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BEEF CATTLE GENOMIC SELECTION IN TROPICAL ENVIRONMENTS

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SUMMARY

Compared to dairy cattle, beef cattle genomic selection is in an early stage. Nevertheless, good perspectives and opportunities for its application are foreseen or are already underway. Genomic selection is expected to benefit beef production by allowing identifying genetic superior animals earlier and more accurately as well as to select for traits that are difficult and expensive to measure such as meat quality and feed efficiency, among other applications. We started this paper discussing the importance of beef cattle production in the tropics, than we presented some results from genomic studies and applications of genomic selection in the tropics, using the Nellore breed (*Bos indicus*) as a case study.

BEEF CATTLE PRODUCTION IN THE TROPICS

Tropical regions correspond to the Earth territories situated between the Tropic of Cancer (northern hemisphere) and the Tropic of Capricorn (southern hemisphere), covering countries from Central (25 countries) and South America (10 countries), Africa (47 countries), Asia (15 countries) and Oceania (17 countries), with over 4779 million ha in extent of land, in which, around 40% correspond to forest ecosystems (Chidumayo and Gumbo 2013). These regions are important for the world food production and security (Foley *et al.* 2011) and cattle are a vital source of animal protein (Porto-Neto *et al.* 2014). According to FAO (Food and Agriculture Organization of the United Nations), there are in the world around 1.47 billion head of cattle and about 65 percent are located in tropical areas. The two countries with the largest number of cattle in the world, India (302 million head) and Brazil (219 million head), are situated in the tropics. The number of cattle is also expressive in other tropical regions such as Africa (312 million head), Central America (47 million head) and Oceania (40 million head). Data from the United States Department of Agriculture (USDA) shows that, in 2016, from a total of 60,486 and 9,439 (1,000 Metric tons) carcass weight equivalent worldwide produced and exported, respectively, 17,489 and 5,340 (~29% and ~57%) were produced and exported by Brazil (9,284 and 1,850), India (4,250 and 1,850), Australia (2,075 and 1,385), and Mexico (1,880 and 255).

The tropics are characterized by warm temperatures throughout the year, usually above 18 °C and seasons are commonly divided in wet and dry. As the beef cattle production in these areas is based on grass-fed, it is common to observe animals gaining body weight during the rainy season and losing or keeping it during the dry season, which usually leads to slaughter of old animals (Millen *et al.* 2011), affecting meat quality. In addition, the natural infestations of ecto and endo- parasites and the high temperature and humidity are challenges that the farmers in the tropics have to deal with (Porto-Neto *et al.* 2014). Because of this, adaptation to tropical environmental conditions is an essential trait to cattle reared in these areas. As a general rule, tropically adapted breeds (Zebu cattle) are more efficient than non-adapted (Taurine cattle) in such tropical environment conditions (Porto-Neto *et al.* 2014), explaining the prevalence of Zebu breeds in the beef production systems in the tropics. In Brazil, for example, about 80% of the cattle have Zebu contribution, mainly of Nellore breed (Carvalheiro 2014).

GENOMIC STUDIES IN THE TROPICS

Genomic selection presents an opportunity for commercial breeders to increase the rates of genetic progress in beef, primarily, through increased accuracy of estimated breeding values on young animals (Johnston et al. 2012). In general, results from several studies support the feasibility of applying genomic selection in tropical regions (Table 1). One of the main advantage of genomic selection is the possibility to accurately select animals early in life, being especially useful for the selection of traits that are difficult or expensive to measure like fertility, disease resistance, methane emissions, feed conversion, and carcass and meat quality (Hayes *et al.* 2013; Carvalheiro 2014). Traditionally, evaluation of these traits in sires requires progeny tests since selection candidates cannot be directly assessed, increasing both costs and generation intervals.

Table 1. Genomic prediction accuracies in tropical beef production

Traits	Prediction accuracy	Reference
Brazilian beef cattle		
Sum of SFA	0.12 to 0.24	
Sum of MUFA	0.07 to 0.13	Chiaia *et al.* (2017)
Sum of PUFA	0.45 to 0.56	
Carcass traits	0.21 to 0.47	Fernandes Júnior *et al.* (2016a)
Feed efficiency	0.06 to 0.58	Silva *et al.* (2016)
Growth, reproductive and visual score	0.17 to 0.74	Neves *et al.* (2014)
Brazilian beef cattle		
Feed efficiency, growth, carcass and meat quality traits	0.13 to 0.48	Bolormaa *et al.* (2013)
Growth, reproductive carcass traits	0.20 to 0.45	Johnston *et al.* (2012)

SFA: saturated fatty acids; MUFA: monounsaturated fatty acids; PUFA: polyunsaturated fatty acids

Genetic markers have also been used in genome-wide association studies (GWAS) in order to identify genomic regions with major effects. Promising quantitative trait loci have already been identified. The QTL that harbors the PLAG1 gene, for example, has been associated with growth and carcass and meat quality traits in both Australian beef cattle and Brazilian Nellore cattle (Fortes *et al.* 2013; Utsunomiya *et al.* 2013; Porto-Neto *et al.* 2014; Fernandes Júnior *et al.* 2016b; Magalhães *et al.* 2016). Genomic studies in the tropics have also been focused on the identification of chromosome regions associated with traits related to sexual precocity. Together, Costa *et al.* (2015) and Regatieri et al. (2017), for example, reported 43 candidate genes for age at first calving, early pregnancy and heifer rebreeding.

Adaptation- and temperament-related QTLs have also been identified. Using GWAS in a crossbred (*taurine x indicine*) cattle population, Porto-Neto *et al.* (2014) identified an extended genetic region centered around the MSRB3 gene on BTA5 affecting several traits related to climatic adaptation of tropical cattle including parasite resistance, yearling weight, body condition score, coat color and penile sheath score. In a Nellore population, Valente *et al.* (2016) reported the existence of nine candidate regions (BTA1 at 73 Mb, BTA2 at 65 Mb, BTA5 at 22 Mb and 119 Mb, BTA9 at 98

Mb, BTA11 at 67 Mb, BTA15 at 16 Mb, BTA17 at 63 Kb, and BTA26 at 47 Mb) affecting animal temperament. According to the last authors, these genomic regions harbor genes such as PARK2, GUCY1A2, CPE and DOCK1 that are, respectively, related to dopaminergic system, memory formation, biosynthesis of peptide hormone and neurotransmitter and brain development. The understanding of genetic control of traits related to adaptation and cattle temperament should contribute to improve the productivity and animal welfare in the tropics.

APPLICATIONS OF GENOMIC SELECTION IN THE TROPICS: NELLORE BREED AS A CASE STUDY

There are different important breeding programs and research groups working on genomic selection applied to beef cattle in the tropics. We will focus on applications of genomic selection for the Nellore breed as a case study because of our research background and due to the importance of this breed for the global beef market (Carvalheiro 2014, USDA 2016). Nellore breeding programs also represent a successful case of partnership between academy and industry. The history behind the establishment and evolvement of the different commercial Nellore breeding programs running independently in Brazil was described by Ferraz and Fries (2004) and Carvalheiro (2014). Currently, these breeding programs jointly control over half a million Nellore cows per year. We will list some genomic selection applications from part of these Nellore breeding programs that are working closely to our research group, so we are more aware of what they are doing. They are CIA de Melhoramento (www.ciademelhoramento.com.br), DeltaGen (www.deltagen.com.br), Nelore Qualitas (www.nelorequalitas.com.br) and PAINT (www.crvlagoa.com.br). We would like to emphasize that there are other important research groups and breeding programs in Brazil also working with genomic selection applied to Nellore and other breeds.

Selection of progeny test candidates

The selection of young sires to be progeny tested in Nellore breeding programs is performed based on selection indexes presenting low to moderate accuracy (~0.5), when genomic information is not used. Under the current breeding scheme, young sires have their semen distributed when they are ~2 years old and have their final proof (based on progeny performance) with ~5 years old. For not presenting highly accurate proofs, these young sires are usually not used intensively until their final proof attests their genetic superiority. As a consequence, the generation interval is increased, constraining the genetic gain.

Genomic selection has increased the accuracy of selection of young sires. For instance, in some breeding programs genotyped young sires have been selected with an average accuracy of 0.75, i.e. 50% higher than the average accuracy of regular proofs. Investments and collaborations among the breeding programs are being done aiming to increase their reference populations and the accuracy of genomic predictions. The target is evaluating young sires with accuracies comparable (>0.85) to proven bulls.

Due to genotyping costs, some breeders perform a first screening based on regular proofs to select the animals to be genotyped, than choose the young sires to be progeny tested based on their genomic enhanced proof. Typically, ten times more candidates are genotyped than the animals to be tested. For example, if a breeding program intents to progeny test 50 young sires in a specific breeding season, the top 500 based on regular proofs are genotyped an their genomic enhanced proofs finally determine those to be selected. Some breeders have already decided to genotype all yearling animals, without pre-screening on regular proofs.

Although this application of genomic selection presents some advantage, increasing the accuracy of selection of young sires would have a limited impact on the genetic gain if they are not used more intensively when they are still young. Fortunately, the increased accuracy of genomic predictions is motivating some breeders to use young sires more intensively.

Intensifying the use of young sires

Historically, Nellore breeders have been using, on average, no more than 30% of young sires to mate their cows (Figure 1a). With few exceptions, generation interval of sires is generally around (or even greater than) seven years. In general, breeders are more comfortable in using proven bulls. Moreover, the trade-off between accuracy and generation interval makes it difficult to technically convince farmers to use young sires more intensively, e.g. the ratio between accuracy and generation interval for young sires (0.5/4.0=0.125) is similar to that for proven bulls (0.9/7.0=0.128). Genomic selection is changing this pattern. As genotyped young sires are presenting higher accurate proofs (compared to young sires without genomic information), some breeders are intensifying their use and, as a consequence, obtaining higher response to selection (Figure 1b).

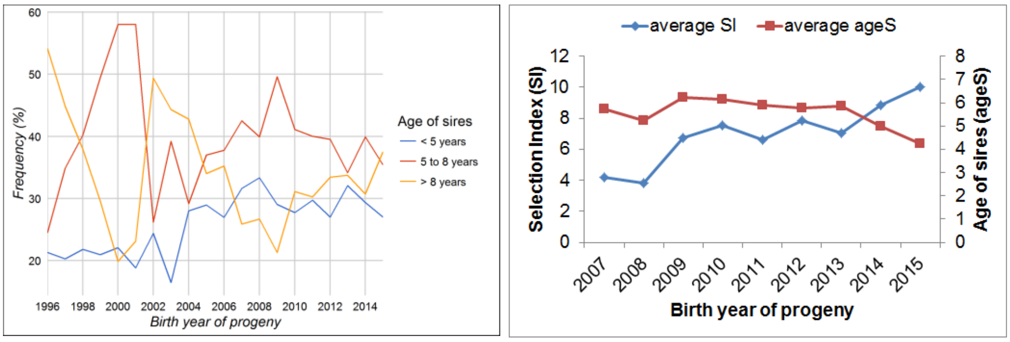

Figure 1. (a: left) Frequency (%) of progeny by age class of sires and year of birth, for Aliança Nelore dataset (~100,000 calves/year); and (b: right) Genetic trend and average age of sires at Jacarezinho farm (~10,000 calves/year).

As the reference population gets better (larger and more representative of the population) and allows obtaining more accurate proofs, genomic selection cancels the trade-off between accuracy and generation interval. It has been predicted that in the near future the seedstock Nellore cows will be mated only with young sires, which is a dramatic 'change of paradigm' on breeder's behavior. Assuming an average accuracy of 0.8 for the genomic enhanced proofs of young sires, this strategy would result in a ratio between accuracy and generation interval equal to 0.2 (0.8/4), a substantial increase compared to the ratio from the scheme without genomics. Indeed, dairy cattle breeders, especially Holstein breeders, had already witnessed this change in their breeding scheme after the advent of genomic selection (Van Eenennaam *et al.* 2014).

Selection of donors

According to the Brazilian Society of Embryo Technology, Brazil has been producing, through *in vitro* fertilization (IVF), more than half a million embryos per year, being, approximately, half of that from beef cattle breeds. In the past, embryo technology was mainly used in Brazil by “elite” herds focused on producing “show type” animals. Lots of embryos used to be produced from cows without any genetic proof and raised in artificial environments. Fortunately, this pattern has changed partially because of the drastic development of IVF, which is becoming more reliable and feasible, but also due to the position conquered by the breeding programs that nowadays lead the genetic market as seedstock providers, position which used to be occupied by “show type” animals.

Previously to genomics, a typical technical recommendation for breeders was to select, as donors, the top cows with reasonably accurate proofs, what generally resulted in selecting old cows. Genomic selection has allowed intensifying the use of young cows or heifers as donors, for increasing the accuracy of their genetic proofs. This strategy, of producing more progeny from genetically superior young animals through the synergistic adoption of genomic selection and reproduction technologies, is predicted to promote substantial increase in genetic gain compared to more conventional breeding schemes (Carvalheiro 2014). Caution should be made to certify that the heifers and young cows have superior and reasonably accurate genomic proofs for maternal and reproduction traits to be selected as donors, in order to produce replacement heifers.

Genotyping of embryos

As previously mentioned, IVF and embryo production have been used in large scale by some farms in Brazil (>1,000 embryos implanted/farm/year, with pregnancy rates around 40%). This reproduction technology provides an outstanding opportunity for increasing the genetic progress if sires and donors are properly chosen and if a reasonably good pregnancy rate of implanted embryos is attained. The genetic progress could be even higher if the genetic merit of embryos were predicted more accurately (using genomic information for example) before they were implanted. Genomic predictions of biopsied and genotyped embryos are already being obtained for dairy cattle (Saadi *et al.* 2014).

A recent study showed the feasibility of genotyping Nellore biopsied embryos and obtaining their proofs more accurately (Carvalheiro *et al.* 2017). Farmers can use this information, for example, to decide which embryos to implant, as their genomic proofs may substantially deviate from what is expected based on parents average. Another application would be to implant the embryos using a customized approach, matching the genomic profile of the embryo with the customers’ needs. For example, farmers more focused on producing high quality beef, could decide to implant just embryos presenting good genomic predictions for marbling and tenderness.

Screening young sires in commercial herds

It is estimated that Brazilian commercial herds have roughly 35 million Nellore cows to be mated under natural mating (NM). If we assume one bull per 25 cows under NM and an annual replacement rate of bulls of 20%, the commercial herds need around 280,000 young replacement bulls per year. Nellore breeding programs running in Brazil jointly control about 500,000 cows, and produce around 40,000 young top bulls per year. So, breeding programs produce less than 15% of the young bulls demanded by the commercial herds, i.e. most of the commercial Nellore cows under NM are being mated with non-proven bulls.

In theory, genomic selection has the potential to change this scenario, as the commercial herds have now a tool to predict the genetic merit of bulls without a traditional proof. This application of genomic selection is technically questionable since there is evidence of the presence of substructures (based on genomic kinship) among Nellore subpopulations (Utsunomiya *et al*. 2013). In this case, the prediction equation developed using data from one subpopulation (e.g. breeding program) will not necessarily work properly in another subpopulation (e.g. commercial herd), particularly if these subpopulations are unrelated and if the developed prediction equation is more influenced by relatedness and co-segregation than by linkage disequilibrium between markers and QTL (Sun *et al.* 2016). This technical issue is even more relevant if we consider that Nellore presents lower level of linkage disequilibrium between markers at short distances compared to taurine breeds (Pérez O'Brien *et al.* 2014).

However, there are some commercial farms that already started using genomic predictions for screening young sires from their own herds. A typical use is being performed by large operation commercial farms (>10,000 cows) that, due to logistical and labor constrain, do not control their herd in a breeding program but have some genetic links with seedstock herds for using their genetic material (bull, semen, etc.). It is believed that these commercial farms could replace part of the bulls used under NM with their own produced young sires. An example is illustrated in Figure 2 where a large commercial farm pre-screened over 2,000 yearling contemporary males based on phenotypic appraisal, chose 272 to be genotyped and selected 69 to be used as replacement, based on their genomic proof (Index>5). A principal component analysis of the genomic relationship matrix revealed that the 272 genotyped animals were within the same cluster of the reference population used to calculate their genomic proofs, suggesting that the accuracy of their genomic predictions (0.38-0.58) were not overestimated.

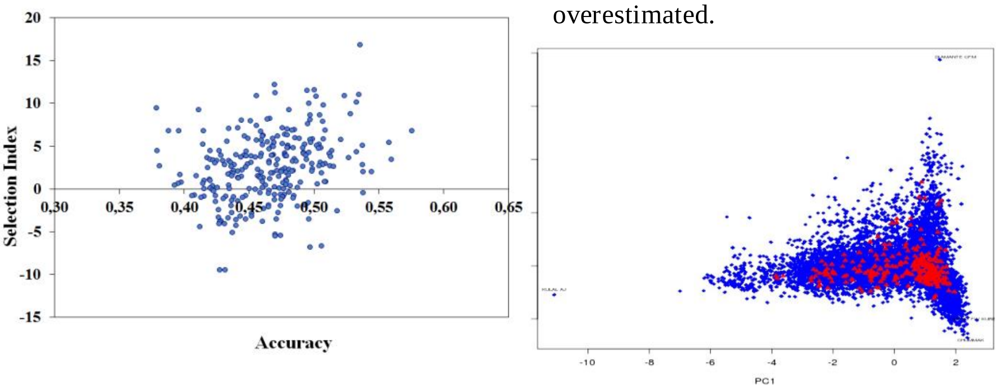

Figure 2. (a: left) Index and accuracy of genomic proofs of young sires from a commercial herd; and (b: right) Principal component analysis plot (x-axis: PC1; y-axis: PC2) based on genomic relationship matrix (blue=reference population, red=selection candidates).

Increasing selection intensity for reproduction traits

The Nellore breeding programs in Brazil use different strategies to select for reproduction traits. The most common are independent phenotypic culling, discarding heifers and cows that are not pregnant at the end of the breeding season, and accounting for reproduction traits in the selection index. In general, the selection indexes adopted give more emphasis to growth and carcass traits than to reproduction traits. This fact is often explained by the low heritability and low accuracy of genetic proofs for reproduction traits.

Motivated by the increase in accuracy obtained with genomic predictions, some breeders are given more weight to reproduction traits on their selection indexes. There are also some programs that are replacing, in their selection indexes, EPDs of indirect traits (e.g. scrotal circumference) by EPDs of traits directly associated with reproduction (e.g. age at first calving or heifer pregnancy). This strategy is expected to promote a substantial increase in genetic gain compared to the conventional strategies (without genomics), given a good prediction equation for reproduction traits.

Selection for expensive and difficult to measure traits

The opportunity to better select for expensive and difficult to measure traits figures amongst the most important applications of genomic selection. A representative example in beef cattle is the selection for meat quality traits. Without genomics, selection for this type of traits is constrained by its cost-effectiveness as it requires huge investments on phenotyping and on progeny testing, resulting in limited genetic gain due to either low accuracy of genetic proofs or long generation intervals.

Despite presenting good adaptation to tropical conditions and an extraordinary capacity to convert (low quality) pasture on meat production, Nellore cattle tends to present lower quality beef (in terms of tenderness, for example) compared to some Taurine breeds. This helps to explain the huge investments and efforts that Brazilian research groups and breeding programs are doing to establish reference populations and develop prediction equations for meat quality traits. Important studies are revealing the existence of genetic variation and the feasibility of applying genomic selection for these traits (Aboujaoude *et al.* 2016; Feitosa *et al.* 2016; Fernandes Júnior et al.

2016a; Gordo et al. 2016; Chiaia *et al.* 2017), attaining prediction accuracies of about 0.4 for some relevant traits (e.g. tenderness) that previously to genomics were not evaluated. Motivated by the results of these studies some breeders are establishing a consortium to develop strategies that would warranty the improvement and maintenance of the prediction equations for carcass and meat quality traits. Efforts and investments are also been made to develop prediction equations for traits related to feed efficiency (Silva *et al.* 2016) and, more recently, methane emission.

Genomic predictions accounting for GxE

Genotypic information has allowed not only obtaining more accurate genetic proofs in different environments but also identifying young animals with less sensitivity to environmental variation (not published). This will help breeders to better explore genotype by environment interaction, which is commonly an important source of phenotypic variation in tropical environments (Cardoso and Tempelman 2012; Chiaia *et al.* 2015; Santana *et al.* 2015). Breeders are now able to select young sires to produce under specific conditions without the necessity to progeny test them in different environments.

Other applications

Many other uses of genotypic information in Nellore breeding programs are emerging. For instance, GWAS are being performed on morphologic and functional traits such as testicular hypoplasia and skin depigmentation, and important candidate major genes are being identified for these traits (H.H.R. Neves, personal communication). If their effects are confirmed, this information could be used on mating plans or on developing genetic tests, aiming to reduce the economic losses caused by the incidence of these problems. Another example of application is the use of genotypic information to perform genomic control of inbreeding (Sonesson *et al.* 2012). As multiple-sire mating is a regular practice in some farms, due to the large number of cows under natural mating, estimates of inbreeding based on genotypic information are expected to be more reliable than those based on incomplete or erroneous pedigree, allowing controlling inbreeding more effectively.

CONCLUDING REMARKS

Genetic improvement has an important role in increasing efficiency and competitiveness of beef cattle production in the tropics. There are several challenges and opportunities to genetically improve more effectively beef cattle herds in the tropics and genomic selection has shown to be a key tool to increase genetic progress of economically relevant traits. Some applications of genomic selection in Nellore cattle from Brazil were listed but more will certainly come or are already been applied by other breeding programs, breeds and countries. Individually, genomic selection applications may have a moderate impact on the breeding programs but considered together they are expected to significantly improve the genetic progress, profitability and sustainability of beef production in the tropics.

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