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Genetic Evaluation of Reproductive Traits: Review

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Abstract: Genetic evaluation systems provide the basis for genetic improvement programs. Breeders and producers need ways to evaluate the genetic merits of cattle and predict the traits and performance of their offspring. The production of high quality, healthy and affordable productivity begins by identifying the best animals for breeding. An evaluation model partitions phenotypic records into genetic and environmental effects. The design goal is to avoid biases by accounting for effects that would influence the estimates of genetic merit. Differences include type of model used, adjustments before analysis, effects included in the model, assumed parameters, solution methods and reported results. With the increasing importance of international use of evaluations, emphasis is placed on harmonization. Phenotypic strategies will remain a key component of an animal breeding strategy to achieve the future as well as providing the necessary tools and information to monitor performance. The inclusion of genomic information in genetic evaluations is and will continue, to improve the accuracy of genetic evaluations which in turn will augment genetic gain; genomics; however, can also contribute to gains in performance over and above support of increased genetic gain.

Key words: Traits · Genetics · Genetic Evaluation · Reproduction · Selection · Improvement

INTRODUCTION

Application of basic science to improve animal production practices is the goal of animal genomics research. In the short-term, the combined use of genomic information with existing animal breeding and animal management programs will provide immediate impacts, such as more accurate and accelerated rates of genetic improvement of breeding stock (especially for traits that have been traditionally difficult to measure), animals that are more adaptable and better suited to various production environments and new genome-based technologies to enable parentage and identity verification (i.e., traceability). Delivery and adoption of new genome-based technologies will require integrated activities involving basic scientists, educators (classroom and extension specialists), animal breeding and artificial insemination organizations and producers working together to utilize these technologies [1].

Genomic evaluation and information will also provide the basis for development of precision management systems. Knowledge of an animal's genotype will allow precise sorting of animals into the optimal production environment, resulting in enhanced animal well-being. For example, the genotype of some beef and dairy cattle may be more suited to pasture-based production systems rather than confinement systems. Feeding regimens and preventative health care programs can also be designed to match an animal's genotype and lead to increased production efficiency, targeted market endpoints and new opportunities for niche markets. The expected amount of genomic information will require development of decision support systems for use in the industries to implement and manage such genome enabled precision management systems [1].

Intended for more accurate genetic evaluations, differences in breed composition, in terms of additive and non-additive effects and of heterogeneous variances,

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should be taken into account [2, 3]. In addition, the interactions between the breeding value of the bull and the genetic group its progenies belong to are important to establish breeding strategies aiming to obtain greater benefits for future generations [4, 5]. Therefore, the genetic evaluation of multiple-breed populations may be improved when the traits of each genetic group are specifically assessed. Multiple-trait models (MTM) allow considering any characteristic (e.g., milk yield) as a distinct one in each group it is measured in. This approach has already been adopted in other studies [4, 5] and allows detecting differences related to variances and co-variances. However, these models tend to become more parameterized as the number of genetic group's increases. This parameterization may be reduced by using random regression models for multiple-breed genetic evaluations. The use of a random regression model using linear splines (RRMLS) is an alternative for cases in which the MTM shows limitations [6] pointed out that polynomial splines can be used to adjust the effect of a continuous variable, such as the expected percentage of alleles of a certain breed. The BLUP procedure has been the method of choice for the genetic evaluation of animals in the last few decades in conventional breeding program [7].

Genetic Evaluation of Reproduction Traits

The Breeding Goal: Setting up a breeding package starts with the definition of a breeding goal and is followed by the design of a scheme that is able to deliver genetic progress in line with this goal. Breeding goals with the relevant traits, collection of performance data, analysis of the data for the identification of superior animals and the use of superior animals to produce the next generation, are the main components of structured breeding programs. Breeding goal traits might be quantitative [8]. Milk, meat or egg production, body measurements or performance expressions are examples of quantitative traits. They are measured in units: in kg or simply in numbers: kg of milk, grams of growth and number of eggs. Breeding goals might be qualitative e.g. the quality of a product or an important trait in the breed standard. Product traits, scores for body traits, disease incidences or performance impressions are examples of qualitative traits. They are measured in classes: e.g. 1-good, 2-moderate or 3-bad for meat quality or simply 0 (not present in the animal) or 1 (present) [8]. Some breeding goals traits cannot be measured at the time when it is relevant. E.g. in meat production, meat quality is an important breeding goal trait. However, you cannot measure carcass composition of a young calf, piglet or lamb at the moment you consider to use the animal for breeding. It can be measured only after slaughter and then breeding with that animal is impossible. Indicator traits, obtained by scanning live animals for body composition before you take breeding decisions may help to predict carcass composition [8].

Breeding goal traits might be complicated consisting of many fundamental traits. E.g. in nearly all food producing species reproduction capacity is part of the breeding goal. Reproduction capacity is composed out of male and female reproduction traits. In male's sperm quality and insemination results are part of their reproductive capacity. In female's age at puberty, interval between litters, number of offspring raised per year is examples of underlying traits. In jumping horses the conformation of the horses and the way they use their legs are very important breeding goal traits. In working dogs, trainability is an important trait in addition to health, behavior and conformation (*Ibid*) [8].

Selection Indices in Reproduction: As with the description of models, it is also hard to determine how the various reproduction traits are included in selection indices and what weighting they receive. Some of the reproduction traits analyzed 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 [9].

Other evaluations, (e.g. Ireland, German Fleckvieh and 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 [9].

Genetic tendencies 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 [9] 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 [9].

Genetic Evaluation Systems: Currently, animal production maintains and executes different genetic evaluation systems based on groups of traits and data used. Specifically, these include production, conformation, longevity, calving ease, milking speed, milking temperament and reproductive performance [10].

Age at First Calving (AFC): AFC is one of the most significant traits high related to fertility and reproductive efficiency in cattle. Lower AFC is associated with heifer cleverness and also high lifetime productivity. Despite of easiness of routine recording, AFC data is not always appropriate to be used in genetic evaluation because of recording mistakes and non-occurrence or delay in communication of the event (parturition) at the moment of genetic evaluation. Also, selection schemes which involve reproductive tools such as multiple ovulation and embryo transfer (MOET) nucleus implemented in Guzerá breed programs in Brazil should have some influence in AFC data. Consequently, these AFC records should not be considered. Usually, animals without AFC phenotype are ignored in routine genetic evaluation. However, their records can also be reconsidered as censored observations (*Ibid*) [10].

Age at first service (AFS) depends mainly on the growth rate and age of the heifer, but is also influenced by genetics, nutrition and health. The decision on when to start breeding is primarily a management one. When the age at first service of the heifer is lower, greater is the useful lifespan of the cow and consequently more calves will be produced. Age at first calving (AFC) is also an important economic trait and a potential measure of reproductive performance in dairy cattle. It encompasses puberty and ability to conceive, gestate and deliver a calf [11]. Decrease in AFC decreases the cost of raising the animals to productive life, increases the annual genetic gain by decreasing the generation interval [12] and raises the average productive life of the animal. In addition, reduced age at first calving increases the number of calves born in the herd.

Longevity: Longevity of dairy cows plays a vital role in international breeding programs and has a high weight in total merit indexes in several countries [13]. It is an economically important trait for farmers and has gained in importance as a global indicator for animal welfare [14, 15]. Longevity is defined as survival at successive time periods. It is genetically often defined as the same trait over the complete life of a cow [16].

Calving Rate: Calving rate is another measure of reproductive performance that has received attention by researchers. While from a genetic point of view, calving rate as defined superior to calving date, from a production perspective, calving rate and calving success have some of the same deficiencies as calving interval. Another potential trait for selection is pregnancy rate, as it has been shown that pregnancy rate measured in the first parity is the same trait as lifetime pregnancy rate. Morris *et al.* [17] estimated genetic parameters for age at first estrus, calving date and pregnancy rates using experimental data. Heritability's for standardized age at first estrus and calving date were 0.27 and 0.09, respectively. Genetic correlations of standardized age at first estrus with calving date and pregnancy rate were 0.57 and -0.36, respectively. Researchers have also attempted to identify physiological parameters, such as endocrine factors, that are related to fertility and are heritable. Mialon *et al.* [17] found a favorable genetic correlation between age at puberty and postpartum intervals in experimental data.

Genomics into Genetic Evaluations: Including genomic data in existing genetic evaluation is becoming routine in many species and countries, especially in dairy cattle where genomic selection is revolutionizing breeding programs and genetic progress. Benefits from genomic selection have also been demonstrated in beef breeding [18, 19]. 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 cooperative research center (CRC) results and several others have published significant single nucleotide polymorphism (SNP) associated with female reproduction traits [20]. Gene expression studies and gene pathway analyses [21] have also been used to identified 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. The clustering of SNP for male reproduction traits, in particular on the X chromosome, may require special consideration in future genetic evaluation [22].

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 [23]. 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 heritability's. 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) [23].

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. Finally, education of industry and individual breeders on genotyping and ongoing phenotype 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 [24].

Genetic Evaluations Models: A key change in approaches to genetic evaluations occurred in the 1970s. Selection index methods popularized by Hazel were generally replaced by the mixed model methodology advanced by Henderson. An advantage of the new approach was that for a given model, the results have best linear unbiased prediction (BLUP) properties. Although mixed models are ideal for normally distributed data, alternative models have been developed for traits that are not normally distributed, such as generalized linear models, threshold, or survival models. Additionally, applications of Bayes' theorem have permitted advances in modeling and especially (co)variance component estimations. Beginning in 1974, the modified contemporary comparison (MCC) was used for evaluation of yield by USDA's Animal Improvement Programs Laboratory (AIPL) [23, 24]. This procedure incorporated many improvements over the previously used herd mate comparison. The major advantages were: consideration of the merit of herd mates, inclusion of genetic groups based on pedigree index and improved weighting of information. The MCC was shown to produce bull evaluations essentially identical to those derived using a linear model with BLUP properties when both models included the same fixed and random effects. The MCC was a sire model and was replaced in 1989 with an animal model (AM). Canada also adopted AM in 1989 and by the 1992 report from Inter bull on national evaluation systems, AM was the standard method. A key technique used in AM computing is "iteration on the data". The advantages of the AM were that it considered all relatives, no matter how distant and all animals of a breed were evaluated simultaneously, male and female [24].

The test-day model (TDM) is also an animal model but focuses on each test-day observation rather than on lactation data. The TDM, first introduced in Australia in 1984, models each test-day observation instead of the lactation record, or pre-adjusts lactation records for the test-day effect. A TDM allows for a more exact specification and consideration of the environment (a day vs. lactation). Often, TDM include consideration of persistency of lactation and rate of maturity. All effective evaluation procedures include fixed or random effects to account for management situations (environment). The more similar the situation within a management group, the better the removal of environmental effects. However, with the MCC and AM, an effort was made to balance between specificity of the environment and the accuracy of estimating the effect of that situation (number of cows). Although test-day data have been collected in the United States since 1905 for management and have contributed to national genetic evaluations since 1936, the TDM was patented in the United States in 1993, later in Canada and a patent was applied for in Europe. This has forestalled its use in the United States except for regional and unofficial evaluations by the patent holder (*Ibid*) [24, 25].

The BLUP procedure has been the method of choice for the genetic evaluation of animals in the last few decades in conventional breeding programs. In 1949, the procedure of genetic evaluation based on the mixed model methodology was introduced by Henderson. Along with the genetic evaluation of purebred animals, genetic merit is considered also for crossbreeds, due to their importance in achievement of economic benefits and their large number in commercial herds. The reliability of comparisons of breeding values and consequently selection decisions across contemporary groups (CG) are influenced by the degree of connectedness between those groups [7]. If the amount of genetic links between CGs in the genetic evaluation is insufficient, comparisons of breeding values between animals from different CGs may be biased. Such a problem was noticed in the species, in which the level of artificial insemination (AI) is low, such as beef cattle [25], sheep [26] as well as some pig breeding programs [27].

Bio-Track: The bio-Track rummage-sale as a whole-farm management system includes functions for animal identification and recording each animal's breeding, genetic evaluation, health, performance, carcass data, economic breeding value and other details useful for herd management. It can also keep track of marketing, transport for traceability records and share appropriate information with in a value chain. There are desktop software programs and apps that take care of one or more of these record-keeping chores but they may not connect with technology you already use to push or pull information from other sources, analyses the data, run comparisons and format reports, or automatically update and back up your data. The full bio-Track program and optional Go360 offer all that and, when the required data is available, produces within-breed and across-breed genetic evaluations for each animal based on its genetic and economic merit to predict the profitability of its progeny [27].

CONCLUSION

Reproduction is a diverse trait and hence, there are many different measures of reproductive performance. 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 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. While several measures of reproductive performance are currently being incorporated into national genetic evaluation, further refinement is still needed. Given the nature of reproductive records, it is unlikely that one individual measure will be able to completely predict reproductive performance. Most likely several measures will need to be used together. The main limitations to genetic evaluation of fertility in the past and currently, are the lack of records available from field data. The adoption of whole-herd reporting schemes by herds will help to alleviate this problem.

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