	0.10	0.30	0.40	0.55	**0.34**	0.10	0.10	-0.25	0.0
SC	0.0	0.53	0.27	0.20	0.20	**0.42**	0.05	0.0	0.0
EMA	0.03	0.25	0.35	0.35	0.20	0.10	**0.30**	0.0	0.0
RIB	-0.04	0.21	0.31	0.31	0.10	0.0	0.19	**0.36**	0.30
IMF	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	**0.31**

Table 20 summarises the final heritabilities and correlations assumed for the International South Devon covariance matrix. Direct heritabilities are given on the diagonal, with genetic and residual correlations given above and below the diagonal, respectively. The correlation between maternal genetic components of birth weight and 200-day weight was 0.0 and no direct-maternal correlations were modelled. The correlation between dam PEV for birth weight and 200-day weight was 0.54.

Table 20. International South Devon covariance matrix: direct heritabilities on the diagonal, genetic correlations above diagonal; residual correlations below diagonal

	BW	200	400	600	MCW	SC	EMA	RIB	IMF
BW	**0.34**	0.66	0.52	0.56	0.35	0.10	0.15	0.05	0.0
200	0.29	**0.09**	0.75	0.70	0.40	0.10	0.20	0.05	0.0
400	0.21	0.53	**0.23**	0.80	0.50	0.15	0.40	0.10	0.0
600	0.16	0.52	0.64	**0.30**	0.75	0.15	0.40	0.10	0.0
MCW	0.10	0.30	0.40	0.55	**0.33**	0.15	0.20	0.10	0.0
SC	0.0	0.50	0.24	0.23	0.20	**0.44**	0.05	-0.05	0.0
EMA	0.03	0.23	0.26	0.30	0.20	0.10	**0.26**	0.20	0.0
RIB	-0.04	0.19	0.24	0.27	0.10	0.0	0.20	**0.22**	0.30
IMF	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	**0.25**

Table 21 summarises the final heritabilities and correlations assumed for a subset of traits in the International Brahman covariance matrix. Direct heritabilities are given on the diagonal, with genetic and residual correlations given above and below the diagonal, respectively. The correlation between maternal genetic components of birth weight and 200-day weight was 0.0 and no direct-maternal correlations were modelled. The correlation between dam PEV for birth weight and 200-day weight was 0.50.

Table 21. International Brahman covariance matrix: direct heritabilities on the diagonal, genetic correlations above diagonal; residual correlations below diagonal

	BW	200	400	600	MCW	SC	EMA	RIB
BW	**0.30**	0.71	0.57	0.61	0.62	0.10	0.29	-0.04
200	0.30	**0.19**	0.83	0.78	0.66	0.19	0.50	0.06
400	0.31	0.69	**0.35**	0.77	0.70	0.20	0.57	0.09
600	0.27	0.61	0.69	**0.48**	0.80	0.20	0.51	0.09
MCW	0.34	0.52	0.60	0.54	**0.45**	0.20	0.41	-0.05
SC	0.0	0.15	0.15	0.15	0.15	**0.44**	-0.05	-0.09
EMA	0.05	0.36	0.36	0.36	0.16	0.10	**0.18**	0.27
RIB	-0.05	0.11	0.15	0.04	0.10	0.05	0.10	**0.35**

4.1.9 Test evaluations

Test runs were completed for the international BREEDPLAN evaluations developed for the Hereford, Brahman and South Devon breeds. Table 22 provides summary statistics for a subset of traits included in each of these test runs. The total number of records per trait is reported.

International BREEDPLAN EBVs were calculated for approximately 5.5M, 1.3M and 410,000 animals representing the Hereford, Brahman and South Devon breeds respectively. For each of these three breeds, Tables 23, 24 and 25 summarise the number of sires from each country with progeny recorded for 200-day weight, the total number of 200-day weight progeny represented by these sires and the number of sires with a 200-day weight of their own in the evaluation.

Table 22. Summary statistics for international BREEDPLAN evaluations: Hereford, Brahman and South Devon

Trait	Hereford	Brahman	South Devon
Birth weight	1,749,276	401,016	212,409
200-day weight	2,229,446	492,168	238,915
400-day weight	1,374,949	231,234	159,225
600-day weight	769,455	194,406	52,299
Mature cow weight	128,461	28,040	7,764
Scrotal circumference	243,517	50,097	9,268
Scan EMA	469,172	44,079	19,978
Scan RIB fat	471,333	42,291	20,195
Scan IMF	270,090	-	13,755

Table 23. Representation of sires in the international Hereford BREEDPLAN evaluation

	Number of sires	Total 200-wt progeny	Own 200-wt record
Argentina	2,193	84,197	1,421
Australia	22,277	643,907	16,733
Canada	27,619	637,547	18,124
Namibia	348	3,754	167
New Zealand	9,827	324,244	8,407
United Kingdom	3,330	50,245	1,999
Uruguay	6,523	240,156	5,212
Total	72,117	1,984,050	52,063

Table 24. Representation of sires in the international Brahman BREEDPLAN evaluation

Brahman	Number of sires	Total 200-wt progeny	Own 200-wt record
Australia	5,443	190,104	3,252
Namibia	757	21,087	681
South Africa	5,849	141,686	3,335
USA	5,951	149,956	3,179
Total	18,000	502,833	10,447

Table 25. Representation of sires in the international South Devon BREEDPLAN evaluation

South Devon	Number of sires	Total 200-wt progeny	Own 200-wt record
Australia	1,176	21,418	895
New Zealand	1,312	32,433	1,068
United Kingdom	2,710	67,781	1,601
USA	3,113	76,594	2,251
Total	8,311	198,226	5,815

In terms of run time, the international BREEDPLAN evaluation reached convergence in 9 hours for Hereford, 3 hours for Brahman and 1.5 hours for South Devon. These times relate to the BREEDPLAN analytical job stream only (ie. exclude all data preparation requirements pre-analysis and result handling post-analysis).

4.1.10 Assets

ABRI purchased a computer server with funds allocated in the project. Compared to its predecessors, this server had 8 times more RAM and 6 times as many cores, better equipping ABRI to assemble large data sets, conduct test runs and multi-country Single-Step BREEDPLAN analyses. This was a Linux server with the latest Intel Xenon E5-2697 V4 CPUs comprising 36 CPU cores and 512GB memory. It allowed ABRI's largest multi-country and Single-Step BREEDPLAN analyses to reach completion in 40% of the total time required by the next largest machine. As a result of this purchase, ABRI was better positioned to conduct the work outlined in this project.

4.1.11 Data sharing agreements

With the exception of the Aberdeen-Angus BREEDPLAN evaluation combining data from the United Kingdom and Portugal, no other international BREEDPLAN evaluations within this project transitioned towards formalising of data sharing agreements.

However, representatives of the Brahman breed associations in South Africa, Namibia and Australia re-opened dialogue with the American association in 2020 to re-engage their participation in the international Brahman BREEDPLAN evaluation. Subject to these negotiations, the data sharing agreements between the four Brahman breed associations might be formalised.

ABRI sent a briefing paper to Interbeef in August 2019 outlining the process by which Hereford populations in Europe might share data for inclusion in an international Hereford BREEDPLAN evaluation. No formal decision was communicated to ABRI.

4.1.12 Pipeline of processes

A schematic of the pipeline of processes required for undertaking routine International genetic evaluations for beef cattle is given in Fig. 1.

From a broad global perspective, there are many database formats used by beef breed associations. Irrespective of how pedigree and performance data is maintained by an individual breed association, an international breed evaluation will necessitate:

(i) the definition and standardising of data extract formats, and
(ii) provision of information to facilitate identification of animals recorded in common across 2 or more databases.

The latter requirement can be achieved by using either an international animal identification approach or the recording of cross-reference information that allows one country identifier to be linked to one or more identifiers as used in other countries. How the individual country extracts are then merged to create the international extracts used in the evaluation will depend on how animals used in common are represented in the country extracts. Use of an international identifier allows separate extracts to simply be amalgamated whereas use of a cross-reference file requires a more sophisticated approach to the merging of data from different sources.

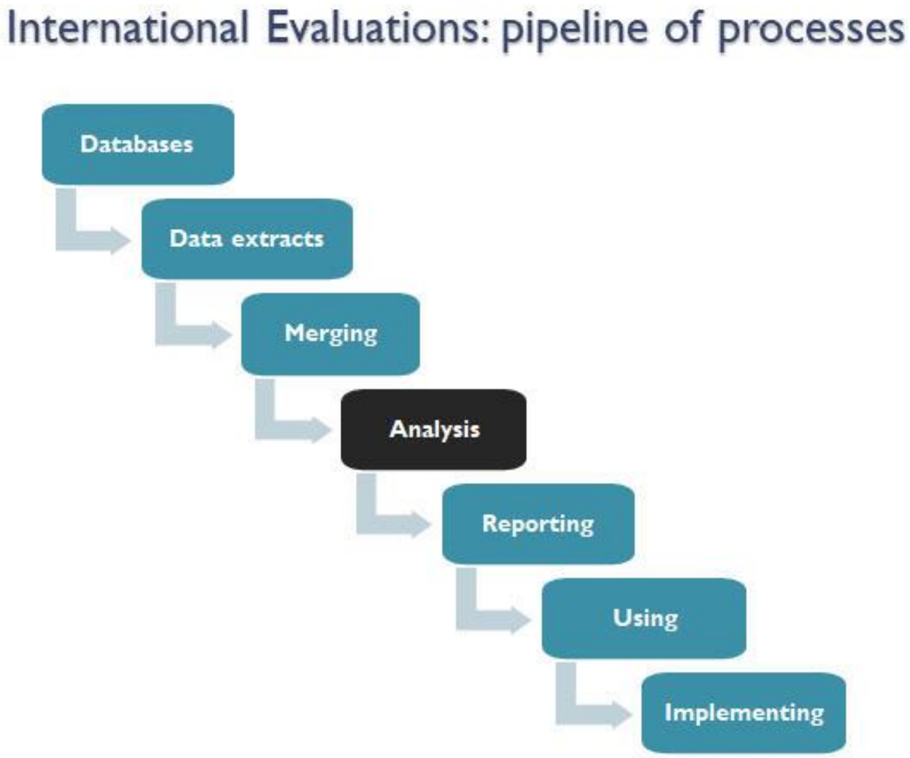


Figure. 1. Schematic of the pipeline of processes required for routine International Genetic Evaluations for beef cattle.

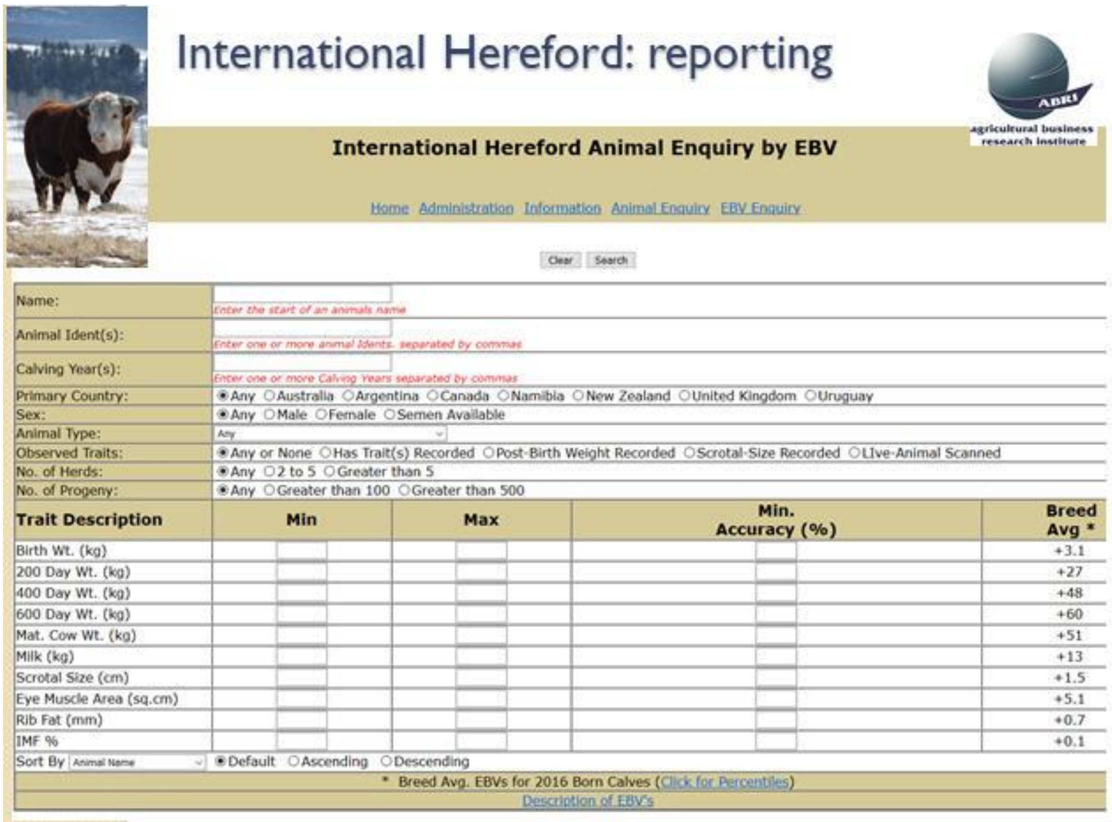
In the current project, BREEDPLAN was chosen as the genetic evaluation technology most appropriate for use in the international evaluation pipeline. Irrespective of the models and software used in the calculation of EBVs and accuracies, however, the reporting and dissemination of international results remains a critical process in the international evaluation pipeline. As to how these international results might then be used – whether as a replacement for individual country evaluations or as an external source of information for inclusion in national evaluations – is another important process that requires consideration.

Finally, the means by which international evaluations are implemented and conducted on a routine basis needs to be determined if such evaluations are to transition into commercial relevance.

4.1.13 Reporting procedures

A web-based browser was developed by ABRI for each of the Hereford and Brahman breeds for the reporting of international BREEDPLAN EBVs. Each browser is an enhancement of the Internet Solutions product currently provided by ABRI, a main difference being that it is populated directly from the international results file without needing to be hosted on any single breed association ILR2 server. In the current prototype systems, EBVs can be reported for sires and young unproven bulls only but could be expanded to reference the entire international breed population.

As shown in Fig. 2, a number of search criteria are available to assist in identifying particular cohorts of sires or bulls. These include primary source country and across-country usage, as well as emphasis on various performance records (on self and/or progeny) and combinations of EBV and accuracy. These prototype systems are currently "de-identified", such that individual sires and young bulls remain anonymous. While technical representatives of participating countries are able to access these test systems, the de-identification of results allows the focus to remain on the process rather than the actual results of international BREEDPLAN evaluations.



Name:	Enter the start of an animals name
Animal Ident(s):	Enter one or more animal Idents. separated by commas
Calving Year(s):	Enter one or more Calving Years separated by commas
Primary Country:	● Any ○ Australia ○ Argentina ○ Canada ○ Namibia ○ New Zealand ○ United Kingdom ○ Uruguay
Sex:	● Any ○ Male ○ Female ○ Semen Available
Animal Type:	Any
Observed Traits:	● Any or None ○ Has Trait(s) Recorded ○ Post-Birth Weight Recorded ○ Scrotal-Size Recorded ○ LIve-Animal Scanned
No. of Herds:	● Any ○ 2 to 5 ○ Greater than 5
No. of Progeny:	● Any ○ Greater than 100 ○ Greater than 500

Trait Description	Min	Max	Min. Accuracy (%)	Breed Avg *
Birth Wt. (kg)				+3.1
200 Day Wt. (kg)				+27
400 Day Wt. (kg)				+48
600 Day Wt. (kg)				+60
Mat. Cow Wt. (kg)				+51
Milk (kg)				+13
Scrotal Size (cm)				+1.5
Eye Muscle Area (sq.cm)				+5.1
Rib Fat (mm)				+0.7
IMF %				+0.1

Sort By Animal Name ● Default ○ Ascending ○ Descending

* Breed Avg. EBVs for 2016 Born Calves (Click for Percentiles)

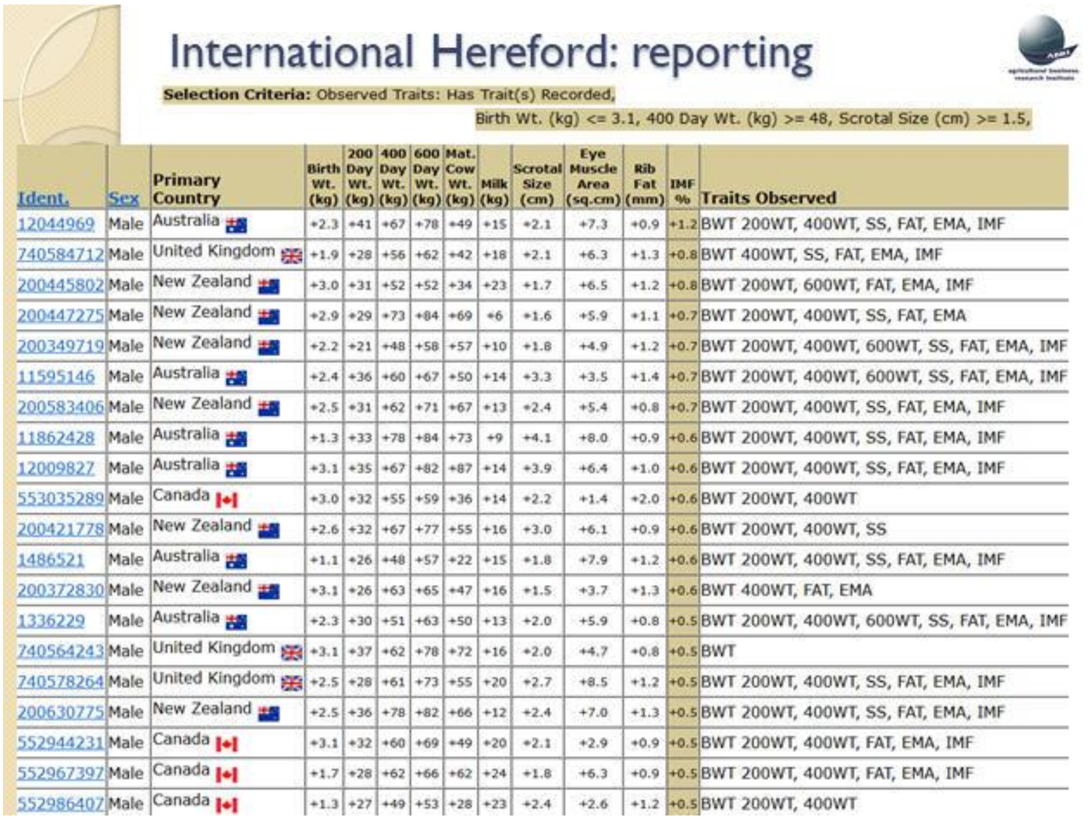
Description of EBV's

Figure. 2. A web-based browser for the reporting of EBVs obtained from International Genetic Evaluations for beef cattle.

As an example, Fig. 3 shows the sires chosen with selection criteria of:

- (i) below international breed average for birth weight EBV;
- (ii) above international breed average for 400-day weight and scrotal circumference EBVs; and
- (iii) has own performance records, regardless of trait.

The list is sorted on scan EMA EBV in descending order and shows individual sires originating from most of the participating countries (as indicated by each national flag icon). Appendix B shows a similar outcome for the reporting of international Brahman BREEDPLAN EBVs.



International Hereford: reporting

Selection Criteria: Observed Traits: Has Trait(s) Recorded,
Birth Wt. (kg) <= 3.1, 400 Day Wt. (kg) >= 48, Scrotal Size (cm) >= 1.5,

Ident.	Sex	Primary Country	Birth Wt. (kg)	200 Day Wt. (kg)	400 Day Wt. (kg)	600 Day Wt. (kg)	Mat. Cow Wt. (kg)	Milk (kg)	Scrotal Size (cm)	Eye Muscle Area (sq.cm)	Rib Fat (mm)	IMF %	Traits Observed
12044969	Male	Australia	+2.3	+41	+67	+78	+49	+15	+2.1	+7.3	+0.9	+1.2	BWT 200WT, 400WT, SS, FAT, EMA, IMF
740584712	Male	United Kingdom	+1.9	+28	+56	+62	+42	+18	+2.1	+6.3	+1.3	+0.8	BWT 400WT, SS, FAT, EMA, IMF
200445802	Male	New Zealand	+3.0	+31	+52	+52	+34	+23	+1.7	+6.5	+1.2	+0.8	BWT 200WT, 600WT, FAT, EMA, IMF
200447275	Male	New Zealand	+2.9	+29	+73	+84	+69	+6	+1.6	+5.9	+1.1	+0.7	BWT 200WT, 400WT, SS, FAT, EMA
200349719	Male	New Zealand	+2.2	+21	+48	+58	+57	+10	+1.8	+4.9	+1.2	+0.7	BWT 200WT, 400WT, 600WT, SS, FAT, EMA, IMF
11595146	Male	Australia	+2.4	+36	+60	+67	+50	+14	+3.3	+3.5	+1.4	+0.7	BWT 200WT, 400WT, 600WT, SS, FAT, EMA, IMF
200583406	Male	New Zealand	+2.5	+31	+62	+71	+67	+13	+2.4	+5.4	+0.8	+0.7	BWT 200WT, 400WT, SS, FAT, EMA, IMF
11862428	Male	Australia	+1.3	+33	+78	+84	+73	+9	+4.1	+8.0	+0.9	+0.6	BWT 200WT, 400WT, SS, FAT, EMA, IMF
12009827	Male	Australia	+3.1	+35	+67	+82	+87	+14	+3.9	+6.4	+1.0	+0.6	BWT 200WT, 400WT, SS, FAT, EMA, IMF
553035289	Male	Canada	+3.0	+32	+55	+59	+36	+14	+2.2	+1.4	+2.0	+0.6	BWT 200WT, 400WT
200421778	Male	New Zealand	+2.6	+32	+67	+77	+55	+16	+3.0	+6.1	+0.9	+0.6	BWT 200WT, 400WT, SS
1486521	Male	Australia	+1.1	+26	+48	+57	+22	+15	+1.8	+7.9	+1.2	+0.6	BWT 200WT, 400WT, SS, FAT, EMA, IMF
200372830	Male	New Zealand	+3.1	+26	+63	+65	+47	+16	+1.5	+3.7	+1.3	+0.6	BWT 400WT, FAT, EMA
1336229	Male	Australia	+2.3	+30	+51	+63	+50	+13	+2.0	+5.9	+0.8	+0.5	BWT 200WT, 400WT, 600WT, SS, FAT, EMA, IMF
740564243	Male	United Kingdom	+3.1	+37	+62	+78	+72	+16	+2.0	+4.7	+0.8	+0.5	BWT
740578264	Male	United Kingdom	+2.5	+28	+61	+73	+55	+20	+2.7	+8.5	+1.2	+0.5	BWT 200WT, 400WT, SS, FAT, EMA, IMF
200630775	Male	New Zealand	+2.5	+36	+78	+82	+66	+12	+2.4	+7.0	+1.3	+0.5	BWT 200WT, 400WT, SS, FAT, EMA, IMF
552944231	Male	Canada	+3.1	+32	+60	+69	+49	+20	+2.1	+2.9	+0.9	+0.5	BWT 200WT, 400WT, FAT, EMA, IMF
552967397	Male	Canada	+1.7	+28	+62	+66	+62	+24	+1.8	+6.3	+0.9	+0.5	BWT 200WT, 400WT, FAT, EMA, IMF
552986407	Male	Canada	+1.3	+27	+49	+53	+28	+23	+2.4	+2.6	+1.2	+0.5	BWT 200WT, 400WT

Figure. 3 An example of Hereford sires in the International Hereford BREEDPLAN evaluation that met particular trait EBV selection criteria

4.2 Assessing the priority of ABRI clients for international evaluations

The ABRI surveyed existing beef clients to gauge the importance of contributing their data to evaluations beyond their current nationally-focussed breed evaluation. Participants were asked to rate on a scale from 1 to 10 the importance given to their breed society or association on three benchmarking scenarios, with 1 as “not important” and 10 as “extremely important”. Undeniably, benchmarking animals of a certain breed internationally was rated to be the most important way to benchmark animals on genetic merit (Fig. 4). Both the Australian and International participants rated international selection as more important than multi-breed analyses, though Australian participants rated their preferences more closely. Notably, there were no results given under 5, representing a neutral response, meaning that all participants rated the benchmarking of their breed population against other populations as important irrespective of whether that be populations of the same breed or of other breeds.

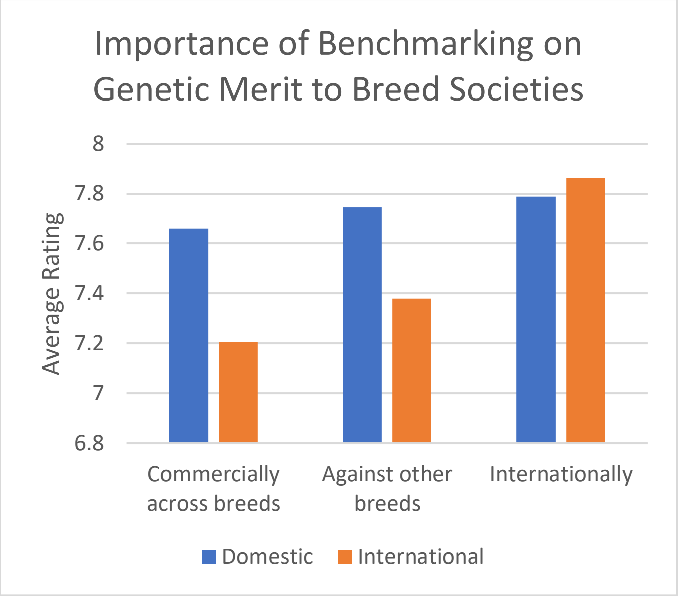


Figure. 4. A comparison of the average ratings given by Australian and International participants to the importance of benchmarking breeds based on different platforms.

However, when asked about the perceived importance of each option to commercial bull buyers, the priority given to selection of genetics from an international gene pool ranked lowest (Fig. 5). This may be explained by the survey participants representing breed societies, with a membership representing seedstock producers who are more likely to buy semen from a wider international market, compared to commercial beef producers who are more likely to use genetics available domestically. Thus, commercial bull buyers have less direct need for international evaluations, even if they would be the recipients of genetic improvements made in the seedstock sector via accessing genetics of greater merit regardless of origin.

When participants were asked as to the reasons why they would consider participating in an international genetic evaluation, all available options received strongly favourable responses (Fig. 6). This indicates a range of perceived benefits to the end-users of such evaluations, with the potential benefits to seedstock producers being the most important. All participants answered in the affirmative regarding their potential participation in a routine international genetic evaluation for their breed. Interestingly, participation in multi-breed evaluations was also rated similarly, with the most significant reason being the benefit to commercial producers. Access to new markets for the export of genetics was important, but not as important as the benefits arising from a wider gene pool for making genetic improvements.

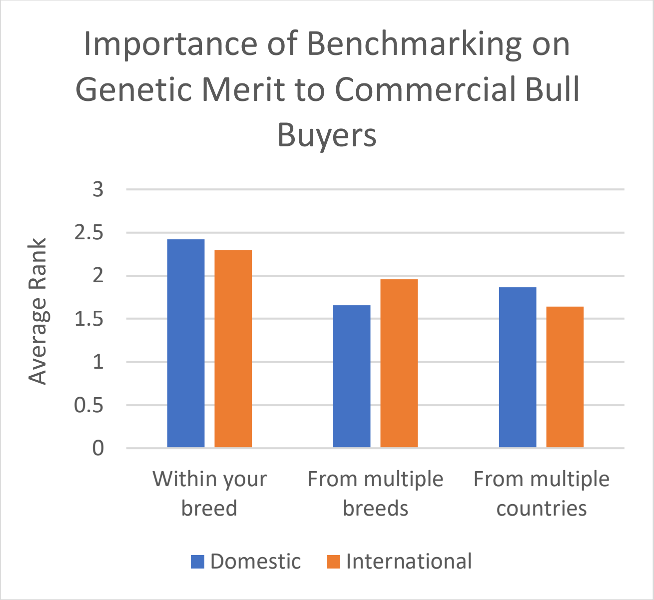


Figure. 5. A comparison of the average ratings given by Australian and International participants of the importance to commercial bull buyers of the benchmarking animals within-breed, across breeds and internationally.

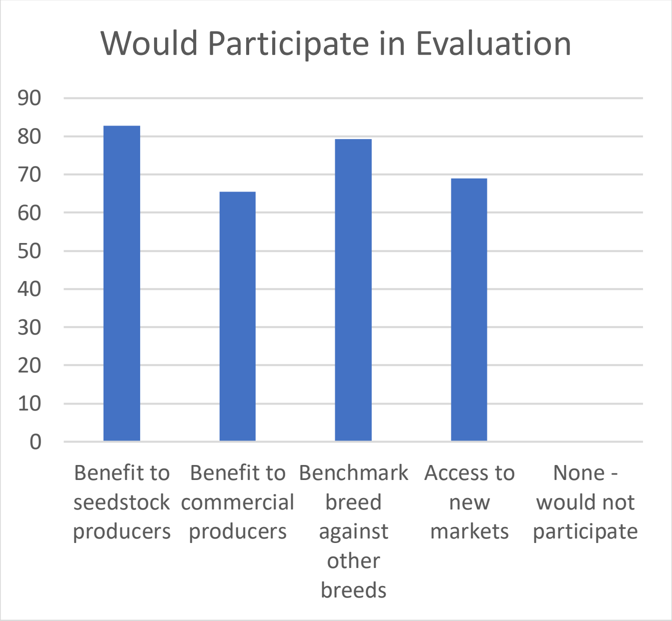


Figure. 6. Average ratings given by participants as to their reasons why they would consider participating in an international genetic evaluation

Participants were also asked for reasons why they might not participate in an international genetic evaluation (Fig. 7). The most significant impediment was the perceived potential for additional costs associated with such evaluations.

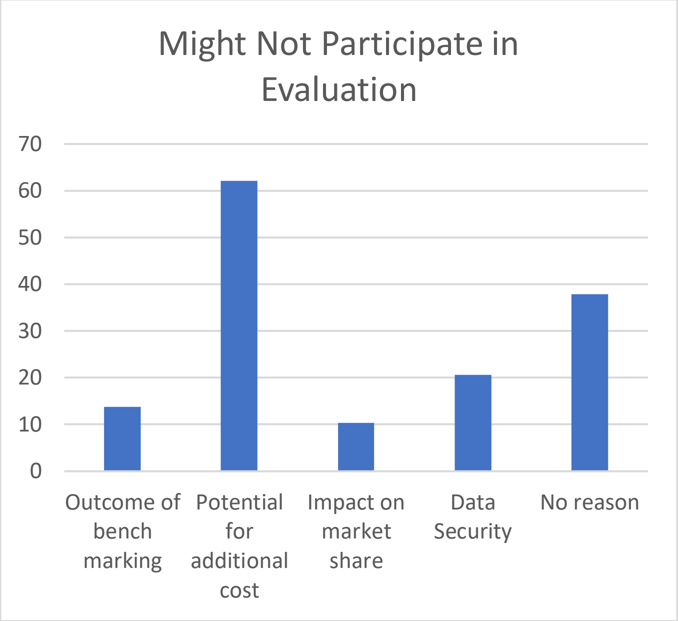


Figure. 7. Average ratings given by participants as to their reasons why they would not consider participating in an international genetic evaluation

The International breed society participants were also asked to score the likelihood of access being given to their pedigree and performance data for use in the research and development needed for international genetic evaluations. Almost 80% of participants indicated that their breed association would contribute data for such purposes (Fig. 8).

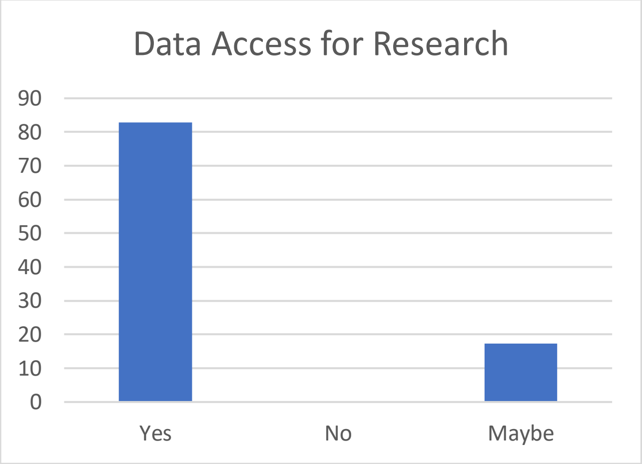


Figure. 8. Percentage of international participants that would provide data access for research projects with an international focus.

4.3 Interbeef

4.3.1 ABRI Full Membership of ICAR

Both ABRI and AGBU have maintained a strong presence at ICAR meetings since 2016. In preparation for the ICAR Conference in Edinburgh (June 2017), both organisations collaborated on preparing background information on the current status of Australian breeds and genetic evaluations for discussion at ensuing Interbeef meetings. This included an overview of the objectives of MDC project P.PSH.0787 and how these could fit current Interbeef activities.

ABRI gained full membership to ICAR and Interbeef following the ICAR Conference in Auckland in February 2018. A strong relationship between ABRI and Interbeef resulted, with Dr Brad Crook (ABRI) joining the Interbeef Technical Committee as well as the Interbeef Operations Group. The ability for ABRI to interact with Interbeef committees and working groups on a more regular basis will help facilitate the reporting of results to future Interbeef workshops. ABRI also offered to provide assistance to Interbeef in estimating across-country correlations, once Australian extracts were available.

4.3.2 Permission to access Australian data

Permission was obtained from Australian Charolais in April 2018 and from Australian Limousin in July 2018 for ABRI to undertake the database processes required to create extracts appropriate for Interbeef analysis of 200-day weight data.

4.3.3 Processes to create Interbeef extracts

Access to Interbeef data formats, pedigree check software and the Interbeef IDEA database was made possible once ABRI gained full membership to ICAR and Interbeef. The ensuing process of creating the required data extracts for Australian Charolais and Australian Limousin required considerable investment of ABRI time, especially to meet the requirement of international formatting for all animal identifiers (e.g. AUSCHAMXXXXXXXXXX, representing 3-character code for country of origin, 3-character breed code, 1-character sex code and the unique animal identifier in the country of origin).

One significant challenge was in determining the correct international identifier for the correct European animal, given that one AI sire could have a number of European identifiers (each relating to the importing country) as well as the identifier in the country of origin, the latter being needed for the Interbeef pedigree extract. This meant, for example, that a French animal appearing in the pedigree of a Canadian Charolais sire used in Australia might be recorded with his Canadian identifier in the Australian Charolais ILR2 cross-reference file – but needed his original French identifier available for the Australian record to link to the correct animal on the Interbeef database. In addition, animal name was not always a useful criterion for matching to European databases as the same name was sometimes given to more than one animal. The process of collating international information required checking of these details against those recorded in European herdbooks available online as well as assistance being sought from the Irish Cattle Breeders Federation (ICBF), with the Interbeef IDEA pedigree checking software lastly used to validate the result. These Interbeef (International format) identifiers were then propagated to the ILR2 cross-reference table for each breed.

A second challenge encountered was the duplicated use of animal identifiers on the Australian databases, resulting in an Interbeef (international format) identifier that was not unique. The former situation arises in Australian animal identification processes that use herd letters and an A-Z year code combined with ear tag. This creates the potential for duplication of animal identifiers if the herd has been in existence for 24 years or longer (noting that alpha “I” and “O” are not used as year codes). While some breed associations address this by adding a year suffix to the identifier of the historic animal (e.g. +84), this is not consistent across all associations nor consistent in all instances. In relation to duplication of Interbeef formats based on the available association identifier, this was addressed manually by adding a two digit year code to the Interbeef record in the cross-reference table (e.g. 84).

Software was developed by ABRI to create data extracts within ILR2 according to Interbeef specifications, with the following selection criteria being used:

- animals born in 1990 and onwards;
- natural-born calves only (ie. exclusion of calves born to embryo transfer);
- single-born calves only (ie. exclusion of calves from multiple births);
- purebred animals only (ie. primary breed percentage >87.5%);
- both parents known (ie. exclusion of calves with missing parent/s or born to multi-sire matings);
- 200-day weight record must meet all other inclusion criteria as required in BREEDPLAN (ie. record has been included in a BREEDPLAN analysis);
- must be the first valid 200-day weight record used in the BREEDPLAN analysis (ie. exclusion of second record, if repeated records exists);
- weight records in BREEDPLAN slice groups containing 2 or more animals (ie. exclusion of single-animal slice groups);
- 5 generations of pedigree (where possible).

Weight records in the Interbeef performance extract were pre-adjusted for age of animal (at weighing) and age of dam. The corresponding BREEDPLAN slice group was included with the weight record to ensure the handling of Australian data in the Interbeef evaluation retained some continuity with data-handling processes in BREEDPLAN.

Variance components derived from each Australian data extract are given in Table 26, these being the variances supplied to Interbeef for use with the Australian data. The variances used in the BREEDPLAN evaluations for each breed as of 2018 are also given in Table 26 for comparison.

4.3.4 Australian data in the Interbeef evaluation

The initial Charolais extracts were uploaded to Interbeef in September 2018, containing 71,840 animals with a 200-day weight record and 106,566 animals in total. Eight countries submitted a total of 4.08M weight records for the Interbeef Charolais analysis: France (92%), Denmark-Finland-Sweden (3.4%), Germany (1.7%), Australia (1.5%) and the remaining 1.8% of records coming from the Czech Republic, South Africa, Ireland and Switzerland (in descending order of contribution). Australia accounted for 16% of all data of non-French origin. Assumed across-country correlations with Australia ranged from 0.70-0.72 for direct genetic and 0.58-0.67 for maternal genetic weaning weight.

The initial Limousin extracts were uploaded to Interbeef in October 2018, containing 66,732 animals with a 200-day weight record and 101,636 animals in total. Nine countries submitted a total of 2.48M weight records for the Interbeef Limousin analysis: France (85%), Great Britain (4.7%), Denmark-Finland-Sweden (2.9%), Germany (2.8%), Australia (2.0%) and the remaining 3.0% of records coming from Switzerland, Spain, Ireland and the Czech Republic (in descending order of contribution). Australia accounted for 14% of all data of non-French origin. Assumed across-country correlations with Australia ranged from 0.74-0.78 for direct and 0.66-0.71 for maternal weaning weight.

Interbeef extracts for both breeds have been created and uploaded twice per year since this initial test phase.

Table 26. Variance component estimates for 200-day weight in Australian Charolais and Limousin: BREEDPLAN and Interbeef estimates[1]

Variance component	AUS Charolais		AUS Limousin	
	BREEDPLAN	Interbeef	BREEDPLAN	Interbeef
V_A	92.56	186.17	75.12	124.32
V_M	83.20	100.52	56.72	70.13
V_C	104.73	99.70	85.89	80.88
V_{sxh}	13.19	-	17.53	-
V_E	365.84	337.35	319.22	282.86
V_P	628.81	664.21	554.48	545.65
h^2_A	0.15	0.28	0.14	0.23
h^2_M	0.13	0.15	0.10	0.13
$r_{g(d,m)}$	-0.35	-0.44	-	-0.13
h^2_C	0.17	0.15	0.16	0.15
h^2_{sxh}	0.02	-	0.03	-

[1] BREEDPLAN parameters were estimated by AGBU using the complete BREEDPLAN data extract, with parameters implemented in 2013 for Charolais and 2014 for Limousin. Interbeef parameters were estimated by ABRI in 2018 using the Australian-only data extracts prepared for Interbeef analysis.

4.3.5 Comparison of Interbeef and BREEDPLAN results

Interbeef results for both breeds were received by ABRI in late December 2018. Comparisons were then made between the Interbeef EBVs for published sires in Australia and EBVs for 200-day weight and milk (maternal weaning weight) as obtained from the following ABRI analyses:

- BREEDPLAN analysis (BP-200): single-trait BREEDPLAN analysis of Australian 200-day weight records (no repeated records), using variance components supplied to Interbeef;
- BREEDPLAN analysis (BP-full): BREEDPLAN multi-trait analysis using current BREEDPLAN parameter files;

Fig. 9 summarises the 200-day weight and milk EBV outcomes for published sires recorded with Australian Charolais. After accounting for differences in base adjustments between Interbeef and BP-200 analyses, changes in EBV ranged from -12.9 to +18.2 kg for 200-day weight and from -11.0 to +13.7 kg for milk, with overall correlations of 0.952 and 0.931 respectively. Correlations between Interbeef and BP-full EBVs were lower (0.858 for 200-day weight; 0.881 for milk) as expected given the impact of a multi-trait model and associated parameters in the BREEDPLAN analysis.

Fig. 10 summarises the 200-day weight and milk EBV outcomes for published sires recorded with Australian Limousin. After accounting for differences in base adjustments between Interbeef and BP-200 analyses, changes in EBV ranged from -9.9 to +14.7 kg for 200-day weight and from -13.2 to +10.5 kg for milk, with overall correlations of 0.914 and 0.856 respectively. Correlations between Interbeef and BP-full EBVs were lower (0.831 for 200-day weight; 0.825 for milk).

A comparison of Fig. 9 and Fig. 10 indicates a greater impact of the Interbeef context on sire EBVs for the Limousin breed compared to the Charolais breed. This reflects the higher across-country correlations assumed for the Australian Limousin population in the Interbeef analysis, a function of stronger genetic linkage between this population and the more significant European populations represented in the analysis.

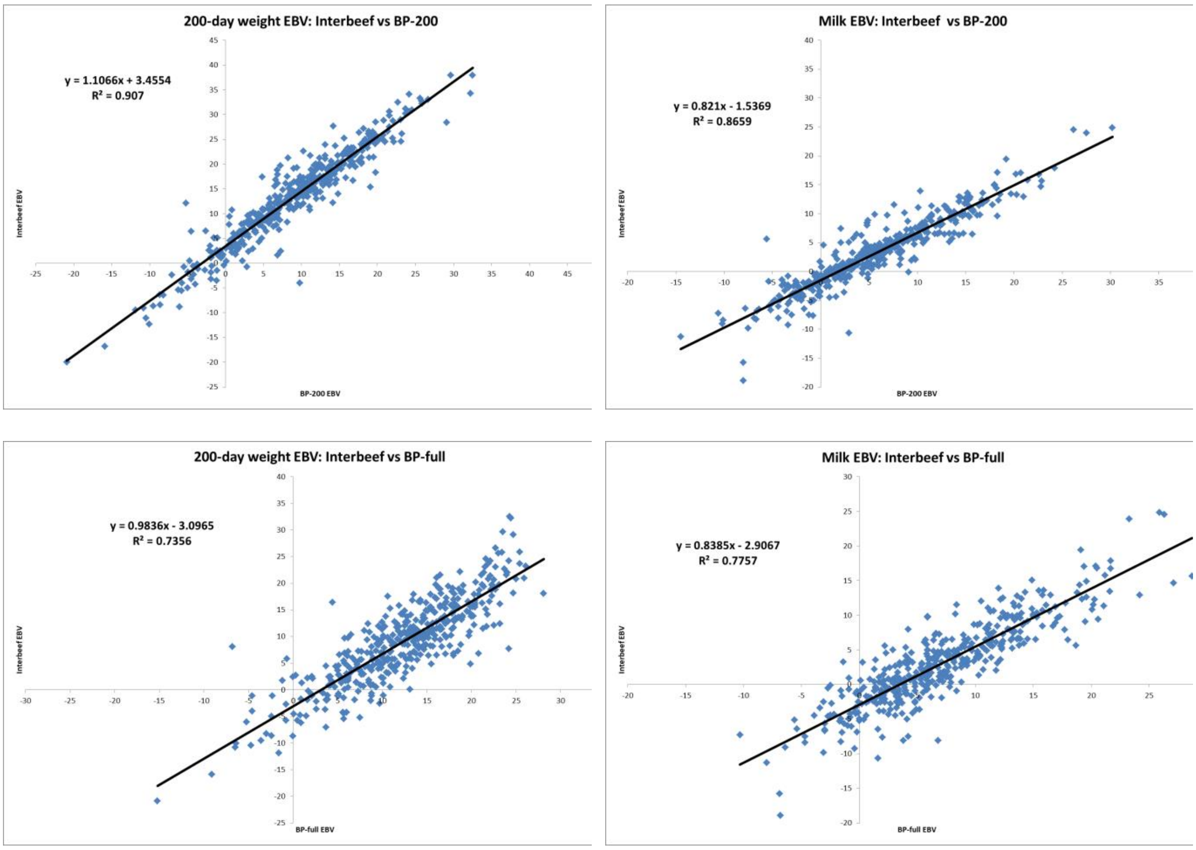
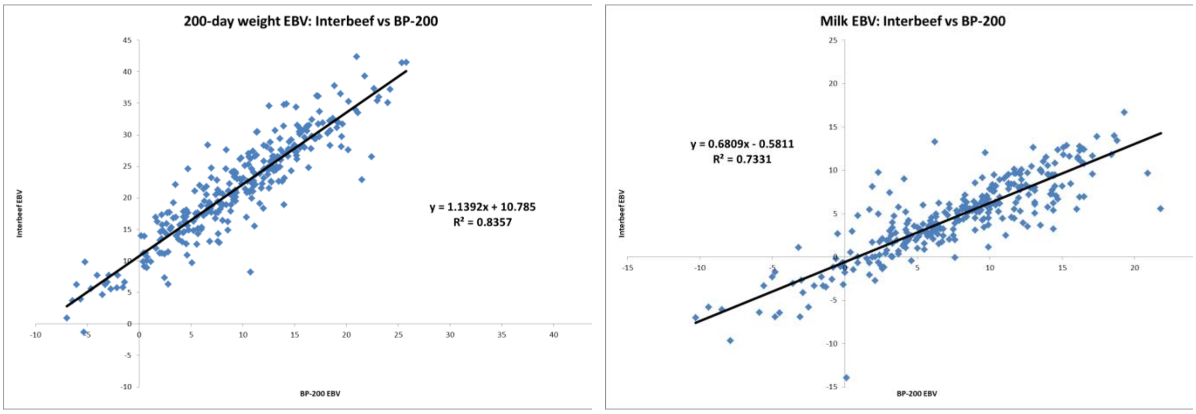


Figure. 9. Interbeef Charolais EBVs for 200-day weight and milk compared with EBVs from the BP-200 and BP-full, for published sires in Australia (n=437)

4.3.6 Meetings

A presentation on developments in multi-source BREEDPLAN genetic evaluations was given at the ICAR 2019 Conference in Prague, as part of the Interbeef technical session on new traits and developments in beef cattle breeding. Developments in the international Hereford and Brahman BREEDPLAN evaluations were highlighted in this presentation (Crook, Skinner and Nivison, 2019).



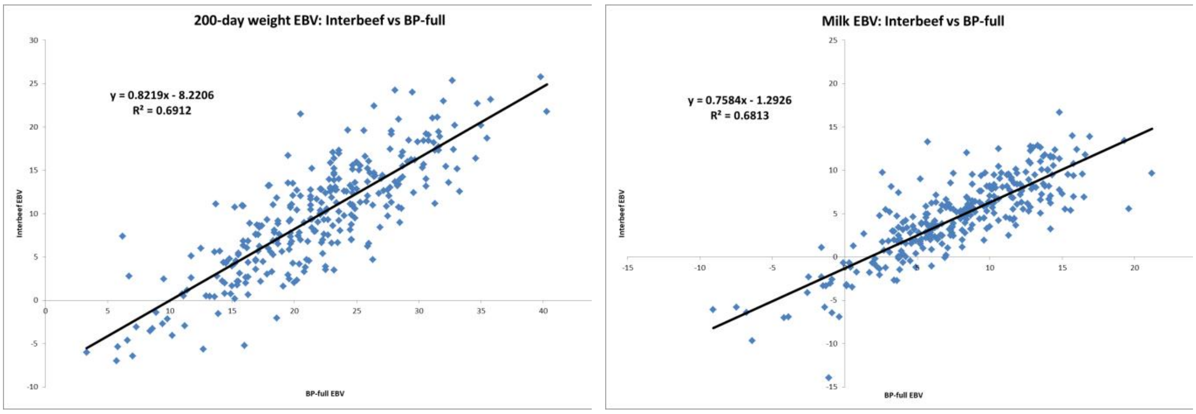


Figure. 10. Interbeef Limousin EBVs for 200-day weight and milk compared with EBVs from the BP-200 and BP-full, for published sires in Australia (n=299)

5 Discussion

5.1 International BREEDPLAN evaluations

5.1.1 Opportunities for international BREEDPLAN evaluations

This project identified a number of Australian breeds with potential for combining with other populations of the same breed for the purpose of an international BREEDPLAN evaluation.

The largest international evaluation conducted was for the Hereford breed, with almost 7.8M performance records for growth, scan and scrotal traits combined in the one multi-trait analysis. With an analytical run time of approximately 9 hours, this would make for ease of implementation of a routine international evaluation, assuming data sharing agreements were formalised. Previous initiatives to progress an international Hereford evaluation focused predominantly on the analytical models and computational requirements, without explicit reference to the pre- and post- analysis processes required for such an evaluation to become commercially feasible and routine (Donoghue, Graser, Johnston and Tier, 2007). The current work completed by ABRI builds upon a foundation of earlier research for the Hereford breed (Graser, 2004; Johnston, 2004) and provides a feasible option for conducting a routine international genetic evaluation for the Hereford breed. Likewise for the Brahman and South Devon breeds, routine international BREEDPLAN evaluations would also be feasible given the approach taken by ABRI.

On the basis of 200-day weight data, the assumption of across-country correlations being sufficiently high seems adequate overall such that country-specific expressions of the trait could be ignored for the Hereford, Brahman and South Devon evaluations. In other words, a more simplified model could be considered in contrast to the approach taken in the Interbeef evaluation of weaning weight in which each country is modelled as a different though correlated traits. In the case of Charolais, the international BREEDPLAN evaluation would yield one 200-day weight EBV per animal compared to 8 different weaning weight EBVs per animal in the Interbeef evaluation. However, this assumption may not be robust for the maternal genetic component of 200-day weight (ie. milk EBV).

Further analyses are needed to estimate across-country correlations for the other traits included in the international BREEDPLAN evaluations.

5.1.2 A commercial process pipeline

One of the on-going primary decisions regarding international evaluations appears to be the "who" and the "how" of transitioning such evaluations into a pipeline of processes for the routine undertaking of International genetic evaluations for beef cattle. There are currently five main commercial service providers where a pipeline has been developed with capacity for delivery of multi-country genetic evaluations: ABRI, Interbeef, International Genetic Solutions (IGS), Theta Solutions and Angus Genetics Inc. (AGI). Note that the IGS evaluation is predominantly a combined American and Canadian multi-breed evaluation, with a markedly smaller representation of beef cattle populations from outside North America (e.g. the Shorthorn breed in Australia). Theta Solutions conducts the current Pan American Hereford evaluation, combining data from America, Canada, Uruguay and Argentina. AGI also provides a multi-country evaluation for each of the Angus and Charolais breeds, combining data for the American and Canadian populations only. A comparison of these services is summarised in Table 27.

Interbeef, IGS and Theta Solutions each require participating countries to take responsibility for preparation of the data extracts to be submitted for analysis. This includes the use of international identification formats to assist in the merging of extracts for analysis. All performance records are assumed to be pre-adjusted for significant non-genetic effects (e.g. age of animal at measurement; age of dam) and for contemporary groups to be pre-defined in the performance files. Results are then returned to participants, where it becomes the responsibility of each participating group as to how such results are reported and subsequently used. There are no options for the reporting of international results in a collective, multi-country platform – although proofs are directly comparable across the country/breed-specific databases that report them. The Interbeef, IGS and Theta Solutions pipelines require considerable involvement of participating breed societies and/or their domestic service providers, especially in correctly identifying the genetics in common with other participating parties.

Table 27. A comparison of commercial service providers with capacity for the delivery of international (multi-source) genetic evaluations for beef breeds

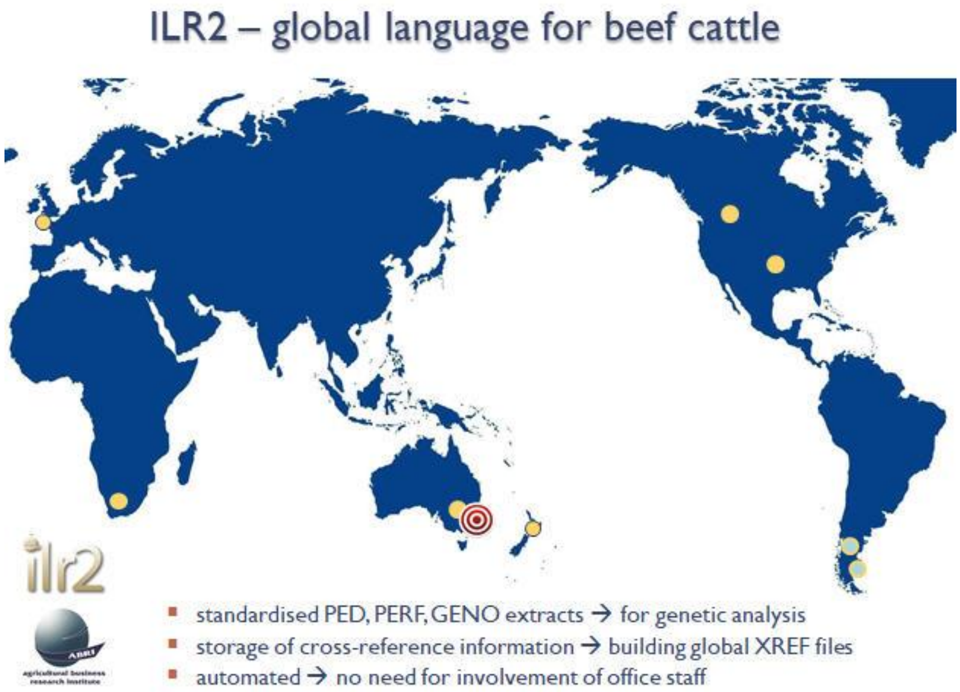
	ABRI	**Interbeef**	**IGS**	**Theta Solutions**	**AGI**
Database services	Yes	No	No	No	No
Analytical software platform	BREEDPLAN	Mix99	BOLT	BOLT	BLUPF90
Multi-source within evaluation	Countries Breeds	Countries	Countries Breeds	Countries	Countries
Multi-country covariance matrix	No	Yes	No	No	No
Multi-trait models	One evaluation combining growth,	Single trait (growth); multi-trait carcase	Separate analyses for growth, fertility and carcase	Separate analyses for growth, fertility and carcase	Separate analyses for growth, fertility and carcase

	fertility, carcase				
Genomics	Yes, using GRM	No	Yes, using marker subset	Yes, using marker subset	Yes, using GRM
Responsibility for creating data extracts	ABRI	Client	Client	Client	Client
Merging process	Cross-reference table	International ID format	International ID format	International ID format	International ID format
Reporting of results	ABRI	Client	Client	Client	Client
International reporting options	Yes	No	No	No	No
Peer-reviewed methodology	Yes	Yes	No	No	Yes
Frequency	Monthly	Twice per year	Weekly	Weekly	Weekly

In contrast to the “global identifier” pathway used by Interbeef, IGS and Theta Solutions, ABRI has established a pipeline of processes based around the “global language” available via its ILR2 database product and associated services (Fig. 11). While each ILR2 system is configured for the specific needs of each client, the architecture behind it remains standardised. This means that pedigree and performance extracts can be created from all ILR2 systems in formats as required for the BREEDPLAN genetic evaluation software. Routine information on imported genetics, such as their foreign herdbook number and/or overseas identifiers, is stored in the ILR2 cross-reference table. Other than the recording of conventional details on imported animals, no further work is required of breed society staff to ensure that later merging for international evaluations can be completed successfully. ABRI software automates the collating of cross-reference records and building of cross-reference files as required for the international BREEDPLAN evaluation given the participating countries (i.e. cross-reference files can be customised “on the fly”).

For breed societies that do not use the ILR2 product (e.g. Herefords in Uruguay and Argentina; Charolais in Hungary), pedigree and performance extracts can be created from their national databases and supplied to ABRI for loading to an ILR2 shell system, from which data extracts can then be prepared. This allows all data extracts to be standardised for BREEDPLAN evaluations, including a consistent use of units for all phenotypic measurements (e.g. kg, cm, cm^2). Data submitted in this way requires provision of the necessary cross-reference information.

The merging of extracts, undertaking of the international BREEDPLAN analysis and de-merging of results can all be conducted using commercial software developed by ABRI and currently available. Associated output, including percentiles and genetic trends, can also be provided, including country-specific and international populations.



ILR2 – global language for beef cattle

- standardised PED, PERF, GENO extracts → for genetic analysis
- storage of cross-reference information → building global XREF files
- automated → no need for involvement of office staff

Figure. 11. Schematic of how ABRI's ILR2 system provides a global language for the handling of standardised data extracts and the recording of cross-referencing information for use in international BREEDPLAN evaluations for beef cattle. The example given is for the Hereford breed.

While the Interbeef pipeline does not currently support genomic information, the IGS, Theta Solutions and ABRI pipelines can accommodate genomic extracts for use in multi-country genetic evaluations. The process as used by ABRI is shown in Fig. 12 and is available to clients of ABRI who have opted for a DNA module in their ILR2 database, whether that be their commercial ILR2 system or an ILR2 shell system. The DNA module allows for SNP data to be extracted in a specific format defined by AGBU for use in their Genomics Pipeline Software (GPS). For multi-country and international contexts, the GPS requires the merged pedigree extract, the ABRI global cross-reference file and the individual SNP extracts in order to create a merged SNP extract and the resulting Genomics Relationship Matrix (GRM). This GRM is configured specifically for use with the Single-Step BREEDPLAN software and requires additional parameter files to allow the GRM to be used. Consequently, a GRM cannot be constructed from third-party sources for use with the Single-Step BREEDPLAN software, nor can the AGBU GRM be used with any third-party genetic evaluation software (e.g. Mix99 and BLUPF90) capable of providing alternate models for International evaluation using genomics.

At present, ABRI does not have access to a commercial version of the genomics pipeline software and as such coordinates with AGBU for delivery of the GRM as required for a Single-Step BREEDPLAN evaluation. The transition to routine international Single-Step BREEDPLAN evaluations therefore remains contingent on an appropriate pathway for generating the GRM using genotypes from a wide range of countries and platforms.

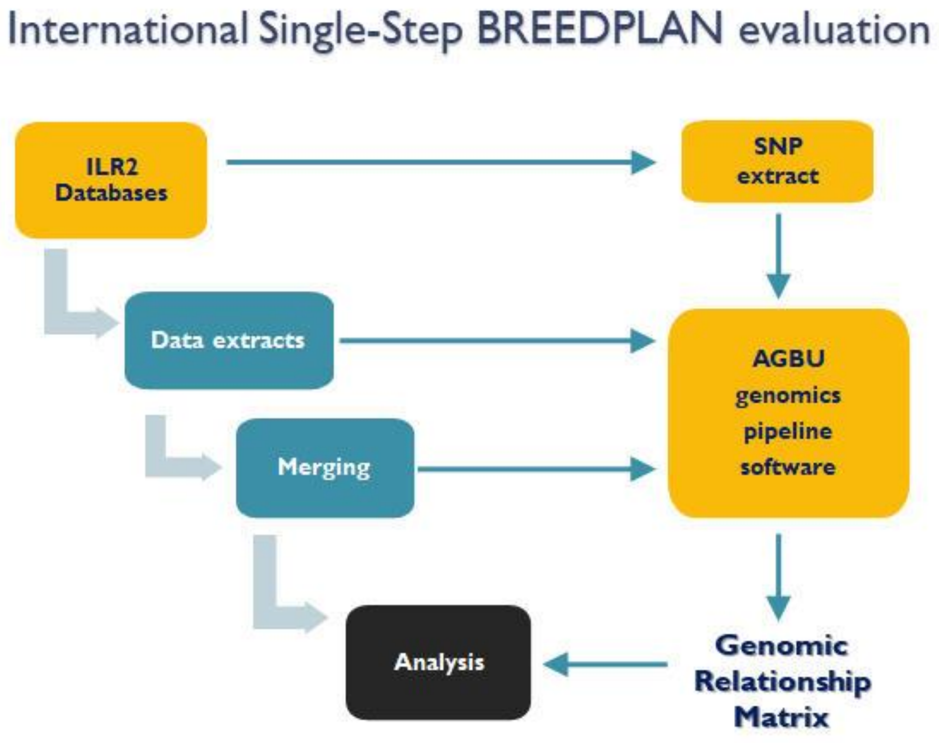


Figure. 12 Schematic of processes necessary for implementation of a Single-Step BREEDPLAN model for use in International Genetic Evaluations of beef cattle.

While documentation of the processes associated with the IGS and Theta Solutions pipelines are not readily available, both evaluations use a marker-effects model based on a subset of markers (Atkins, Spangler, Golden and Shafer, 2020; Saatchi and Garrick, 2019). The selection of informative markers requires ongoing validation for the breeds and traits in the evaluation – but whether this extends to validation of breed populations in other countries remains unclear.

5.1.3 Validation and implementation strategies

All international BREEDPLAN evaluations conducted by ABRI in this project are commercially feasible and could be transitioned into commercial production using ABRI's existing database and applications software. These outcomes suggest that such international evaluations could be provided as a regular, commercial service. However, progression towards a commercial outcome necessitates two important considerations: the validation of international BREEDPLAN results and strategies for implementation.

Validation of international BREEDPLAN EBVs is necessary to demonstrate the potential usefulness of outcomes. One approach to this would be to compare EBVs from the international evaluation with those calculated in single-country evaluations. These latter evaluations can also be conducted using both the international covariance matrix and the country-specific covariance matrix to allow an assessment of assumptions regarding the covariance matrix used in the international evaluation. A second approach would be to conduct cross-validation studies using LR method (Legarra and Reverter, 2018) in order to demonstrate the extent to which future phenotypes can be predicted within country on the basis of international EBVs. The same approach could be taken using single-country evaluations, as benchmarks against which the predictive merit of international EBVs can be compared.

The research required for validation of international EBVs falls outside the scope of the current project.

Consideration should also be given to the means by which international BREEDPLAN EBVs could be used and/or reported, with three options currently available:

(i) routine (monthly) international BREEDPLAN evaluation as a replacement for the various country-based BREEDPLAN evaluations;
(ii) regular (scheduled) international BREEDPLAN evaluation to supplement separate country-based BREEDPLAN (or other) evaluations; or
(iii) Regular (scheduled) international BREEDPLAN evaluation, providing de-regressed proofs to improve the modelling of imported genetics represented in each separate country-based BREEDPLAN (or other) evaluations;

Option 1 is an extension of the approach currently taken in Trans-Tasman BREEDPLAN evaluations, as well as the Southern African BREEDPLAN evaluations (combining South Africa and Namibia) and Southern Limousin BREEDPLAN evaluation (Australia, South Africa and Namibia). This was the approach taken in developing the initial international Brahman BREEDPLAN evaluation, seeking to include all traits encompassed by the three separate Brahman BREEDPLAN evaluations that would be superseded. This is also a suitable option for countries that have linkage to the international breed population but are relatively small in comparison in terms of performance records. The suitability of option 1 is, however, conditional on the magnitude of across-country correlations for traits in the analysis.

Option 2 is the approach taken in developing the international BREEDPLAN evaluation for the Hereford and South Devon breeds, restricting the traits to a subset of those recorded across the countries represented. This option provides a valid comparison of alternative genetics using an international EBV benchmark, while still accommodating the needs of some countries for a local evaluation (especially if there are additional traits included in the local evaluation). This option is also the current approach used by some of the countries participating with Interbeef.

Option 3 is an approach currently being explored by the ICBF to make use of the Interbeef proofs in the Irish national evaluation, with their methodology being presented at the Interbeef technical committee meeting in Prague. ABRI sought collaboration with the ICBF in validating the approach, using de-regressed Interbeef proofs and BREEDPLAN EBVs for the Australian Charolais and Limousin breeds. Although this research falls outside the scope of the current MDC project, the outcomes may provide a valid approach whereby international BREEDPLAN EBVs might be reported separately (option 2) as well as being used to augment the BREEDPLAN EBVs for imported animals and their relatives.

The Brahman and Hereford breeds represent two different approaches to transitioning from their respective “national” evaluation to a larger scale International evaluation. In the case of the Brahman breed, the goal was to develop an international evaluation combining Australia, the USA, South Africa and Namibia yet using the Australian model as the framework. For traits in common across two or more countries, international variance components were estimated and used in place of the Australian variances. For traits recorded in Australia only, the Australian variances were retained. It was anticipated that the international evaluation would subsequently replace the three separate BREEDPLAN evaluations, providing opportunity for more objective across-country selection decisions for Australian breeders as well as developing more effective global marketing opportunities for Australian genetics. However, on-going enhancements to the Australian Brahman BREEDPLAN evaluation – such as introduction of additional fertility traits, genomic data and, more recently, integration of the northern Repronomics multi-breed data (Johnston, Schatz, Burns, Fordyce and Lyons, 2017) – required on-going development and testing of the International evaluation. This created unexpected delays in progressing towards a routine International evaluation, which eventually stalled following changes in the American Brahman office and the inability for genotypes from Southern Africa to enter the genomics pipeline managed by AGBU.

A different approach was proposed for the Hereford breed, building on the experience gained by ABRI in collaborating with Interbeef. Rather than developing an International BREEDPLAN evaluation that would replace the current Hereford BREEDPLAN evaluation provided jointly to Australia, New Zealand and Namibia, an evaluation was developed to provide International BREEDPLAN EBVs for a range of production traits recorded in two or more of the countries participating. Country-specific adjustment factors and international (co)variances were estimated for the subset of traits. The International Hereford evaluation would be run separately from each participating country's "national" evaluation (i.e. regardless of the software platform used for each national evaluation) and less regularly than the national evaluations, perhaps only 2-4 times per year. International EBVs could be reported as per 4.1.13 and for some participating countries (e.g. smaller populations in Europe), this might be all that is required for their respective in-country purposes. For those countries with larger populations and a well-developed national evaluation already in operation, the international EBVs could be incorporated using methods similar to those outlined by the ICBF for use with Interbeef proofs (Pabiou, Pitkanen, Evans, Herpje, and Vandenplas, 2018). This is likely to improve the modelling of imported genetics, retaining some continuity with International results, while also allowing each population to retain ownership of their own evaluation and service provider.

In comparing the two approaches, it is the latter one as used in the international Hereford evaluation that is considered the more practical to maintain, develop and operate commercially.

5.1.4 Genomics

One of the objectives of this project was to develop and implement international BREEDPLAN evaluations in which genomic data was included using single-step methods. As noted previously, a Single-Step BREEDPLAN job stream does exist and is currently used in a number of routine commercial runs for Australian breeds. This job stream has also been used in developing the international BREEDPLAN evaluations, but genomic data has not been incorporated. None of the breeds involved in international BREEDPLAN evaluations have as yet progressed to using single-step methods for the following reasons:

(i) ABRI does not yet have access to commercial genomics pipeline software to construct the genomics relationship matrix needed for Single-Step BREEDPLAN evaluations. While a G matrix does exist for the Hereford and Brahman breeds and for animals included in the international BREEDPLAN evaluations, each G matrix has been created for an Australian- (Brahman) or Trans-Tasman- (Hereford) specific pedigree extract and cannot be directly used in a much larger international evaluation without being manually recoded. In addition, these G matrices do not currently include genotypes available in other countries (e.g. Brahman genotypes from South Africa and Namibia);

(ii) while there is considerable genomic data available for some breeds internationally, a number of breed associations agreed to participate in the project on condition that their genotypes would <u>not</u> be required. In terms of data security, there appears to be greater concern over access being given to genomic data compared to pedigree and phenotypic data. This resulted in very limited access to genomic data, restricting the scope for enhancing international BREEDPLAN evaluations through the use of genomics;

(iii) while some international breed associations do have a genotyping strategy, some do not currently store their genomic data in formats directly accessible to ABRI for use. Further developments are required in this regard.

In spite of these challenges, ABRI has continued to assist its clients to collect and store SNP data in the ILR2 DNA module. Brahman in South Africa and Namibia, Hereford in the UK, South Devon in the UK, Charolais in the UK and Hungary and Aberdeen Angus in the UK have each installed a DNA module and are presently loading SNP data with a goal of including this in their respective BREEDPLAN evaluations once a Single-Step option becomes available for them. In relation to the Simmental breed, genotypes are currently available in the ILR2 DNA module for both Australia and New Zealand. The South African society is starting to genotype animals and has installed a DNA module to their ILR2 system. The priority given to collection of SNP data for Simmental cattle is still subject to discussion in the UK.

In terms of an international Brahman BREEDPLAN evaluation, formal permission was given by the Australian, South African and Namibian associations for their respective genotypes to be used in the current project. For the international Hereford BREEDPLAN evaluation, formal permission was given by Herefords Australia (HAL) only.

At this stage, there is only limited access to genomic data for inclusion in international BREEDPLAN evaluations. This should not be interpreted as an impediment to further developing such evaluations, especially if the international evaluation is not viewed as a replacement for national evaluations. This would allow each country to utilise genomic information in their national evaluation, in addition to a potentially wider range of traits included.

5.1.5 Challenges for international BREEDPLAN evaluations

Regarding the Brahman breed, progression towards a routine international BREEDPLAN evaluation remains stalled by changes arising in the American Association since the current project commenced, such that access to American Brahman data remains uncertain since their departure from ABRI's client base and their transition to an alternative provider of their genetic evaluation service. Without access to the American pedigree and performance data, genetic linkage between the Australian and Southern African populations will be insufficient to progress developments further. At present, the remaining breed associations have taken responsibility for re-opening dialogue with the American Brahman Breeders Association to gauge interest in developing further the International Brahman BREEDPLAN evaluation and to negotiate access to the American pedigree and performance data. Interest remains strong in Southern Africa as highlighted in the following correspondence:

> "From the Southern African Brahman Breed Improvement Forum, we would like to emphasize that we are especially interested in the first place to continue with the International Genetic Evaluation for Brahmans (over the 3 continents) for Australia, USA, South Africa and Namibia. The first test run was made by ABRI some 3 years ago – but due to various circumstances not to be elaborated here, this development was unfortunately put on hold…..If BREEDPLAN wants to extend its international market share then it would be imperative to engage in these combined international evaluations. More breed societies would be interested in these developments and skills."
>
> - Mecki Schneider: Chair of the Southern African Brahman Breed Improvement Forum (6/4/20)

Regarding the Hereford breed, interest remains strong in having an international evaluation developed and routinely available. Such an evaluation is considered to serve a range of purposes, including:

(i) access to a genetic evaluation service for the smaller Hereford populations, especially those in Europe and the UK;
(ii) across-country selection of potential new genetics;
(iii) across-country benchmarking of local genetics, and
(iv) access to international proofs for use in local/national evaluations to enhance the modelling of imported genetics.

However, there are no final agreements in place for the sharing of data for an international Hereford evaluation because consensus has not been reached as to the software platform preferred for the running of such an evaluation. Even though the pipeline of processes for an International Hereford BREEDPLAN evaluation has now been developed and could be available for routine evaluation, the insistence of the American Hereford Association on using BOLT software instead of BREEDPLAN software has stalled any final agreements being reached. That said, an International Hereford BREEDPLAN evaluation could still be progressed without the American pedigree and performance data, providing the Canadian Hereford population remains in the evaluation to provide the predominant source of genetic linkage between the other populations.

It is worth noting that some of ABRI's beef clients were already participating in multi-country evaluations prior to commencement of the current project. These include:

(i) the joint evaluation of breeds in Australia and New Zealand, such as Angus, Charolais, Simmental, Shorthorn, Gelbvieh, South Devon, Salers and Devon;
(ii) the joint evaluation of breeds in South Africa and Namibia, such as Brahman, Santa Gertrudis and Brangus; and
(iii) multi-country evaluations of the Limousin (Australia, New Zealand, South Africa and Namibia), Hereford (Australia, New Zealand and Namibia), Murray Grey (Australia, New Zealand, the UK, Canada and the USA) and Salers (Canada and USA) breeds.

However, none of these breeds have transitioned to an international BREEDPLAN evaluation of the magnitude originally conceived as an objective in this project.

The Charolais and Limousin breeds in Australia could continue to provide data for inclusion in the respective Interbeef evaluations, accessing international proofs on Australian genetics as well as imported genetics of relevance to Australia. These benefits are limited in scope because:

(i) data is only being contributed to the Interbeef weaning weight evaluation;
(ii) the Australian-based BREEDPLAN evaluation provides EBVs for a more diverse range of economically relevant traits;
(iii) genetic linkage to the European populations tends to be more historic in nature, and
(iv) a higher proportion of more recently imported genetics appears to be derived from North America, which is not represented in the Interbeef evaluations.

A stronger case could be made for each of the Australian breeds to combine with their North American counterparts. For Australian Charolais, there might be opportunity for data to be incorporated in the single-step Charolais evaluation provided by AGI for the combined American and Canadian population.

For Australian Limousin, data could be incorporated in the IGS multi-breed analysis, which includes both the American and Canadian Limousin populations.

Shorthorn is one Australian breed that has recently moved away from using BREEDPLAN software in a joint evaluation with New Zealand, favouring the much larger multi-source evaluation delivered by IGS. The latter includes both the American and Canadian Shorthorn populations, providing Australian Shorthorn breeders with capacity to make across-country selection decisions on suitable genetics. Surprisingly, the lack of validation of the IGS multi-source proofs, especially in their capacity to predict future progeny performance for breed populations outside North America, has not been appreciated by those breeds in Australia (and elsewhere) that are considering the IGS multi-source (international) evaluation. This process of validation is an essential component of the history and development of the BREEDPLAN technology (Jeyaruban, Gurman, Johnston, Swan, Banks and Girard, 2019) and should remain an essential step in developing routine international BREEDPLAN evaluations.

South Devon represents another breed considered for possible development of an international BREEDPLAN evaluation. However, a declining interest in using BREEDPLAN among the largest Australian herds, combined with the recent transition of American South Devon from BREEDPLAN to IGS, renders an international BREEDPLAN evaluation of the South Devon breed highly unlikely. In a similar way, the recent change made by American Salers to include their data in the IGS evaluation and discontinue their BREEDPLAN evaluation would presumably hinder any further multi-country BREEDPLAN developments that may have been of benefit to the Australian population.

Both domestically and internationally, there is strong and positive interest in seeing international genetic evaluations for beef breeds come to fruition. Likewise, there are pipeline processes and analytical models currently available to facilitate the conduct of routine international evaluations, with options already in place for the reporting of outcomes from these evaluations. In spite of this, the greatest challenges seem to be pragmatic and political ones rather than technical ones: who will drive the international evaluation initiative, who will deliver the commercial service and with what frequency and at what cost, and perhaps most importantly, who will be best positioned to reap the benefits from international evaluations for beef breeds.

6 Conclusions/recommendations

6.1 International opportunities

This project identified the development of international genetic evaluations as being of very high priority to most of the beef breed clients of ABRI, both domestically and internationally. For seedstock breeders and for those involved in the international marketing of semen and embryos, access to large-scale international evaluations for a given breed was ranked as being of higher priority than access to multi-breed evaluations.

This project delivered outcomes for commercial consideration by a range of beef breeds. A pipeline of processes has been developed, at least one option for the reporting of international EBVs is available and suggestions have been proposed as to how international evaluations might be of use in practical ways.

6.2 International collaborations

This project demonstrated that ABRI as a commercial service provider and BREEDPLAN as the genetic evaluation service are each held in very high regard internationally. Opportunities for the on-going development of international BREEDPLAN evaluations will be dependent on the international reputation of each being reinforced through strategic collaborations (via ABRI) and continual enhancement of the BREEDPLAN technology to better service the requirements of the international market.

6.3 International challenges

This project did highlight an increasingly competitive market in the provision of commercial genetic evaluation services. The marketing strength and speed of delivery of other organisations, such as IGS and Theta Solutions, does mean the priority given to developing international evaluations requires careful consideration of the models and methods available. The growing interest in these other service providers becoming evident within Australian breed associations should not be taken lightly, given their capacity to facilitate multi-country evaluations.

In this regard, the need for validation of outcomes from international models of evaluation will remain ever critical. It is one matter to combine data extracts with a degree of commonality in usage of genetics and run these through analytical models that generate estimates of breeding value and accuracy. It is quite another matter to validate these outcomes and demonstrate the international EBVs as having a degree of reliability in predicting the phenotypes of future offspring.

7 Key messages

International genetic evaluations for beef breeds could assist in accelerating rates of genetic gain in the Australian beef population by providing a more objective basis on which selection decisions are made regarding foreign genetics. International evaluations also have potential to enhance Australia’s high-value genetic export opportunities by demonstrating how Australian genetics compare to other genetics available internationally for a range of production traits.

The development of international genetic evaluations is considered a very high priority to many beef breeds, both domestically and internationally. For seedstock breeders and for those involved in the international marketing of semen and embryos, access to large-scale international evaluations for a given breed is viewed as a higher priority than access to multi-breed evaluations.

A commercial pipeline of processes is necessary for international beef evaluations to be conducted on a routine basis. Such a pipeline requires consideration of requirements that extend beyond the model and analytical software chosen for the calculation of breeding values and is best served by a commercial service provider capable of coordinating all stages of the international evaluation pipeline. The need for validation of outcomes from international beef evaluations remains ever critical, particularly the potential for international EBVs to predict the performance of future progeny in Australia.

Routine international genetic evaluations could be considered as supplementing current national evaluations, rather than replacing them. While international EBVs could be used directly for benchmarking and marketing purposes, there may also be potential for these international EBVs to be used in national evaluations to improve the modelling of imported genetics represented in the national population.

Regardless of breed, there will be specific populations needed to provide the genetic linkage on which international evaluations depend. This highlights the importance of collaboration between countries to ensure key populations are represented in international beef evaluations.

Opportunities for the on-going development of international BREEDPLAN evaluations will depend on strategic collaborations between breed associations and service provider combined with continued enhancement of the BREEDPLAN technology to better service the requirements of an international market.

8 Bibliography

Atkins, J., Spangler, M., Golden, B. and Shafer, W. 2020. Updates to growth trait predictions. *IGS*.

Crook, B.J., Skinner, S.J. and Nivison, H.P. 2019. Developments in multi-source genetic evaluations for beef cattle: A BREEDPLAN perspective. *ICAR Technical Series* 24: 41-47.

Donoghue, K., Graser, H.U., Johnston, D.J. and Tier, B., 2007. AGBU's approach to across-country genetic evaluation for beef cattle. *Interbull Bulletin* 37:12.

Graser, H.U., 2004. Issues and options for global evaluations. *Proc. 14th World Hereford Conference, Armidale Australia*.

Jeyaruban, M.G., Gurman, P.M., Johnston, D.J., Swan, A.A., Banks, R.G. and Girard, C.J., 2019. Validation of Single Step genomic best linear unbiased prediction in beef cattle. *Proc. Assoc. Advmt. Anim. Breed. Genet.* 23: 79-82.

Johnston, D.J., 2004. A global Hereford genetic evaluation – making it happen. *Proc. 14th World Hereford Conference, Armidale Australia.*

Johnston, D.J., Ferdosi, M.H., Connors, N.K., Boerner, V., Cook, J., Girard, C.J., Swan, A.A. and Tier, B., 2018. Implementation of single-step genomic BREEDPLAN evaluations in Australian beef cattle. *Proc. World Congr. Genet. Appl. Livest. Prod*. 11:269.

Johnston, D.J., Schatz, T.G.T., Burns, B.M., Fordyce, G. and Lyons, R.E., 2017. The Repronomics Project: Enabling genetic improvement in reproduction in Northern Australia. *Proc. Assoc. Advmt. Anim. Breed. Genet.* 22: 385-388.

Legarra, A. and Reverter, A., 2018. Semi-parametric estimates of population accuracy and bias of predictions of breeding values and future phenotypes using the LR method. *Genetics Selection Evolution*, 50(1): 53-70.

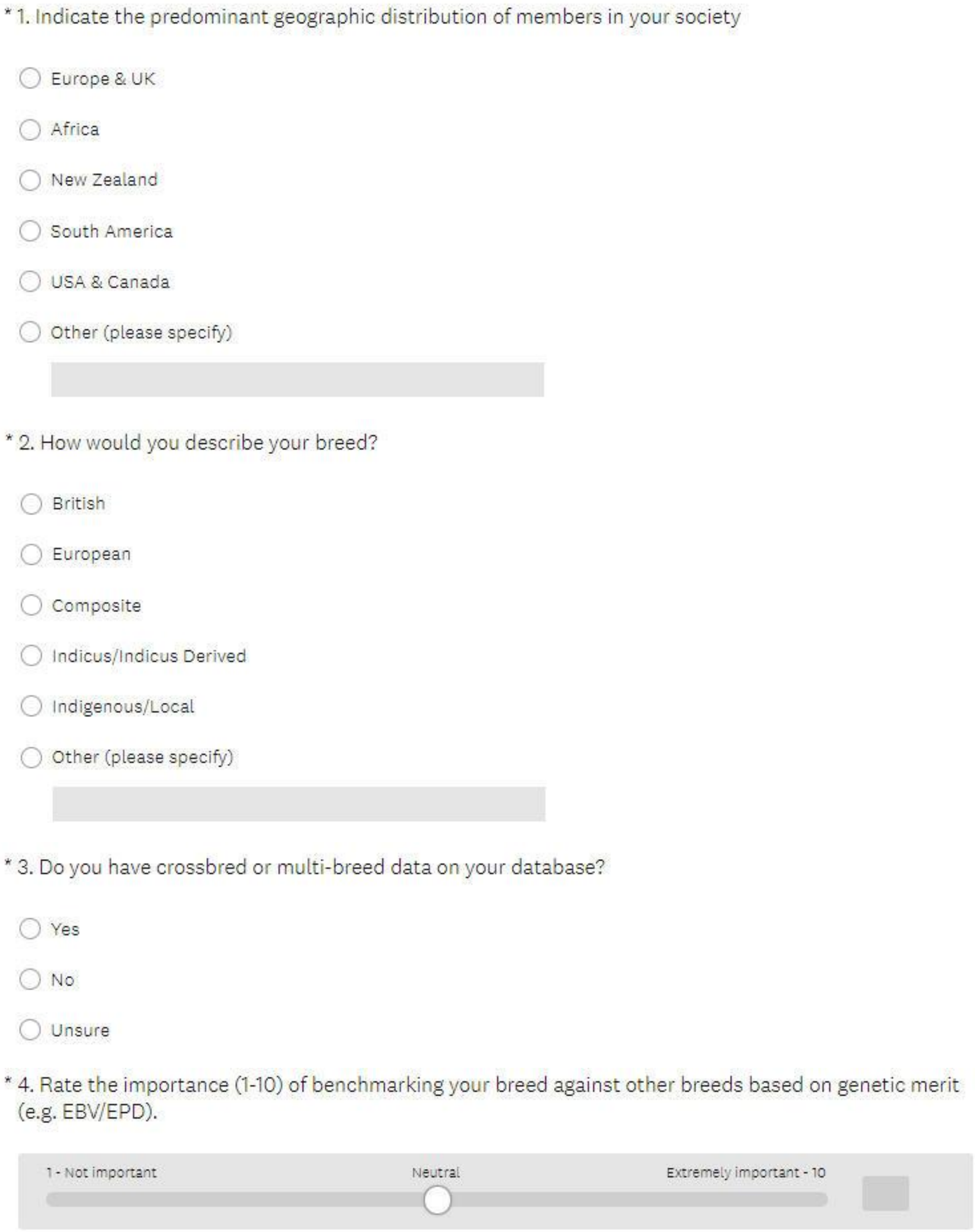
Meyer, K., 2011. WOMBAT: a program for mixed model analyses by restricted maximum likelihood.

Pabiou, T., Pitkanen, T., Evans, R., Herpje, E. and Vandenplas, J., 2018. Using direct and maternal Interbeef information to increase genetic gains in Irish beef. *http://interbull.org/static/web/1630ThierryPabiou.pdf.*

Saatchi M. and Garrick D., (2019). MSRP: A Multi-Breed Selected Reduced Panel for Efficient Genomic Selection in Beef Cattle, *Iowa State University Animal Industry Report* 1(16).

9 Appendix

9.1 Appendix A – Survey template for assessing ABRI client priorities for international evaluations



* 1. Indicate the predominant geographic distribution of members in your society

○ Europe & UK

○ Africa

○ New Zealand

○ South America

○ USA & Canada

○ Other (please specify)

* 2. How would you describe your breed?

○ British

○ European

○ Composite

○ Indicus/Indicus Derived

○ Indigenous/Local

○ Other (please specify)

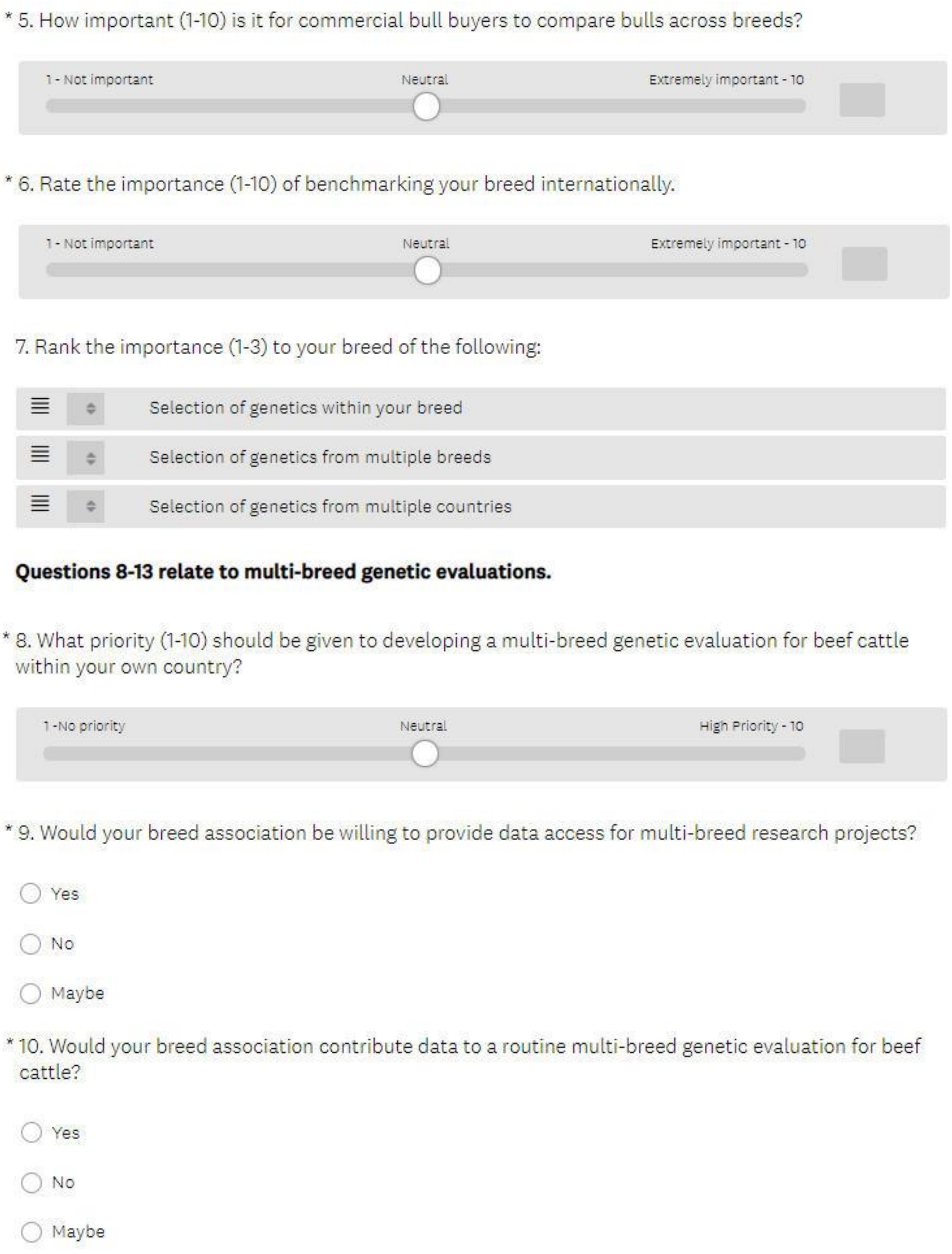
* 3. Do you have crossbred or multi-breed data on your database?

○ Yes

○ No

○ Unsure

* 4. Rate the importance (1-10) of benchmarking your breed against other breeds based on genetic merit (e.g. EBV/EPD).



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

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

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

Questions 8-13 relate to multi-breed genetic evaluations.

* 8. What priority (1-10) should be given to developing a multi-breed genetic evaluation for beef cattle within your own country?

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

○ Yes

○ No

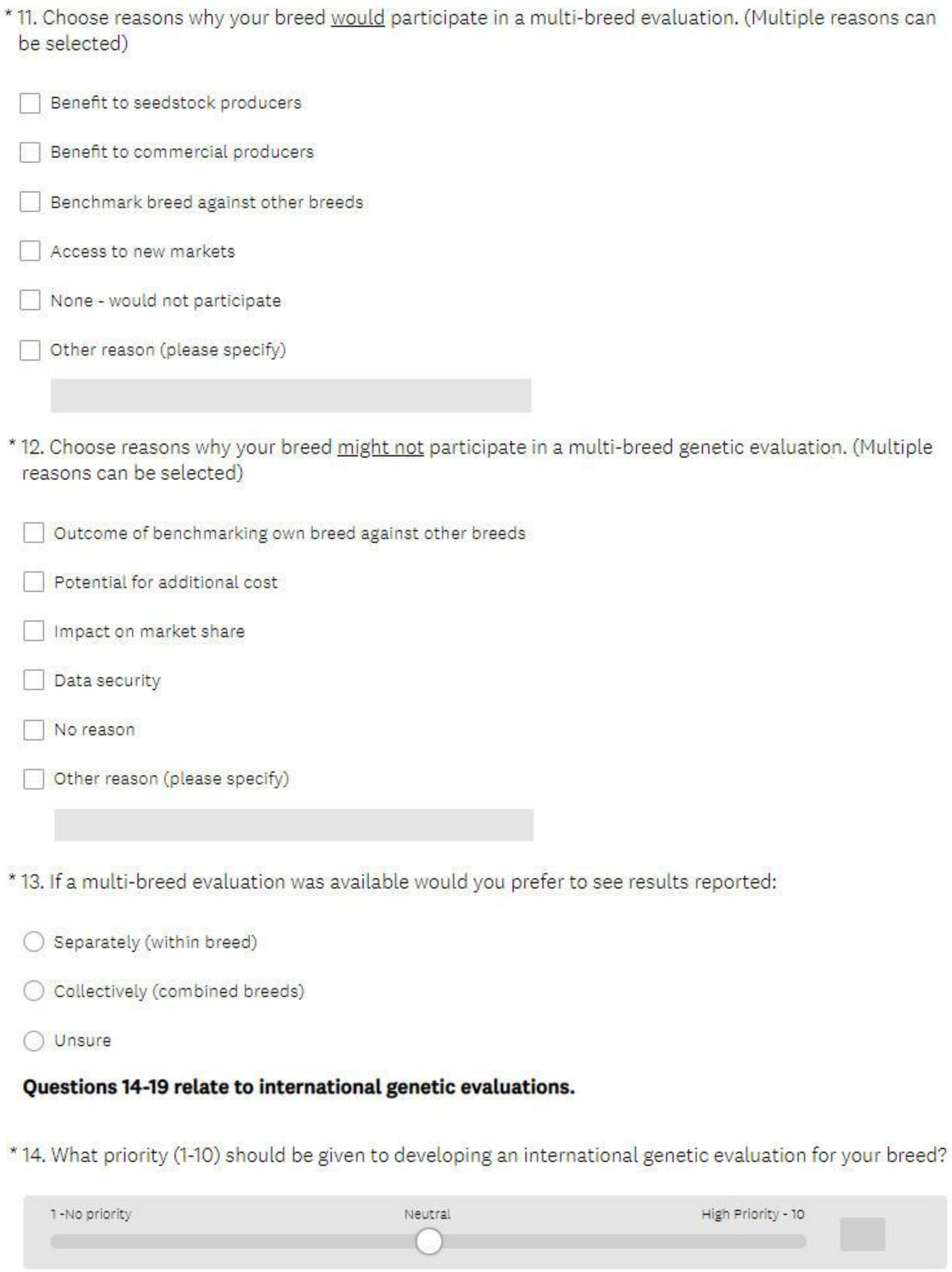
○ Maybe

* 10. Would your breed association contribute data to a routine multi-breed genetic evaluation for beef cattle?

○ Yes

○ No

○ Maybe



* 11. Choose reasons why your breed would participate in a multi-breed evaluation. (Multiple reasons can be selected)

☐ Benefit to seedstock producers

☐ Benefit to commercial producers

☐ Benchmark breed against other breeds

☐ Access to new markets

☐ None - would not participate

☐ Other reason (please specify)

* 12. Choose reasons why your breed might not participate in a multi-breed genetic evaluation. (Multiple reasons can be selected)

☐ Outcome of benchmarking own breed against other breeds

☐ Potential for additional cost

☐ Impact on market share

☐ Data security

☐ No reason

☐ Other reason (please specify)

* 13. If a multi-breed evaluation was available would you prefer to see results reported:

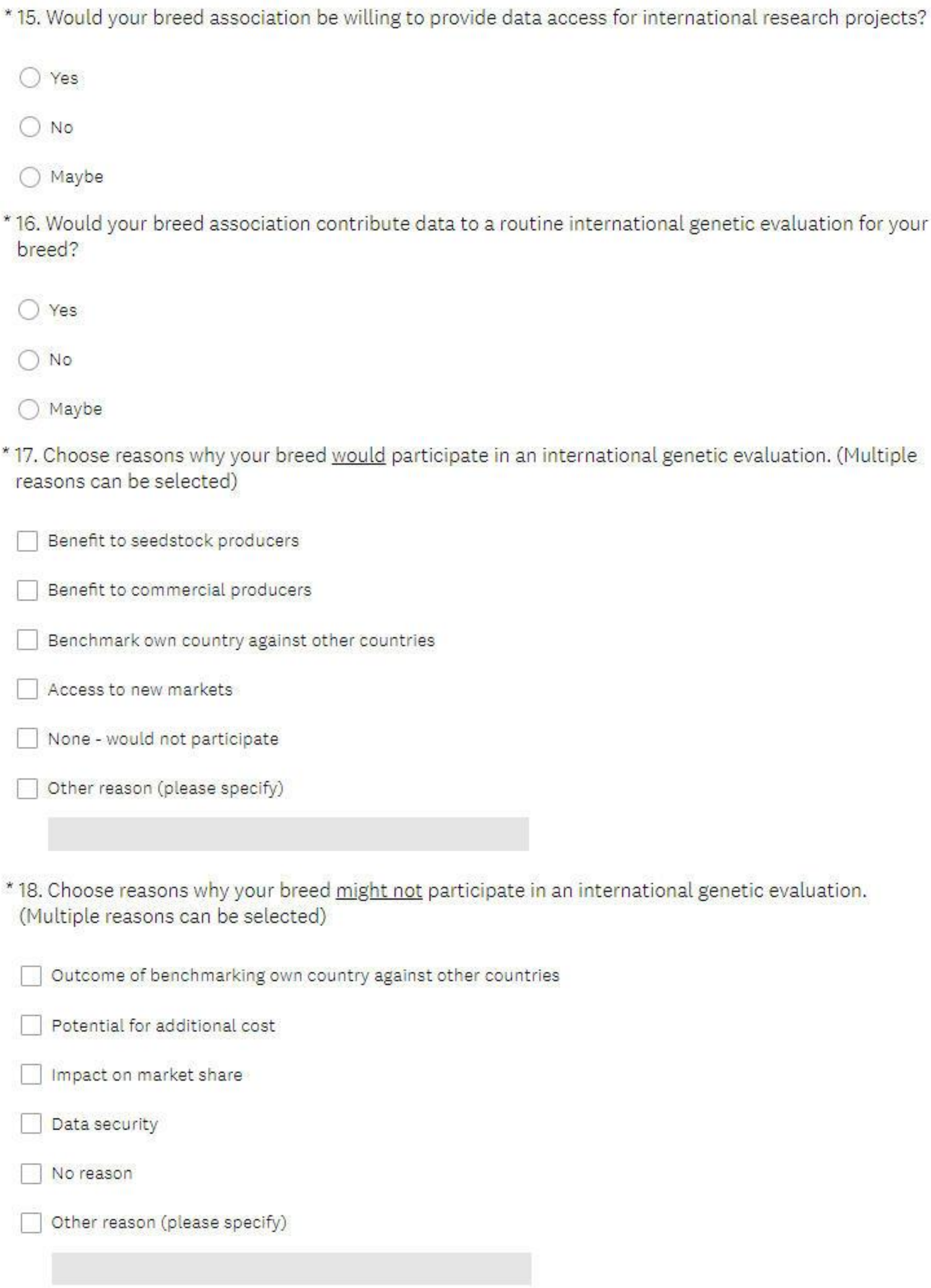
○ Separately (within breed)

○ Collectively (combined breeds)

○ Unsure

Questions 14-19 relate to international genetic evaluations.

* 14. What priority (1-10) should be given to developing an international genetic evaluation for your breed?



* 15. Would your breed association be willing to provide data access for international research projects?

○ Yes

○ No

○ Maybe

* 16. Would your breed association contribute data to a routine international genetic evaluation for your breed?

○ Yes

○ No

○ Maybe

* 17. Choose reasons why your breed would participate in an international genetic evaluation. (Multiple reasons can be selected)

☐ Benefit to seedstock producers

☐ Benefit to commercial producers

☐ Benchmark own country against other countries

☐ Access to new markets

☐ None - would not participate

☐ Other reason (please specify)

* 18. Choose reasons why your breed might not participate in an international genetic evaluation. (Multiple reasons can be selected)

☐ Outcome of benchmarking own country against other countries

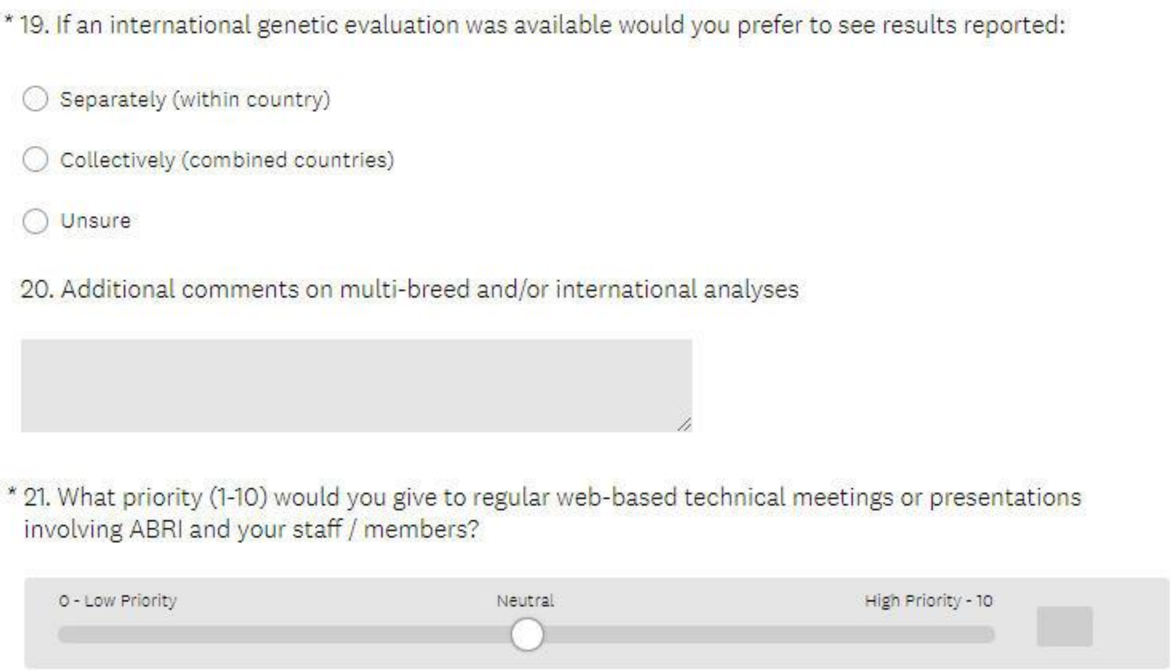
☐ Potential for additional cost

☐ Impact on market share

☐ Data security

☐ No reason

☐ Other reason (please specify)



* 19. If an international genetic evaluation was available would you prefer to see results reported:

○ Separately (within country)

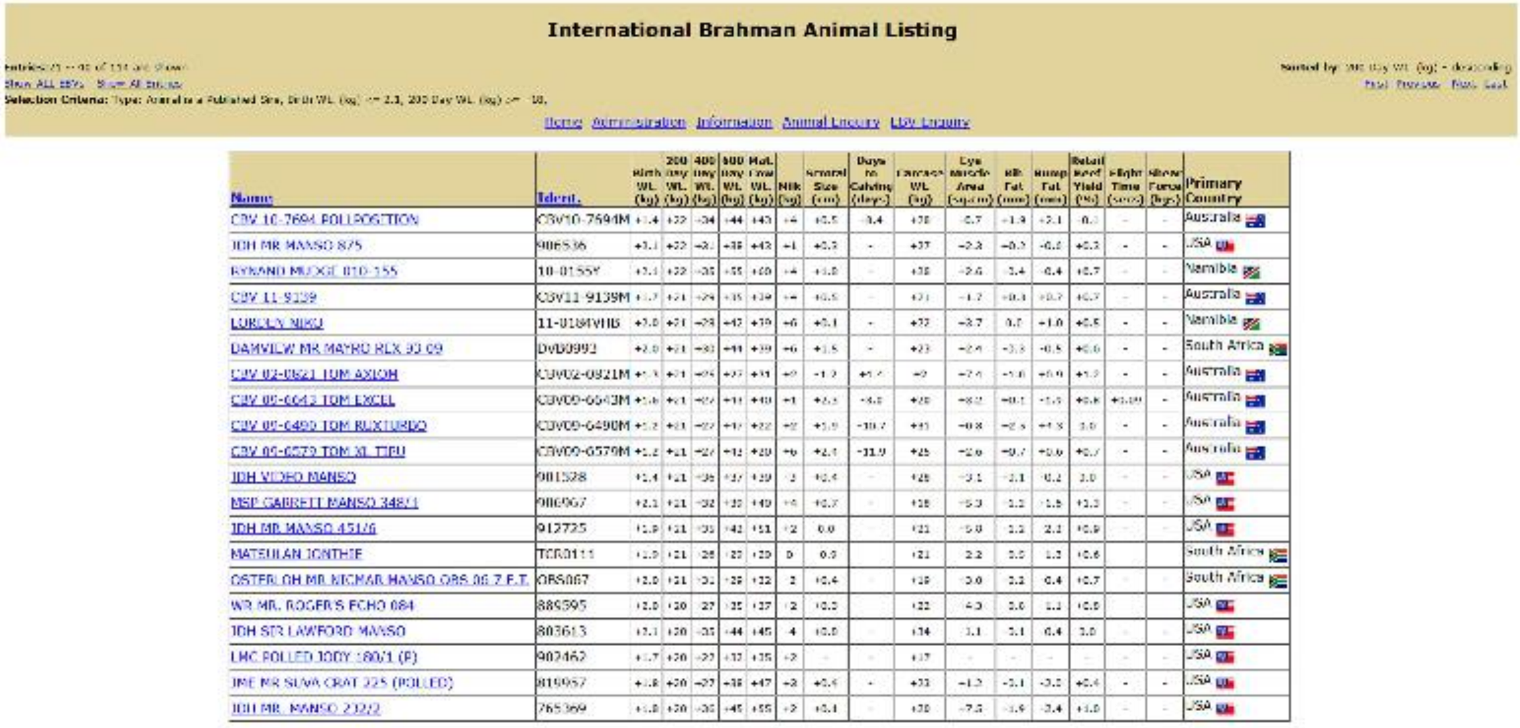
○ Collectively (combined countries)

○ Unsure

20. Additional comments on multi-breed and/or international analyses

* 21. What priority (1-10) would you give to regular web-based technical meetings or presentations involving ABRI and your staff / members?

9.2 Appendix B - Example of EBV reporting from the international Brahman BREEDPLAN evaluation



International Brahman Animal Listing

Entries 21 -> 40 of 131 are shown
Show ALL EBVs Show All Entries
Selection Criteria: Type: Animal is a Published Sire, Birth Wt. (kg) <= 2.3, 200 Day Wt. (kg) >= 18.

Sorted by: 200 Day Wt. (kg) - descending
First Previous Next Last

Home Administration Information Animal Enquiry EBV Enquiry

Name	Ident.	Birth Wt. (kg)	200 Day Wt. (kg)	400 Day Wt. (kg)	600 Day Wt. (kg)	Mat. Cow Wt. (kg)	Milk (kg)	Scrotal Size (cm)	Days to Calving (days)	Carcase Wt. (kg)	Eye Muscle Area (sq.cm)	Rib Fat (mm)	Rump Fat (mm)	Retail Beef Yield (%)	Flight Time (secs)	Shear Force (kgs)	Primary Country
CBV 10-7694 POLLPOSITION	CBV10-7694M	+1.4	+22	+34	+44	+43	+4	+0.5	-3.4	+28	-0.7	+1.9	+2.1	[illegible]	-	-	Australia
IDH MR MANSO 875	906536	+3.1	+22	[illegible]	+38	+43	+1	+0.3	-	+37	-2.3	-0.3	-0.6	+0.3	-	-	USA
RYKAND MUDGE 010-155	10-0155Y	+2.1	+22	+35	+55	+60	+4	+1.0	-	+38	-2.6	1.4	-0.4	+0.7	-	-	Namibia
CBV 11-9139	CBV11-9139M	+1.7	+21	+24	+35	+39	+4	+0.5	-	+31	-1.7	+0.3	+0.7	+0.7	-	-	Australia
LORELY NIKO	11-0184VHB	+2.0	+21	+28	+42	+39	+6	+0.1	-	+22	-3.7	0.0	+1.0	+0.5	-	-	Namibia
DAMVIEW MR MAYRO RLX 93 09	DVB0993	+2.0	+21	+30	+41	+39	+6	+1.5	-	+23	-2.9	-3.3	-0.5	+0.6	-	-	South Africa
CBV 02-0821 TOM AXIOM	CBV02-0821M	+1.3	+21	+25	+27	+31	+2	-1.2	+1.4	+9	-2.6	-1.0	+0.9	+1.2	-	-	Australia
CBV 09-6643 TOM EXCEL	CBV09-6643M	+1.6	+21	+27	+11	+40	+1	+2.3	-4.8	+20	-8.2	-0.1	-1.5	+0.8	+0.09	-	Australia
CBV 09-6490 TOM RUXTURBO	CBV09-6490M	+1.2	+21	+22	+17	+22	+2	+1.9	-10.7	+41	-0.8	-2.5	+1.8	0.0	-	-	Australia
CBV 09-6579 TOM XL TIFU	CBV09-6579M	+1.2	+21	+27	+13	+20	+6	+2.1	-11.9	+25	-2.0	-0.7	+0.6	+0.7	-	-	Australia
IDH VIDEO MANSO	901528	+1.4	+21	+36	+37	+39	+3	+0.4	-	+28	-3.1	-1.1	-0.2	0.0	-	-	USA
MSP GARRETT MANSO 348/1	906967	+2.1	+21	+32	+33	+49	+4	+0.7	-	+18	-5.3	-1.2	-1.5	+1.3	-	-	USA
IDH MR MANSO 451/6	912725	+1.9	+21	+31	+42	+51	+2	0.0	-	+21	-5.0	1.2	2.2	+0.9	-	-	USA
MATEULAN JONTHIE	TCR0111	+1.9	+21	+28	+23	+20	0	0.0		+21	2.2	3.0	1.3	+0.6			South Africa
OSTERLOH MR NICMAR MANSO OBS 06 7 E.T.	OBS067	+2.0	+21	+31	+29	+32	2	+0.4	-	+19	-3.0	2.2	0.4	+0.7	-	-	South Africa
WR MR. ROGER'S ECHO 084	889595	+2.0	+20	27	+35	+37	+2	+0.3		+22	4.3	3.0	1.1	+0.8			USA
IDH SIR LAWFORD MANSO	803613	+2.1	+20	+35	+44	+45	4	+0.0	-	+34	1.1	3.1	0.4	3.0	-	-	USA
LMC POLLED JODY 180/1 (P)	902462	+1.7	+20	+22	+32	+35	+2	-	-	+17	-	-	-	-	-	-	USA
JME MR SUVA CRAT 225 (POLLED)	819957	+1.8	+20	+27	+38	+47	+3	+0.4	-	+33	-1.2	-3.1	-3.2	+0.4	-	-	USA
IDH MR. MANSO 232/2	765369	+1.8	+20	+30	+45	+55	+2	+0.1	-	+20	-7.5	-1.9	-3.4	+1.0	-	-	USA