## Genomic Selection in Nelore Cattle in Brazil

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**ABSTRACT**: Despite a favorable business model, genomic selection is still not a popular tool for genetic improvement of Nelore cattle in Brazil mainly due to the lack of a cost-effective strategy for its application. Different independent Nelore breeding programs have already developed prediction equations for usual and difficult/expensive to measure traits. Unfortunately, some programs are using genomic predictions more as a marketing than a selection tool. Different breeding schemes were compared aiming to envisage opportunities to better apply genomic selection in Nelore cattle. Breeding schemes combining genomic selection and reproductive technologies provided the best results in terms of genetic gain. Benefit of using genomic selection in the Nelore breed is also expected to occur in commercial herds, allowing them to buy young replacement bulls with more reliable proofs for a comprehensive number of economically relevant traits.

**Keywords:** beef production; *Bos indicus*; breeding scheme; genetic gain; genomic prediction

### Introduction

The objective of this paper was to present the current status of genomic selection in Nelore cattle in Brazil. As most of the studies treating this subject are under development, the paper was written focusing on the perspectives and opportunities of applying genomic selection in Nelore cattle, rather than providing a comprehensive review of the already published results, although a section was dedicated to partially explore that. Despite being a breed predominantly raised in a specific country, Nelore has a global impact in the beef market. Some numbers are presented in the next section to reinforce this argument. To better understand the current applications and the business models for genomic selection in Nelore cattle in Brazil, one needs to know the history behind the evolvement of the different Nelore breeding programs existing in the country. One section was dedicated to briefly summarize this topic. Results from research on genomic selection in Nelore cattle are presented and particular aspects relative to its application are discussed. As will become evident throughout the text, genomic selection in Nelore cattle in Brazil is still in an early stage. Nevertheless, good perspectives and opportunities for its application are foreseen, especially if combined with reproductive technologies, exploring new relevant traits and disseminating genetic gain to commercial herds. Arguments to sustain these perspectives are provided in the section "foreseen opportunities". The paper ends with some concluding remarks, including Brazilian beef production target.

### Brazilian Beef Business and the Importance of Nelore Breed

Brazil is one of the largest beef producers and exporters in the word. In 2012, the country was responsible for 16% of the world beef production and 19% of global exports (USDA 2013). The amount of beef exports in 2013 alone, which represented less than 20% (in volume) of the national production, generated US$ 6.6 billion revenue to Brazil (ABIEC 2014). Projections indicate that Brazil will have a continuing importance as a beef supplier to meet the increasing world demand (FAO 2013; FIESP 2013).

The Brazilian beef cattle industry is predominantly based on Zebu animals raised on pasture. According to the Brazilian Association of Zebu Breeders (ABCZ), between 75 and 80% of the Brazilian herd, around 200 million heads currently, has *Bos indicus* contribution, and the beef breed with the largest number of animals is Nelore, comprising around 80% of the beef herd (Josahkian 2000). All these estimates suggest that for every 10 pounds of beef produced in the world one comes from Nelore animals raised in Brazilian lands, highlighting that the breed has a huge impact not just locally but also in the global beef market.

### Nelore Breeding Programs

Although the vast majority of the Brazilian herd has *Bos indicus* contribution, only less than 7,000 purebred Zebu animals were imported from India from 1868 to 1962, when the importation was banned. The Brazilian *Bos indicus* herd, including Nelore - originally Ongole in India, was mainly formed by mating the imported *Bos indicus* bulls (or their descendants) with *Bos taurus* cows, brought to America by Portuguese and Spanish colonizers (Santiago 1987; cited by Ferraz and Felício 2010).

Official initiatives to objectively select the animals started in the 1950's, but it was not until the 1980's that well organized breeding programs started to be established in Brazil (Ferraz and Fries 2004). The history behind the evolvement of the Nelore breeding programs in Brazil is peculiar and sometimes difficult to understand. Independent groups of farmers, and also ABCZ, started (almost concomitantly) different Nelore breeding programs to meet their interests and needs. In partnership with universities, research institutes and private companies, these groups implemented independent genetic evaluations and started using breeding value estimates to select the animals and to adopt oriented mating systems in their herds. The groups became strong and today there are around 10 different Nelore breeding programs running in parallel in Brazil, with the number of controlled calves per program varying approximately from 20 thousand to more than 100 thousand per year. Jointly, they control roughly 500 thousand Nelore cows per year, and this number is rising each year.

The lack of a unique national genetic evaluation can be seen as a disadvantage but, on the other hand, the existence of different Nelore breeding programs generates competitiveness and helps to maintain genetic variability, which ultimately benefits the Brazilian beef industry. The existence of different breeding programs also spreads the training of the students across the Universities. An interesting feature of the Nelore breeding programs is that there are genetic links between them due to the use of common AI (artificial insemination) top sires, irrespective of the origin of the sire, i.e. although the programs compete they also (involuntarily) cooperate with each other. Another remarkable aspect is that, with the exception of few governmental policies and some public funds to invest in research, the breeding programs are in general funded by the farmers.

An unprecedented governmental policy was made in 1989, when the Brazilian Ministry of Agriculture (MAPA) instituted a decree allowing credited commercial breeding programs to emit a certificate of genetic superiority (called CEIP) for their top yearling animals. Currently, nine Nelore breeding programs are accredited by MAPA to issue CEIP. Each one has its own selection index and is allowed to issue CEIP just for the top 20% yearling animals based on that index. Certified animals have the same fiscal benefits as breeder association registered animals, irrespective of being registered by the association or not. The advent of CEIP has stimulated breeders to increase selection intensity and changed dramatically the market of genetics in the country. For instance, nowadays the top sires dominate the semen market, which used to be led by "show bulls".

**Genomic Selection Research in Nelore**

As happened in other countries, studies exploring genotypic information started in Brazil with a notable participation of multi-national private companies, focusing mostly in the identification of "informative" markers, aiming to offer genetic tests to be used in marker assisted selection (MAS). With the advent of dense marker panels, the "informativeness" of the markers started to be estimated by genome-wide association (GWA) studies. Results of MAS and GWA studies will not be presented here as they are outside the scope of the present paper.

Different groups are doing research on genomic selection for the Nelore breed in Brazil. The main interest is to determine whether genomic selection can accelerate genetic improvement and contribute to produce better beef in a more efficient manner. Some attempts were made to encourage the different Nelore breeding programs and research groups to join forces to develop prediction equations together but just part of them agreed. It seems that each Nelore breeding program (or groups which decided to join forces) is going to have its own prediction equations. Further details about that will be provided in the next section. The different research groups are usually characterized by a multi-institutional and multi-national cooperation.

Besides monetary constraint, a difficulty faced by all the research groups was the absence of a centralized DNA repository of the Nelore breed. For instance, from an original list of more than four thousand bulls with highly accurate proofs in the Aliance Nelore database, the Zebu Genome Consortium (Garcia *et al.* 2012) was only able to find biological samples from approximately one thousand of them. As a consequence, the different research groups needed to also genotype animals with less reliable proofs to increase the size of their reference populations.

Studies investigating the pattern of linkage disequilibrium (LD) in the Nelore breed revealed that it presents lower levels of LD at short distances than taurine breeds (Espigolan *et al.* 2013; Pérez O'Brien *et al.* 2014). The average LD between adjacent markers obtained with the Illumina® Bovine HD (HD) panel (~777K SNPs) in Nelore cattle (~0.29) is similar to the values obtained in Holstein animals (Hayes *et al.* 2009) with the Illumina® Bovine SNP50 panel (~54K SNPs). According to Meuwissen *et al.* (2001) and Calus *et al.* (2008), this level of LD is sufficient to produce accurate genomic predictions, provided enough phenotypic information is used to estimate marker effects. Brito *et al.* (2011) evaluated the accuracy of genomic predictions in simulated populations that mimicked the extent and pattern of LD reported in real beef cattle populations, and predicted that a large reference population would be needed for successfully implementing genomic selection in beef cattle.

Neves *et al.* (2014) assessed the quality of genomic predictions in Nelore cattle, for 13 growth, carcass composition and reproduction traits, by using a set of 685 bulls, from different Nelore breeding programs, with high accuracy proofs and genotyped with the HD panel. Different validation strategies and prediction methods were adopted. Accuracies of genomic predictions ranged from 0.17 (navel at weaning) to 0.74 (finishing precocity). Across traits, the average empirical accuracy was 0.44 for the method presenting the highest accuracies (BayesC). Accuracies for two selection indices including either weaning traits or both weaning and yearling traits were 0.39 and 0.55, respectively, being equivalent to the accuracies of regular proofs (indexes based on EBVs) presented by calves and yearling animals with own performance. Despite the small number of genotyped animals, the study demonstrated the technical feasibility of applying genomic selection in Nelore cattle.

Results of a principal component analysis based on the genomic relationship matrix of bulls from different Nelore breeding programs evidenced the existence of two subgroups of the sampled population (Utsunomiya *et al.* 2013). Further inspection revealed that the clustering of the two subgroups was coincident with selection emphasis of the different breeding programs: one with bulls belonging to breeding programs that emphasize selection for weaning and yearling weight, and the other with bulls belonging to breeding programs that emphasize selection for carcass conformation, finishing precocity and fertility traits. Using one of these two subgroups as the reference set and the other as the validation set to obtain genomic predictions resulted in very poor predictive ability, suggesting that if developed independently the prediction equation for one

group would not be so useful for the other and vice versa (H. Neves, personal communication).

Further research is also being done in genomic selection applied to relevant traits that are difficult and/or expensive to measure. Preliminary studies, including HD genotypes from approximately 830 Nelore animals, found empirical accuracies of genomic predictions around 0.30 for traits like carcass weight, marbling and tenderness, indicating that genomic selection is a feasible alternative for improving these traits in Nelore cattle, as they are hard to improve by conventional selection (Fernandes Junior *et al.* 2013; Magalhães *et al.* 2013). An area of relevance for developing research is to investigate how to properly incorporate these "novel" traits in the selection indexes.

It is not clear yet if the HD panel should be considered as the target panel for genomic selection in the Nelore breed, or if a lower density panel would provide similar predictive ability. The results from imputation analyses carried out by Carvalheiro *et al.* (2014) indicated that if the HD is considered as the target panel for applying genomic selection in the Nelore breed, its cost effectiveness can be improved with the strategy of genotyping part of the animals with a panel containing around 15K useful SNPs and imputing their HD missing genotypes. As imputation accuracy from 15K to HD was very high (~0.98), this strategy is expected to provide similar reliabilities of genomic predictions than the more expensive strategy of genotyping the animals using only the HD panel.

Due to the low margins of beef cattle operations, it will not be reasonable to genotype all selection candidates, even with lower density panels, so different strategies need to be investigated to decide which animals will be genotyped (selective genotyping), aiming to enhance cost-effectiveness of genomic selection. Using simulated beef cattle populations, Neves (2013) evaluated the long-term consequences of different selective genotyping strategies to update the reference population for genomic prediction. Conversely to results from other studies (Boligon *et al.* 2012; Jiménez-Montero *et al.* 2012), there was no evidence that would, in the long-term, discourage using the strategy of updating the reference population by genotyping only superior animals, based on their regular proofs (EBVs). According to the author, the single-step approach (Misztal *et al.* 2009) is more appealing for genomic prediction under selective genotyping, because it provided more accurate and less deflated predictions than a multiple-step approach using EBVs to estimate marker effects. The single-step approach also presented advantage over multi-step prediction in terms of inbreeding incidence and accumulated genetic gain (Neves 2013).

### Genomic Selection Applications in Nelore

Applications of genomic selection in Nelore cattle in Brazil are currently following two distinct business models, represented in Figure 1. In one of them (Figure 1A), the prediction equations are treated as an intellectual property of the multinational private company that invested in their development. In this model the breeders or the breeding programs do not have access to the genotypes, and the proofs enhanced by genotypic information are derived, for example, by combining "molecular predictions" (MP), calculated based on the prediction equations, and regular proofs as correlated traits in a multiple-trait mixed animal model analyses (Garrick 2011). In this business model the breeding programs become dependent on the company that sells the MP. Its sustainability relies on the interest of the commercial company to constantly invest in recalibrating the prediction equations. Another more flexible business model is also being applied (Figure 1B), in which the breeding programs and the breeders have full access to the genotypes. This is a very attractive model because no dependencies exist between any two segments. It allows the breeding programs to change their service providers without any prejudice if they are not satisfied, for example, with the genotyping cost or with the quality of the genetic evaluations. It also allows breeders to move to another
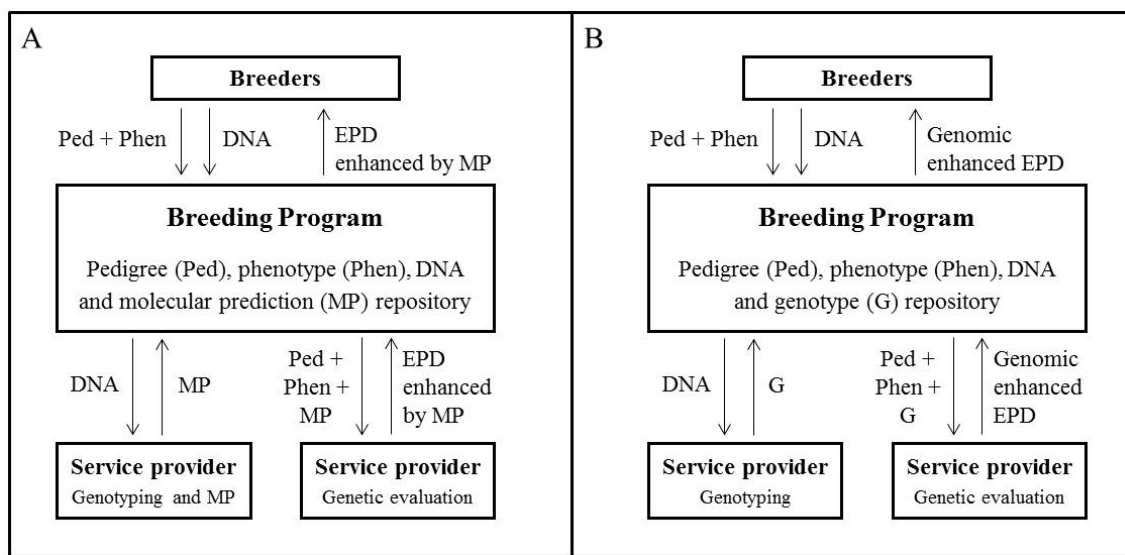


**Figure 1. Business model for genomic selection application with (A) or without (B) dependence of the service provider.**

breeding program without loosing information. In addition to being less vulnerable, this model promotes competition between service providers, what ultimately benefits the Brazilian beef industry.

Despite the existence of a favorable business model, unfortunately some Nelore breeding programs are using genomic predictions more as a marketing than a selection tool. For instance, some breeders are only genotyping few pre-selected young bulls aiming to add value in their auction prices. This is mainly happening due to the lack of a cost-effective strategy for a more correct use of genomic selection. In general, the quality of the current prediction equations also needs to be improved, and economic indexes including the "novel" traits need to be developed. Some breeding programs that already have good prediction equations are having difficulty to use genomic selection more effectively due to genotyping costs. Aiming to increase return on the investments, some breeders started using genomic predictions to identify superior donor cows and intensify their use by embryo production through *in-vitro* fertilization (IVF). As presented in the next section, this seems an appealing strategy in terms of possibility to improve the genetic gain.

## Foreseen Opportunities

Opportunities for applying genomic selection in dairy cattle were well envisioned even before commercial dense marker panels were available. With an expected drastic reduction in the cost of identifying superior bulls and an estimated substantial increase in genetic gain, the genomic selection was correctly predicted to become popular in dairy cattle breeding programs (Schaeffer, 2006).

As previously mentioned, cost-effective strategies for applying genomic selection in beef cattle are still not well established. Seeking to identify opportunities, comparisons of the expected genetic gains from different beef cattle breeding schemes were carried out and are presented in Table 1. Serving as a base for comparison, the current breeding scheme (S1) adopted by a regular farm participating in a Nelore breeding program is characterized by having half of its calves being born from AI proven bulls and the other half from natural mating (NM) sires. The genetic change per year in S1 was estimated assuming that CEIP sires (top 20%) were used under NM, with ages varying from 2 to 6 years old (replacement rate of 20%/year) and an average accuracy of selection equal to 0.50. Higher values for selection intensity, accuracy and generation interval were assumed for AI sires. From the female side, common practices are to discard non-pregnant cows, besides those presenting poor genetic evaluation (e.g. bottom 10%), and to incorporate around 60% of the top heifers per year in the cow herd. These assumptions resulted in an annual genetic gain of 0.134 genetic standard deviation in S1, which is in agreement with the trend estimated with real data by Boligon *et al.* (2013).

Another scheme that is becoming very popular in Brazil (S2 in Table 1) is to almost eliminate the use of sires under NM by using fixed time AI (FTAI). In fact, some farms already eliminated NM by adopting hormone protocols to resynchronize the cows ("multiple" FTAI). It was assumed in S2 that 80% of the calves have an AI sire. As shown in Table 1, the expected benefit of S2 compared to S1 is an increase of 22% in the annual genetic gain. An interesting consequence of the popularization of FTAI is that it reduces the use paternity tests as a by-product of genomic selection. Parentage testing is important in schemes like S1 as the calves born by NM are usually from multiple-sire mating.

**Table 1. Genetic gains (ΔG) from different beef cattle breeding schemes, varying in at least one of the following parameters: selection intensity (i), accuracy of selection ($r_{TI}$), generation interval (L) and percentage of progeny (% progeny) being born by artificial insemination (AI) or natural mating (NM) sire, NM dam or donor.**

| Scheme | Type of parent | Selection % | i | $r_{TI}$ | L | % progeny | ΔG |
|---|---|---|---|---|---|---|---|
| **S1: Current** | AI sire | 3 | 2.27 | 0.85 | 6.5 | 50 | **0.134** |
| | NM sire | 20 | 1.40 | 0.50 | 5.0 | 50 | |
| | NM dam | 60 | 0.64 | 0.50 | 6.5 | 100 | |
| | Donor | - | - | - | - | 0 | |
| **S2: Current + FTAI** | AI sire | 3 | 2.27 | 0.85 | 6.5 | 80 | **0.163** |
| | NM sire | 10 | 1.75 | 0.50 | 4.0 | 20 | |
| | NM dam | 60 | 0.64 | 0.50 | 6.5 | 100 | |
| | Donor | - | - | - | - | 0 | |
| **S3: FTAI + Genomics** | AI sire | 3 | 2.27 | 0.85 | 6.5 | 80 | **0.172** |
| | NM sire | 10 | 1.75 | 0.80 | 4.0 | 20 | |
| | NM dam | 60 | 0.64 | 0.50 | 6.5 | 100 | |
| | Donor | - | - | - | - | 0 | |
| **S4: FTAI young sire + Genomics** | AI sire | 3 | 2.27 | 0.80 | 3.0 | 80 | **0.212** |
| | NM sire | 10 | 1.75 | 0.80 | 4.0 | 20 | |
| | NM dam | 60 | 0.64 | 0.50 | 6.5 | 100 | |
| | Donor | - | - | - | - | 0 | |
| **S5: FTAI young sire + IVF + Genomics** | AI sire | 3 | 2.27 | 0.80 | 3.0 | 80 | **0.240** |
| | NM sire | 10 | 1.75 | 0.80 | 4.0 | 20 | |
| | NM dam | 55 | 0.72 | 0.50 | 6.0 | 95 | |
| | Donor | 2 | 2.42 | 0.80 | 3.0 | 5 | |

The first scheme applying genomic selection considered was S3. Compared to S2, no change in the breeding scheme occurred except for the increase in accuracy of selecting genotyped young sires for NM. The estimated genetic gain in S3 revealed that no important change is expected for regular traits if genomic selection is applied without "redesigning" the breeding scheme.

A more pronounced difference was observed when only genotyped young sires were used in FTAI (S4 in Table 1). An increase of 30% and 23% in genetic gain was observed when S4 was contrasted with S2 and S3, respectively. The adoption of S4 implies abandoning progeny testing, which would represent a remarkable change for some beef cattle breeders accustomed to mostly use "consecrated" AI bulls.

The last investigated scheme (S5) explores the use of IVF, with embryos being produced by genotyped donors, which would be responsible for 5% of the calves being born. Compared to S1, S2 and S4, this scheme resulted in genetic gain increases of 79%, 47% and 13%, respectively. It is important to mention that the production of embryos through IVF is becoming very accessible in Brazil, costing about US$150 per calf born.

Although refinements to better compare these breeding schemes are needed, considering for example their cost-effectiveness, the estimated genetic gains highlighted two important aspects regarding the application of genomic selection in beef cattle breeding programs. Firstly, that genomic selection in beef cattle is expected to generate a more modest increase in genetic gain for regular traits compared to dairy cattle. Secondly, that it is possible to obtain more pronounced genetic gains if genomic selection is applied in combination with reproductive technologies, as postulated by Garcia *et al.* (2013).

An important benefit of using genomic selection in the Nelore breed is expected to occur in commercial herds, i.e. those herds not participating in breeding programs. Considering that they have roughly 35 million Nelore cows to be used under NM, they need around 280,000 young replacement bulls per year (assuming one bull per 25 cows and an annual replacement rate of 20%). Nowadays, most of the bulls mated with commercial cows have no genetic proofs, and those that have (e.g. CEIP bulls) are bought with relatively low accurate proofs (~0.50). Genomic selection will not just allow breeders to select and sell young bulls to commercial herds with higher accuracy, but will also serve as a tool to predict the genetic merit of the bulls in commercial herds without a traditional proof.

Opportunities for applying genomic selection are also envisaged for economically relevant traits that are difficult and/or expensive to measure. For instance, the possibility of directly selecting for meat quality, feed efficiency and gas emission related traits provides the opportunity to produce better beef in a more sustainable manner. However, it is still not clear who is going to pay the development and the maintenance of good prediction equation for these traits, since the breeders are not stimulated to select for them because slaughter houses payment system in Brazil is mainly based on carcass weight. The pressure of the society to increase the sustainability of beef production and the establishment of governmental policies to foster low carbon livestock agriculture practices will probably change this scenario.

## Concluding Remarks

The Brazilian government has set a target of increasing beef production by 40% and reducing the occupied area with pasture by 29% in the next 10 years, which would result in a production by 2023 of 13.6 million tons of carcass weight equivalent, on 114 million hectares (MAPA 2014). Genetic improvement of Nelore cattle will certainly have an important role to reach this target and genomic selection can serve as a tool to enhance and disseminate the genetic gain of Nelore breeding programs, consequently increasing the efficiency of beef production in Brazil.

The current available prediction equations for Nelore cattle, which will be constantly refined, already allow increasing the genetic gain for a comprehensive number of relevant traits. Currently, the lack of a cost-effective strategy for applying genomic selection is the main drawback for its widespread use. Genotyping strategies need to be defined to better identify the proper densities of marker panels to be used for each category of animal and in which proportion they should be genotyped. Combined with imputation methods, proper genotyping strategies have the potential to drastically reduce the genotyping cost and make investments in genomic selection feasible.

The popularization of genomic selection in Nelore cattle also relies on designing new breeding schemes, intensifying the use of genetically superior young animals through the synergistic adoption of genomic selection and reproductive technologies. As profit margins in beef production are low, the right dose of each technology to be applied in the different Nelore breeding programs will define their competitiveness and success.

## Acknowledgments

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