

INFLUENCE OF GENOMIC TECHNOLOGIES ON GENETIC SELECTION IN NELORE CATTLE AND COMMERCIAL BEEF PRODUCTION

Jason B. Osterstock, DVM, PhD

Zoetis

Kalamazoo, MI, USA

Genomic technologies are rapidly emerging as a standard component of genetic evaluation in beef and dairy breeds globally. The ability to leverage genomic data to gain accurate insight into the genetic potential of cattle, particularly in young animals, helps mitigate risks associated with genetic selection decisions. Classically, this is expressed as the impact of increased accuracy of breeding values on genetic progress. From a practical perspective, it is avoiding selection mistakes and doing a better job of identifying those animals that truly express superior genetic merit.

The history of genetic testing, while relatively short, is quite dramatic. Early applications focused on relatively few traits and relied upon a small number of markers. The preferred application of genomic data today is as a component of genetic evaluation as a complement to existing pedigree, performance, and progeny data. Many of the major breeds support the use of genomic data within their genetic evaluation programs as a means to improving the accuracy of genetic predictions for traits of merit. In these evaluations, genomic data from tens of thousands of DNA markers are used to describe genomic similarity of tested animals and derive estimates of genetic merit for a host of traits.

There are several different statistical methodologies available for the integration of genomic data within genetic evaluation. The most broadly applied methodology in terms of numbers of tested animals is the use of the selection index method as routinely employed for the Council on Dairy Cattle Breeding US dairy genetic evaluation.¹ This method combines results from traditional genetic evaluation with molecular breeding values weighted based on the relative accuracy of the DNA-based prediction. A similar approach to combining classical and genomic data is to include the molecular breeding value as a correlated trait in a multi-trait model.² This method has been most commonly applied in beef cattle evaluations including the evaluation supported by Associação Nacional dos Criadores e Pesquisadores (ANCP) for Nelore cattle. The final method is the use of single-step methodology whereby genomic data is used to construct a genomic relationship matrix that informs the genetic evaluation.³ This method is being applied more routinely and is anticipated to improve the efficiency of genomic evaluation. However, regardless of the method employed, the effects of genomic data on accuracy of resulting breeding values are very similar.

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Much like the statistical methods employed to integrate genomic data into genetic evaluation, there are many options for the underlying genotyping platform. There have been two major transitions over the last 10 to 15 years. The first was the move away from assays with few markers, primarily targeting few quantitative trait loci (QTL) or candidate genes, to more dense arrays with thousands of markers that provide a more comprehensive, genome-wide evaluation. This transition was required because it became evident early on that the polygenic nature of most traits required that more genetic markers be considered. For example, Costa et al. identified 42 markers that were significantly associated with reproductive traits in Nelore cattle.⁴ Of those identified, the marker with the largest effect described less than 1.5% of the phenotypic variance in heifer rebreeding and age at first calving. Therefore, when considering the number of significant markers that need to be evaluated to describe a meaningful amount of phenotypic variation, and the number of traits that would need to be evaluated, it is clear that information must be derived from a large number of genetic markers to provide useful information.

A challenge associated with the need for more genetic markers is price. A second major advancement that has helped to overcome this challenge is the use of lower density genotypes that can be imputed to derive higher density genotypes that are more informative. This process relies upon a reference set of higher density genotypes, preferably derived from animals with many progeny in the target population. Lower density genotypes are then compared against the reference set to identify common patterns that can be used to predict the remaining genetic markers. The process of imputation is extremely accurate, generally achieving greater than 95% accuracy of imputed genotypes in Nelore cattle.⁵ Importantly, imputation accuracy does not increase significantly with the addition of more markers above approximately 15,000. The result is a system that is quite robust and insensitive to genotyping platform provided a suitable number of genetic markers have been evaluated.

The impact of genomic data on genetic evaluation in Nelore cattle can be examined using data available from the ANCP genetic evaluation. The addition of genomic data, in the form of molecular breeding values, to existing pedigree and performance records results in an increase in the accuracy of the resulting genomically enhanced expected progeny difference. Data from the ANCP evaluation is reported in Table 1. Accuracy gains range from approximately 10 to 20 percentage points across the traits evaluated. As a means of helping to understand what that increase in accuracy really means, one can estimate the number of progeny required to achieve a given level of accuracy based on the heritability of the trait. For many of the traits evaluated, the number of progeny required to achieve a similar level of accuracy is equivalent to one or more calf crops from a natural service sire, and many more progeny than most females would produce in their lifetime. Therein lies the benefit of genomic technologies as a complement to traditional genetic evaluation. Genomic data provides an additional source of information that provides insight into the true genetic merit of selection candidates to help inform selection and breeding decisions.

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Table 1: Heritabilities (h^2), accuracy of traditional EPD, accuracy of genomic EPD, and associated progeny equivalents based on integration of CLARIFIDE Nelore results in the ANCP genetic evaluation.⁶ (IPP – Age at first calving; PG – gestation length; STAY – stayability; PAC – accumulated production; MP120/210 – maternal component of weight at 120/210 days; P120/210/365/450 – direct weight at 120/210/365/450 days; ALT – height)

Trait	h^2	Traditional Accuracy	Genomic Accuracy	Progeny Equivalents
IPP	0,11	0,24	0,38	28
PG	0,38	0,28	0,41	9
STAY	0,12	0,22	0,37	26
PAC	0,20	0,22	0,35	18
MP120	0,11	0,27	0,48	59
MP210	0,11	0,26	0,47	56
P120	0,23	0,37	0,48	20
P210	0,25	0,37	0,52	28
P365	0,32	0,42	0,57	28
P450	0,34	0,42	0,59	32
ALT	0,25	0,16	0,28	7

At this point, one might logically conclude that if we have a wide array of genotyping platforms that are suitable for genomic evaluation and well established methods for genomic evaluation, the Nelore breeder should be well poised to leverage the technology today. In some instances that may be true, but it is not quite that simple. It is true that all of the necessary tools are available. The complexity becomes linked to one of the nuances of genomic evaluation, that the predictions and accuracy thereof are relevant to the population from which the reference set was derived. To a significant degree, the associations between genetic markers and traits of interest are driven by the ability of the genetic markers to characterize relatedness, not the location of those markers in the genome relative to causal mutations.

To that end, it becomes apparent that a single set of genomic prediction equations cannot be applied to all Nelore cattle, especially when one considers the number of EPD programs available to breeders. This necessary degree of specificity is underscored when considering evidence that genomically distinct sub-populations exist within the breed.⁷ This can be attributed to differences in selection strategies and patterns of segregation within and among sub-populations. The net effect is manifest in the accuracy of the resulting molecular breeding values – higher than expected in close relatives and lower than expected in other sub-populations. Thus, there may be need for optimized genomic evaluations specific to the respective EPD programs.

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This becomes particularly important when considering the potential applications of genomic technologies for non-registered, commercial progeny. Outside of seedstock production, the technology works in the same fashion, but cannot complement genetic evaluation since the vast majority of commercial cattle lack the necessary pedigree and performance records to inform traditional evaluation. Nonetheless, genomic predictions can provide valuable guidance for selection and breeding in these herds that would otherwise have very little other than phenotype to rely upon for selection and mating decisions. It follows that, given the importance of connectedness on the accuracy of genomic prediction, commercial producers should prioritize use of genomic applications derived from the same information used to inform the bulls / semen they purchase.

Of note is that the power of genomic technologies, just like any other statistical endeavor, is driven to a large degree by population size. This applies principally to the number of genotyped animals in the reference population used to derive the genomic prediction equations. However, it also applies to the phenotypes that go into genetic evaluation. In commercial application of genomic technologies, both of these are driven to a large extent by the producers themselves. The current calibration used by the American Angus Association and Angus Genetics, Inc. is based on data from nearly 50,000 genotyped animals, of which commercial genotypes outnumber research genotypes 10:1.⁸

Genomic predictions available through Zoetis and ANCP have been well validated in commercial conditions. In a trial conducted in 2015,⁹ the top third of heifers ranked based on genomic predictions for a maternal selection index and heifer pregnancy rate had a fixed-time artificial insemination conception rate 15 percentage points higher than those in the bottom third. Recognizing the relatively low heritability of reproductive traits, the observed phenotypic differences are quite large. Similar results have been obtained in other herds. Zoetis has also partnered with ANCP and Agro Maripa in a 5 year study contrasting genomic selection with traditional, phenotypic selection in commercial Nelore heifers. The results of this work will help to document the long-term benefits of genomic selection in commercial herds.

The emergence of genomic technologies have not altered how genetic improvement is achieved. There are effectively only three selection decisions that any producer can make. The first is choosing which animals will be retained / enter the herd. This applies to both replacement females and herd sires. The second selection decision is defining how to assign matings to address individual weaknesses and complement existing strengths. The final selection decision is how many progeny each animal will produce. Elite animals are assigned to produce many progeny, as may be the case with AI sires and donor females.

To execute any of these selection decisions, the breeder needs to be able to rank animals from best to worst based on their selection criteria. In seedstock production, this requires balancing of

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many different traits, whereas in commercial production this can often be simplified through use of selection indexes. Regardless of the application, this process requires a genetic prediction for economically relevant traits with sufficient accuracy to make the right selection decisions – and avoid mistakes. Genomic technologies, by virtue of their contribution to accuracy, help to ensure that animals are ranked more dependably relative to their true differences in genetic merit.

For Nelore breeders, both seedstock and commercial, there are well validated genomic technologies available today. There is no longer a question regarding the effectiveness of genomic data in predicting economically relevant traits. Furthermore, the differences in statistical methodologies used for genomic evaluation or the underlying genotyping platforms are largely academic with limited impact on the producer. To that end, there is no clear incentive to wait and very little to decide regarding implementation. The technology is being used extensively in other beef and dairy populations worldwide to great effect. The Nelore breed is well poised to follow suit.

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