

Genetic Improvement of Reproduction in Beef Cattle

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ABSTRACT: Reproduction is a key profit driver in beef cattle production systems around the world. However genetic evaluation for reproduction traits is generally limited or non-existent. This is likely a function of low levels of recording reproduction traits, and low heritabilities. Traditional BLUP based genetic evaluations have been used effectively in beef for generating estimated breeding values and, in conjunction with selection indices, have generated significant improvement in growth and carcass traits. Recent studies in Australia have shown component traits of both female and male reproduction have moderate to high heritabilities and there are promising results for the application of genomic selection. This paper summarises genetic evaluation of reproduction in beef cattle world-wide and presents results from a large, long-term Australian research project that provides a blueprint for building future genetic evaluations to increase the rate of genetic improvement in beef cattle reproduction.

Keywords: beef cattle; reproduction; genetic evaluation; genomics

Introduction

Productivity in many beef production systems, including those in the northern Australian pastoral zone, is predominantly driven by sale weights and weaning rates. However reproduction rates are often low in these environments, commonly the result of extended post-partum anoestrous intervals, especially in *Bos indicus* cattle. Traditionally selection has played little role in improving reproduction in beef breeds due to low levels of recording and slow selection response. However, selection line experiments in Droughtmaster (Davis et al. 1993) and Brahman (Schatz et al. (2010)) have shown significant improvement in reproduction rates. Despite this, there is limited inclusion for reproduction traits in genetic evaluations and selection programs of beef breeds around the world. Recent research finding from the Australian Beef CRC northern breeding project has shown opportunities exist to increase rates of genetic improvement for female reproduction through a greater understanding of the genetic control of component traits in both females and males. This paper reviews current genetic evaluation of reproduction in beef cattle world-wide, with a focus on the results of the Beef CRC project as a model for the development of new phenotypic measures, and the application of genomics, to enhance future genetic evaluation and selection for reproduction traits in beef cattle.

Current genetic evaluation of reproduction traits in beef
Traits evaluated. Genetic evaluation of male and female reproduction traits around the world is limited. This

contrasts to genetic evaluation of growth and carcass traits where numerous programs exist, with millions of beef animals evaluated annually across a range of breeds and countries. Table 1 presents a summary of reproduction traits currently included in beef genetic evaluation schemes around the world. By far the most common trait included in genetic evaluations is scrotal circumference (SC). Its ease of measurement has clearly aided its adoption, and without female traits being recorded, it has been evaluated as a proxy for female reproduction (i.e. heifer age at puberty) based mainly on the results of Brinks et al. (1978).

Table 1. Example of countries with reproduction traits as part of beef genetic evaluation programs.

Trait	Country [*]
Scrotal circumference	AU, NZ, SA, NA, AR, UK, IR, BR, FR, US, CA, ME
Days to calving	AU, NZ, SA, NA,
Heifer pregnancy	US, VE, BR
Heifer calving success	FR
Age at 1 st calving	IR, UK, BR
Calving interval	IR, DE, UK
Stayability/productive life	US, CA, VE, UK, FR, BR

^{*}AU=Australia; NZ=New Zealand; BR=Brazil; VE=Venezuela; UK = United Kingdom; IR=Ireland; SA= South Africa; FR=France; US=United States of America; CA=Canada; DE=Denmark; AR=Argentina; NA = Namibia; ME=Mexico.

Researchers have developed a number of female reproduction traits for beef cattle (see review of Cammack et al. (2009)) and heritability estimates reveals their potential use in selection. However net reproduction rate is a function of many components, and for beef cattle, continues through to the weaning of the calf. Therefore it is often difficult or costly to record in extensively managed beef breeding herds. Additionally, to collect suitable data for genetic evaluation of female reproduction traits often requires implementation of whole-herd-recording. This ensures the capture of necessary fixed effects, but most importantly, the recording of females in the herd that fail to express the trait (i.e. not pregnant or did not calve). Female reproduction traits currently used in beef genetic evaluations around the world include: days to calving, heifer pregnancy rate, calving success, age at first calving, calving interval and stayability.

The trait days to calving (DC) was developed as part of the Australia's national genetic evaluation (i.e. BREEDPLAN) and requires the recording of start date for natural mating and the service sire for each mating (Meyer et al. (1990)). The date of birth of the subsequent calf is

used to compute the DC record, with non-calvers receiving a penalty value. Days to calving has been used since 1993 in the genetic evaluation for Australian Angus and has been introduced to a number of breeds (both temperate and tropical) in Australia, New Zealand, South Africa and Namibia.

Heifer pregnancy (HP) is a binary trait that simply records the success or failure of heifers to conceive at their maiden mating. However it is not always clear if evaluations include records from both natural and AI matings, and whether AI synchronisation methods are considered. Examples include the HP EPD used in US Red and Black Angus breeds, and several tropical beef breeds in Venezuela. In France, an evaluation has recently been developed for female fertility in Charolais and Aubrac breeds. The EBV is computed from the calving success from the first AI mating of heifers and includes a correlated calving success trait of cows (Venot et al. (2013)).

Two other related traits used extensively in Ireland (<http://www.icbf.com/>) and some breeds in Canada and the US are age at first calving and calving interval. These traits are computed using calving dates from first mating of heifers, and subsequent calvings. In South American evaluations, heifer precocity/maturity EBVs are produced for a number of breeds and is based on age at first calving or heifer pregnancy (Eler et al. (2002)) in yearling heifers.

Genetic evaluations also exist for traits associated with lifetime reproduction and longevity of beef females. The trait stayability uses production and reproduction records to determine whether or not (0, 1) a cow is present in the herd at a given age (at 6 years of age). Stayability genetic evaluation exists for a number of breeds in US (e.g. Red Angus, Simmental, Limousin) and South America. In France, a productive life trait has been developed and records total number of calves at 78 months of age.

For comparison, all major dairy cattle genetic evaluations globally (including some dual purpose breeds e.g. German Fleckvieh) have added reproduction traits in the past decade. The intensive management of dairy cows and the high use of AI has allowed collection of large amounts of data, and the construction of reproduction traits based heavily around known insemination dates. This has led to the development of traits such as number of days open and non-return rate 56 days post-partum (NR56). Many evaluations have developed these traits further and have introduced new traits such as daughter progeny rate (e.g. US Holstein). Some evaluations have moved to a multiple trait approach including component traits such as calving interval, lactation length, pregnancy rate, first service non-return rate and age at first insemination. Commonly, heritabilities of reproduction traits in dairy cattle evaluations are very low (1-3%). Research has investigated other reproduction measures, targeting particular biological and physiological processes e.g. progesterone concentrations in milk. Although, it is not clear if any routine national genetic evaluation is occurring for these traits.

Models used in beef. The heritabilities reported for female reproduction traits from beef genetic evaluations from around the world tend to be low. For example, heifer calving success in French Charolais (1.5%), Australian

Angus DC (7%) and US Angus HP (13%). In contrast, SC has a heritability of around 40% in many evaluations. It is also difficult to determine the model structure used in each evaluation (i.e. single versus multiple trait) and whether linear versus threshold models are used. BREEDPLAN evaluations that include both DC and SC are analysed in a multiple trait model (Graser et al. (2005)), with a low genetic correlation between the two traits. Van Melis et al. (2010) also reported a low correlation (0.29) between SC and HP in Brazilian Nellore cattle.

One of the challenges commonly faced with the genetic evaluation of reproduction traits is the binary nature (i.e. 0, 1) of many of the traits. These are often related to the output or rate variables such as conception rate and calving success. This creates analytical difficulties because most evaluations are configured as linear models. However, threshold models are routinely used in beef evaluations of calving ease and temperament, and can also be used for binary female reproduction traits (e.g. US Angus HP).

Reproduction in selection indices and selection.

As with the description of models, it is also difficult to determine how the various reproduction traits are included in selection indices, and what weighting they receive. Some of the reproduction traits analysed are selection criteria (e.g. SC) while others could be considered traits in the breeding objective (e.g. HP). In Australia, for those breeds with a DC EBV it is included in self-replacing indexes as selection criteria for cow weaning rate which is the female reproduction trait in the breeding objective (Barwick and Henzell (2005). Other evaluations, (e.g. Ireland, German Fleckvieh, South American) include their reproduction EBVs in their maternal indexes. At this stage the HP EPD is not used in the computation of US Angus selection indexes.

Genetic trends are reported in some evaluations and generally show positive trends for growth and carcass traits, while trends for reproduction traits are generally not informative due to their relatively recent introduction and limited numbers of animals evaluated. Barwick and Henzell (2005) concluded from Australian breed genetic trends for numerous indexes that low rates of gain and low index accuracies were primarily the result of low levels of performance recording, and this was particularly the case given many self-replacing indexes place considerable emphasis on female reproduction. Johnston et al. (2012) reported low average accuracies in young beef bulls for a range of breeds, particularly for the days to calving EBV.

New reproduction phenotypes for beef- Northern Australia reproduction project

Project design. The Beef CRC northern breeding project involved both Brahman (BRAH) and Tropical Composite (TCOMP) cattle generated in sub-tropical and tropical regions of northern Australia (see Barwick et al. (2009a)). These were the progeny of more than 50 sires per genotype, with the heifer progeny (N=2174) allocated at weaning to one of four Queensland Research Stations that represented a range of northern Australia's breeding environments. Heifers were recorded post-weaning for growth and body composition traits (Barwick et al. (2009b)), tropical adaptation traits (Prayaga et al. (2009)) and age at puberty (Johnston et al. (2009)). All heifers were

naturally mated to first calve at approximately 3 years of age. Subsequently the cows were naturally mated annually with full reproduction data collected, including reproductive tract ultrasound scanning to determine resumption of cycling after calving. Cows remained in the project until the weaning of calves from their 6th mating when they were approximately 8.5 years of age, unless they failed to wean a calf in consecutive years or were culled for other management reasons. Cows were also regularly weighed and measured for body composition throughout their lifetime and analyses of these traits in first-calf cows are presented in Wolcott et al. (2014). All male progeny (N=3,500) generated from the project cows remained entire and were measured for a range of production and reproduction traits from 4 to 24 months of age. The reproduction traits included: scrotal circumference, hormone concentrations, crush-side semen traits and sperm morphology (Burns et al. (2013)).

Full genetic analyses were undertaken for all female and male traits to estimate heritabilities (h^2) and genetic correlations (r_g) among traits. All cows were genotyped using SNP 50K and a subset with the HD SNP chip (i.e. 770K). All genotypes were imputed to HD and genome-wide association studies were performed for several early-in-life female production and reproduction traits (Hawken et al. (2012)). Female reproduction data and HD genotypes were also used by Zhang et al. (2014) to construct genomic prediction equations. A subsample of the young male BRAH and TCOMP progeny were also genotyped with the SNP 50K and HD, respectively. Genome wide associations studies (GWAS) were performed for male puberty traits in BRAH (Fortes et al. (2012)) and TCOMP (Fortes et al. (2013a)).

Key reproduction traits. The intensive measurement of females (i.e. regular ovarian ultrasound scanning, body measures, mating, calving and weaning records) allowed the construction of numerous traits related to components of female reproduction from puberty through to lifetime performance (Johnston et al. (2014a)). These included traits associated with heifer puberty (age, weight, body condition score, hip height, fatness, pubertal rates), and those describing reproductive performance in maiden heifers and 1st calf cows. These included traits describing particular intervals (DC, lactation anoestrous) and binary traits (i.e. conception, pregnancy, calving, cyclicity and weaning rates). Finally, calving and weaning records across the whole experiment (i.e. up to 6 matings) were used to construct traits for lifetime reproductive output (calving rate and weaning rate) for each cow, and for the sub-set of cows still present at the end of the experiment.

Average lifetime annual weaning rate from the experiment was 65%, but rates were considerably lower in first lactation cows. For example, pregnancy rate for BRAH was only 27% in this class of cow. This low performance was influenced by an extended lactation anoestrous interval experienced by these 1st calf cows, where only 53% cycled while lactating. These effects were also apparent in the TCOMP but to a lesser extent. Differences between calving and weaning rates revealed the occurrence of significant calf losses (Bunter et al. 2014). These results are in line

with average performance in northern Australia and illustrate the opportunity that exists to increase productivity.

Genetic analyses showed many of the component traits of early reproductive performance had moderate to high heritabilities (Table 2). Heifer age at first observed *corpus luteum* (AGECL) had heritability estimates of 0.57 and 0.52 in BRAH and TCOMP, respectively. First lactation anoestrous interval (LAI) was moderately to highly heritable 51% and 26% in BRAH and TCOMP, respectively. Heritabilities of binary reproductive output traits (conception rate, pregnancy rate, calving rate and weaning rate) from 1st and 2nd annual matings were also moderately heritable in BRAH, and lower in TCOMP. More consistent with expectations, heritabilities of lifetime reproduction traits were low, with estimates of 11% and 7% for lifetime annual weaning rate (LWR) in BRAH and TCOMP, respectively.

Table 2. Heritabilities of reproduction traits^s in Brahman (BRAH) and Tropical Composite (TCOMP).

Time [®]	Trait [*]	h^2	
		BRAH	TCOMP
Puberty	AGECL	0.57	0.52
	WTCL	0.56	0.46
	FATCL	0.55	0.39
	PR rate	0.33	0.13
Mating 1	PREG1	0.42	0.10
	CR1	0.22	0.11
	DC1	0.22	0.13
Mating 2	PREG2	0.35	0.06
	CR2	0.32	0.11
	DC2	0.20	0.17
	LAI2	0.51	0.26

[®] Puberty = heifers recorded between 10-24 months; Mating 1 = start annual mating period of maiden (2yr old heifers); Mating 2 = start of 2nd mating period; Lifetime = records from up to 6 annual matings; Male = bulls recorded between 4-24 months.

Table 2. Heritabilities of reproduction traits^s in Brahman (BRAH) and Tropical Composite (TCOMP). (continued)

TIME [*]	TRAIT [*]	h^2	
		BRAH	TCOMP
Lifetime	LCR	0.16	0.04
	LWR	0.11	0.07
Male	INH	0.74	0.72
	IGF-I	0.44	0.36
	SC	0.75	0.46
	PNS	0.25	0.41
	AGE26	0.78	0.58

^s adapted Johnston et al. 2009, 2014a; Corbet et al. 2013; Fortes et al. 2012
^{*} AGECL = age at 1st CL; WTCL = weight at 1st CL; FATCL = P8 fat at 1st CL; PR rate = pubertal rate into mating; CR1,2 = calving rate; DC 1,2 = days to calving; PR1,2 = pregnancy rate; LAI2 = lactation anoestrous interval; LCR = lifetime annual calving rate; LWR = lifetime annual weaning rate; IGF-1 = insulin-like growth factor - I; SC = scrotal circumference; INH = inhibin concentration; PNS = % normal sperm; AGE26 = age at 26 cm SC.

Genetic correlations between early-in-life reproductive measures and lifetime reproduction traits were moderate to high (Table 3). AGECL was correlated with

early reproductive performance in BRAH and with mating 2 traits in TCOMP. But AGECL was only moderately correlated with lifetime reproductive performance. LAI was genetically associated with higher LWR (BRAH $r_g = -0.60$; TCOMP $r_g = -0.85$). These results represent an opportunity to genetically improve weaning rates in tropical breeds by focusing recording and selection on early-in-life female reproduction traits, particularly those traits associated with lactation anoestrus in BRAH.

Table 3. Genetic correlations^s of key female reproduction traits (1) with male* and female (in italics) indicator traits (2) in BRAH and TCOMP.

Trait 1 ^{&}	Trait 2 ^{&}	r_g	
		BRAH	TCOMP
AGECL	<i>IGF-I</i>	-0.70	-0.35
	<i>WT</i>	-0.35	-0.40
	<i>Fat</i>	-0.35	-0.20
	<i>IGF-I</i>	-0.55	-0.45
	<i>SC</i>	-0.25	-0.20
	<i>PNS</i>	-0.50	-0.05
CR1	<i>AGECL</i>	-0.60	-0.15
	<i>DC1</i>	-0.95	1.00
	<i>IGF-I</i>	0.45	-0.00
	<i>SC</i>	0.25	0.10
	<i>PNS</i>	-0.00	-0.15
LAI2	<i>AGECL</i>	0.30	0.70
	<i>DC2</i>	-1.00	-0.90
	<i>SC</i>	-0.25	0.15
	<i>PNS</i>	-0.50	-0.35
	<i>WWTm</i>	0.05	0.40
CR2	<i>AGECL</i>	-0.10	-0.60
	<i>DC2</i>	-1.00	-1.00
	<i>LAI2</i>	-1.00	-0.85
	<i>PNS</i>	0.30	0.55
	<i>SC</i>	0.25	0.15
	<i>WWTm</i>	-0.05	-0.70
LWR	<i>AGECL</i>	-0.35	-0.30
	<i>LAI2</i>	-0.60	-0.85
	<i>DC1</i>	-0.50	-0.55
	<i>DC2</i>	-0.95	-0.75
	<i>HH</i>	0.50	0.10
	<i>WT</i>	0.55	-0.10
	<i>WWTm</i>	-0.50	-0.25
	<i>MOT</i>	0.80	0.10
	<i>SC</i>	0.15	-0.30

^sadapted Johnston et al. 2009, 2014a,b; Wolcott et al. 2014.

* Male traits recording time BRAH at 18mth and TCOMP at 12mth.

[&] see descriptions Tables 1 and 2. WT = liveweight; Fat = P8 fat depth; WWTm = weaning weight maternal; HH = hip height; MOT = % motile sperm.

Male reproduction traits measured on bulls between 4 and 24 months of age had moderate to high heritability estimates in both BRAH and TCOMP (Table 2 and Corbet et al. (2013)). In general, estimates were higher when measured at 12 months of age for TCOMP bulls, and 18 months of age for BRAH.

Early-in-life indirect measures. Several traits measured early-in-life were genetically correlated with female reproduction traits (Table 3). IGF-I in heifers and

bulls was correlated with AGECL. SC was genetically correlated with heifer AGECL ($r_g = -0.25$ in BRAH for SC at 18 months; $r_g = -0.20$ in TCOMP for SC measured at 12 months) however the genetic correlations were lower with later measures of female reproduction. Semen quality traits were genetically correlated with LAI, and with female lifetime reproduction rates in both genotypes, although the magnitudes of the relationships differed with bull age at measurement. Several novel traits, including heifer adaptive measures (e.g. hip height and coat score) and bull traits (e.g. sheath and preputial eversion score) were also genetically associated with lifetime reproduction rates in both genotypes and could contribute to significant improvement in genetic progress for female lifetime reproductive performance (Barwick et al. (2014)). In general, cow weight and body composition at 18 months and at start of 2nd mating period were not highly genetically related to subsequent reproductive performance, with the exception of maternal weaning weight (i.e. genetic milk) and, to a lesser degree, cow eye muscle area in BRAH (Wolcott et al. (2014)).

Genomics for reproduction. GWAS results for early-in-life traits in the females (Hawken et al. (2012)) showed large number of associations, with clusters of SNPs for BRAH on BTA14 and for TCOMP on BTA5. Fortes et al. (2012) investigated Brahman age at puberty in both the heifers and bulls and reported many common SNPs. This result supports the moderate to large genetic correlations in these cattle reported by Johnston et al. (2014b) for heifer AGECL with a range of male reproduction traits. GWAS results for male reproduction traits in TCOMP (Fortes et al. (2013a)) also showed a large number of explanatory SNPs. For male pubertal traits many were located on the X chromosome. Further investigations (Fortes et al. (2010, 2013b)) showed the presence of complex gene networks associated with puberty and interaction of regions and selection signatures for genomic regions associated with production and reproduction in these tropical beef genotypes.

Zhang et al. (2014) developed genomic prediction equations for female reproduction traits AGECL and PPAI from GBLUP analyses. The resultant GEBVs were assessed using internal cross-validation analyses and genomic accuracies ranged from 0.14 to 0.33 for AGECL and PPAI in BRAH and TCOMP. Further, independent validation of the genomic predictions using populations recorded outside the training dataset showed accuracies up to 0.4 for industry recorded pregnancy rate. An analysis using BREEDPLAN trait DC in Brahman yielded genomics accuracies of 0.36 and 0.22 using genomic predictions of AGECL and PPAI, respectively. These results, while only modest, were shown to contribute significantly to increased rates of predicted genetic gain in female reproduction (Barwick et al. (2014)). However, larger numbers of phenotypes and genotypes are required to lift genomic accuracies above 0.4, and thus increase the utility of genomic information in future selection.

Future genetic evaluation for reproduction

World perspective. There is significant scope to increase the genetic evaluation of reproduction traits in beef

cattle world-wide. Although limited, there are several examples of reproduction traits in beef cattle genetic evaluations and selection indexes, and this should offer encouragement to others. Current evaluations have been based on ease of recording reproduction data. There is potential to expand the recording for existing, and new traits, but cost will clearly be a constraint, particularly in extensive beef production systems. However, it is likely to be more cost effective if the data can also be used to drive increased accuracy through genomic selection.

New reproduction phenotypes for genetic evaluation. With advances in technology (e.g. electronics and computing) opportunities exist to expand recording and more actively capture phenotypic data which describes components of female and male reproduction. This may allow a greater proportion of the population to be measured, and for traits with higher heritabilities. This will allow increased selection intensities and accuracy of selection, and the potential to increase rates of genetic progress. As seen in the Beef CRC project, a range of additional female measures could be considered (e.g. ovarian scanning). Other technologies exist that could be used to record individual behaviour, mating and calving outcomes, and calf survival. This may include remote sensing, satellite tracking, pedometers, location loggers, electronic mount detectors for oestrus activity, body temperature or hormone assays. There is also potential to use new measures of male reproduction. The Beef CRC identified several male traits recorded during bull breeding soundness evaluations that are candidates for genetic evaluation (Corbet et al. (2013)) and research is underway to determine their suitability for inclusion in BREEDPLAN for tropical beef breeds. Remote sensing may also offer new methods for recording bull libido and mating outcomes.

For any of these new measures to contribute useful data to genetic evaluation requires precise trait definition (included necessary fixed effects) to provide a repeatable and heritable trait that can be measured consistently across herds and years. If they are indicator traits then an estimate of the genetic correlation is needed with the related female (or male) reproduction trait. It is also likely that some of these new measures will generate large volumes of data, requiring effective data transfer and database storage and retrieval. New algorithms will be required for interpreting and turning the raw data into meaningful traits for genetic evaluation.

Genomics into genetic evaluation. Including genomic data in existing genetic evaluation is becoming routine in many species and countries, especially in dairy cattle where genomic selection is revolutionising breeding programs and genetic progress. Benefits from genomic selection have also been demonstrated in beef breeding (e.g. Van Eenennaam et al. (2011) and Saatchi et al. (2011)). The major advantage is the increase in accuracy for traits that can't be measured (or are too costly) before selection of young bulls occurs (e.g. 1-2 years of age). Benefits of genomic selection to dairy breeding comes mainly from greatly reduced generation intervals due to the need to record daughters, and this applies equally to female reproduction traits in beef cattle.

The potential for genomics to contribute to the genetic improvement of female reproduction traits is evident from Beef CRC results and several others have published significant SNP associated with female reproduction traits (Allan et al. (2009); Luna-Nevarez et al. (2011)). Gene expression studies and gene pathway analyses (Snelling et al. (2012); Beltman et al. (2010)) have also been used to identify complex interactions of genes involved in beef female fertility (e.g. heifer puberty) which may lead to more sophisticated SNP assays and use in selection. Opportunities also exist to exploit genomics of male reproduction as demonstrated in Beef CRC (Fortes et al. (2013a)) and summarized in a review by Fortes et al. (2013c). The clustering of SNP for male reproduction traits, in particular on the X chromosome, may require special consideration in future genetic evaluation.

Swan et al. (2012) summarised different analytical methods for including genomic data into beef and sheep genetic evaluations. Currently several beef evaluations report the use of genomic information in their genetic evaluations (e.g. Ireland, and Angus in US and Australia). There is scope to increase accuracies for reproduction traits as demonstrated in the Australian studies. However the lack of phenotypes for traditional genetic evaluation of female reproduction is also a limitation for genomic selection. Therefore, beef breeding programs need to genotype and phenotype increased numbers of animals in their populations. However, evaluations that continue to use existing lowly heritable traits will require considerable more records compared to evaluations that can develop new traits with higher heritabilities. Advances in genomic technologies will almost certainly occur and may include the routine use of denser chips, use of whole genome sequencing, identification of copy number variants affecting genes and chromosome anomalies (e.g. Y chromosome in females; McDanel et al. (2012)). These developments should lead to more effective genomic tools for determining genetic differences controlling traits of economic importance (i.e. reproduction).

Using genomics in routine genetic evaluations will require effective storage and retrieval of genotypic data and if genomic data is included using selection index (i.e. blending) or a multiple trait approach it requires the correct weighting on the genomic data (i.e. genomic accuracies) for each trait and breed. Research has shown GEBVs will not be predictive for breeds not in the training set or that are distantly genetically related. Therefore knowledge of genomic distance of the animals from the training population may be required. Genomic selection using GBLUP or single-step requires the construction of a genomic relationship matrix and its inversion, which may add to computing and storage requirements. Both methods may need to address the modeling of SNP of large effect and evaluation of combined breeds (or genetic groups). Finally, education of industry and individual breeders on genotyping and ongoing phenotyping strategies will be needed. Wide-scale adoption of genotyping in the beef breeding sector will depend primarily on cost genotyping, and the level of accuracy achieved.

Reproduction in multiple trait selection. Reproductive performance will continue to be an important

trait in beef breeding objectives for many breeds and countries. As discussed, there needs to be wide-scale recording of reproduction, suitable genetic evaluation and importantly, inclusion in breeding objectives and selection indexes for effective selection. Therefore, before any new traits are considered, estimates will be required of their relationships to reproduction traits in the breeding objective and their impact on index accuracy. It is also likely as new female reproduction traits are included that additional measures of cow longevity/survival will be required, and correlations with other key traits are known e.g. cow weight, body condition score, and genetic milk. Similarly, for male traits to be included it will require the establishment of suitable traits in the breeding objective, including computation of economic values and relationships to selection criteria. Inclusion of genomics is not expected to alter the formation of the breeding objective, with the exception of single genes that may be considered directly as objective traits.

Conclusions

Beef genetic evaluations and selection programs world-wide have generally ignored reproduction traits. However, advances in recording and application of new technologies have meant increased numbers of evaluations including reproduction traits. Opportunities exist to greatly increase the accuracy of selection for reproduction traits in beef by increasing levels of recording and through the inclusion of correlated early-in-life traits in females and males. These enhancements, along with genomics, need to be incorporated into existing genetic evaluations and selection indices to allow increase rates of genetic progress through improved selection.

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