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**UNIVERSIDADE ESTADUAL PAULISTA - UNESP
CÂMPUS DE JABOTICABAL**

**Application of ssGBLUP for variance components
estimation and genomic prediction in two Zebu cattle
populations**

Daniel Cardona Cifuentes
Zootecnista, M.Sc.

2024

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Orientadora: Profa. Dra. Lucia Galvão de Albuquerque

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IMPACTO POTENCIAL DESTA PESQUISA

A estimativa de componentes de variância é essencial nos programas de avaliação genética do gado de corte. Este trabalho estabelece se a informação genômica deve ser considerada nesse processo. Isso é importante para as associações de produtores, pois permite otimizar os recursos computacionais, aumentar a precisão na seleção de reprodutores e obter animais com maior capacidade reprodutiva no trópico.

POTENCIAL IMPACT OF THIS RESEARCH

The variance components estimation is essential in breeding programs for beef cattle. This work establishes whether genomic information should be considered in this process. This is important for producer associations, as it allows them to optimize computational resources, increase the accuracy of sire's selection, and obtain animals with greater reproductive capacity in the tropics.



UNIVERSIDADE ESTADUAL PAULISTA

Câmpus de Jaboticabal




CERTIFICADO DE APROVAÇÃO

TÍTULO DA TESE: APPLICATION OF ssGBLUP FOR VARIANCE COMPONENTS ESTIMATION AND GENOMIC PREDICTION IN TWO ZEBU CATTLE POPULATIONS


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AUTHOR'S CURRICULAR DATA

Daniel Cardona Cifuentes was born on February 6, 1991, in Medellin, Colombia, the son of Carlos Cardona and Nancy Cifuentes. In 2008, he started a career in animal science at the Universidad Nacional de Colombia. Daniel became interested in animal breeding and genetics during his studies and took an advanced course in variance components and genetic parameter estimation. In 2015, he completed his undergraduate studies and, in the same year, began a master's in biotechnology at the same university. He worked in the genetics and breeding of dairy cattle and participated in the research group "Biología y Genética Molecular – BIOGEM." In 2016, he started his career as a professor at Universidad de Antioquia, and in 2018, he finished his master's degree. The same year, Daniel worked on the Colombian national plan for animal breeding and, in 2019, became a professor at Universidad Nacional Abierta y a Distancia and at Corporación Universitaria la Sallista. In 2020, Daniel began doctoral studies in genetic and animal breeding at Faculdade de Ciências Agrárias e Veterinárias (FCAV) from Universidade Estadual Paulista (UNESP) in Jaboticabal, São Paulo, Brazil. Daniel obtained a scholarship awarded by La Fundación para el Futuro de Colombia (COLFUTURO) and the Ministerio de Ciencias from the Colombian Republic to develop his doctoral studies.

EPIGRAPH

“El capitán miró a Fermina Daza y vio en sus pestañas los primeros destellos de una escarcha invernal. Luego miró a Florentino Ariza, su dominio invencible, su amor impávido, y lo asustó la sospecha tardía de que es la vida, más que la muerte, la que no tiene límites.

- *¿y hasta cuándo cree usted que podemos seguir en este ir y venir del carajo?*
– *le preguntó.*

Florentino Ariza tenía la respuesta preparada desde hacía cincuenta y tres años, siete meses y once días con sus noches.

- *Toda la vida – dijo.”*

El Amor en los tiempos del Colera, Gabriel García Márquez.

DEDICATION

I dedicate this thesis to my parents, Nancy and Carlos, for their unconditional support and continuous efforts that have allowed me to develop my academic and professional life.

To my sister for always giving me words of motivation and whose kindness brightens the lives of everyone around her. To the three of you, thank you for your infinite love.

To Daniela, the woman I am fortunate to call my partner and future wife, for her patience during this journey, for giving me light in the darkest moments, and for staying despite the adversities.

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Los amo.”

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APPLICATION OF SSGBLUP FOR VARIANCE COMPONENTS ESTIMATION AND GENOMIC PREDICTION IN TWO ZEBU CATTLE POPULATIONS

ABSTRACT – The ssGBLUP combines genomic and pedigree information, which can increase the accuracy in the estimation of variance components (VCE). In cases such as the traits traditionally evaluated in commercial genetic improvement programs for Nelore cattle in Brazil, the use of ssGBLUP often involves mixing information from an old pedigree-based selection program with current genomic selection (GS) information. This is controversial because selection decisions are based on genomic information, and only subsets of animals are genotyped, which represents an additional selection step that can introduce bias into genomic estimated breeding values (GEBV). On the other hand, ssGBLUP can improve VCE in GS programs for breeds with fewer records, such as Brahman cattle, especially in traits with low heritability, such as gestational loss (PL), and when considering genotype-environment interaction (GxE). Therefore, the overall objective was to evaluate the application of ssGBLUP for VCE and genomic prediction of production and reproduction traits in two Zebu cattle populations. In the case of Nelore cattle, the first specific objective was to estimate variance components for growth and reproductive traits using two different relationship matrices (relationship matrix **A** based on pedigree and relationship matrix **H** based on pedigree and genomic information), as well as considering phenotypic records collected before or after the implementation of GS in Brazilian Nelore cattle. Additionally, we evaluated how GEBV are affected by VCE and by excluding records prior to the implementation of GS. In this case, the traits evaluated were weight at 120 days (W120), weight at 450 days (W450), and scrotal circumference at 450 days (SC450). Three datasets were used for VCE: 1) including all phenotypes (All), 2) only records of animals born before 2010 (Before), or 3) records of animals born since 2010 (After), according to the start of GS. We used matrix **A** in all three datasets (A_before, A_after, and A_all), while H was used in two situations: H_All and H_After. Different VCE were used for the prediction of GEBV through ssGBLUP. This stage used two possible datasets: all available records (Dataset 1) and only records collected since 2010 (Dataset 2). Validation was conducted using the LR method. For the three traits, heritability increased using A_After, and for W450 and SC450 heritability decreased with the use of matrix H. For W120, Dataset 1 and VCE from A_After showed the highest accuracy for direct and maternal GEBV. For W450 and SC450, Dataset 1 and VCE using H_After allowed high accuracy for GEBV. Furthermore, in both traits, using Dataset 2 did not add bias or dispersion and maintained high accuracy of GEBV. For W450 and SC450, genetic variance and heritability increased with GS. For W120, GEBV were more accurate using **A** for VCE. It was possible to obtain high accuracy of GEBV for W450 and SC450 using **H** in VCE and discarding records prior to GS. It is possible to exclude records prior to the implementation of GS without increasing bias and dispersion in predictions. In the case of Brahman cattle, the second specific objective was to estimate variance components and genetic parameters for PL and evaluate its genetic correlation with growth and reproductive traits assessed in a commercial genetic improvement program, comparing the use of matrices **A** and **H**. For this, PL records from three pregnancy orders (heifers, primiparous cows, and

multiparous cows) were collected for two herds in Bolivia. Univariate and multivariate threshold models were fitted for PL in the three pregnancy orders, and multivariate models were also fitted between PL and traditional traits such as weights adjusted at 450 (W450) and 550 (W550) days of age, scrotal circumference adjusted at 450 (SC450) and 550 (SC550), cow accumulated productivity (ACP), age at first calving (AFC), and stayability (STAY). Matrices **A** and **H** were tested in all models. Heritability for PL was low in the three orders, but the use of matrix **H** increased heritability in heifers. High genetic correlation was observed between PL in the pregnancy orders. Using matrix **H** reduced the posterior standard deviation of the genetic correlations between PL and other traits. The genetic correlation between PL in heifers and STAY increased with the use of matrix **H**. Moderate to high and positive genetic correlations were observed between PL and STAY in primiparous and multiparous cows. High and moderate positive genetic correlations were observed between AFC and PL. Negative genetic correlation was observed between PL and SC450 or SC550. The genetic correlation between PL and ACP was generally medium to high and negative, with the greatest change in heifers when using matrix **H**. Medium or low genetic correlation was always observed between PL and W450 or W550. Including genomic information increased heritability for PL in heifers and improved the accuracy of genetic correlation estimates between PL and commonly evaluated traits. The third specific objective was to test the use of a reaction norm model (RNM) to identify GxE affecting PL in Brahman cattle, evaluating the inclusion of genomic information on VCE, predictive ability, and accuracy of GEBV. PL records in heifers were used along with meteorological data collected from NASAPOWER. The daily temperature and humidity index (THI) was calculated, and the date of pregnancy confirmation was used to associate PL records with the accumulated THI 30 days before and after confirmation. Threshold RNM were fitted for PL using matrices **A** and **H**. The use of matrix **H** increased the heritability of the regression intercept. The average heritability for PL on the accumulated THI gradient was similar using matrix **A** or matrix **H**. GxE affecting PL was confirmed by the negative genetic correlation between coefficients and between extreme values of accumulated THI. A significant reclassification between THI levels was observed because of GxE. VCE and genetic parameters changed with the use of matrix **H**, although no clear advantage was observed. However, the use of matrix **H** allowed more accurate and robust GEBV for random coefficients. There is evidence of GxE affecting the genetic response for PL in Brahman cattle under tropical conditions.

Keywords:

Genomic selection, beef cattle, accuracy, genetic variance

APLICAÇÃO DO SSGBLUP PARA ESTIMATIVA DE COMPONENTES DE VARIÂNCIA E PREDIÇÃO GENÔMICA EM DUAS POPULAÇÕES DE GADO ZEBU

RESUMO – O ssGBLUP combina informações genômicas e de pedigree, o que pode aumentar a precisão na estimativa de componentes de variância (VCE). Em casos como os das características tradicionalmente avaliadas em programas comerciais de melhoramento genético de gado Nelore em Brasil, o uso do ssGBLUP frequentemente envolve a mistura de informações de um antigo programa de seleção baseado em pedigree com informações atuais da seleção genômica (GS). Isso é controverso porque as decisões de seleção são baseadas em informações genômicas, e apenas subconjuntos de animais são genotipados, o que representa um passo adicional de seleção que pode acrescentar viés nos valores genéticos genômicos (GEBV). Por outro lado, o ssGBLUP pode melhorar as VCE nos programas de GS para raças com menos registros, como é o caso do gado Brahman; principalmente nas características com pouca herdabilidade, como a perda gestacional (PL), e quando considerada a interação genótipo – ambiente (GxE). Portanto, o objetivo geral foi avaliar a aplicação do ssGBLUP para VCE e predição genômica de características de produção e reprodução em duas populações de gado Zebu. No caso do gado Nelore, o primeiro objetivo específico foi estimar os componentes de variância para características de crescimento e reprodutivas utilizando duas diferentes matrizes de relacionamento (matriz **A** de relacionamento baseado no pedigree e a matriz **H** de relacionamento por pedigree e genômico), assim como considerando registros fenotípicos coletados antes ou depois da implementação da GS no gado Nelore Brasileiro. Além disso, avaliou-se como os GEBV são afetados pelas VCE e pela exclusão de registros anteriores à implementação da GS. Nesse caso, foram avaliadas as características peso aos 120 dias (W120), peso aos 450 dias (W450) e circunferência escrotal aos 450 dias (SC450). Foram utilizados três conjuntos de dados para a VCE: 1) incluindo todos os fenótipos (All), 2) apenas registros de animais nascidos antes de 2010 (before) ou 3) registros de animais nascidos desde 2010 (After), de acordo com o início da GS. Utilizamos a matriz **A** em todos os três conjuntos de dados (A_before, A_after e A_all), enquanto **H** foi usada em duas situações: H_All e H_After. Diferentes VCE foram usadas para a predição dos GEBV através do ssGBLUP. Esta etapa utilizou dois possíveis conjuntos de dados: todos os registros disponíveis (Dataset 1) e apenas registros coletados desde 2010 (Dataset 2). A validação foi conduzida com método LR. Para as três características, a herdabilidade aumentou usando A_After, e para W450 e SC450 a herdabilidade diminuiu com o uso da matriz **H**. Para W120, o Dataset 1 e VCE de A_After mostraram a maior precisão para o GEBV direto e maternos. Para W450 e SC450, o Dataset 1 e VCE usando H_After permitiram alta acurácia para os GEBV. Além disso, em ambas as características, usar o Dataset 2 não acrescentou viés nem dispersão e manteve alta a acurácia dos GEBV. Para W450 e SC450, a variância genética e a herdabilidade aumentaram com a GS. Para W120, os GEBV foram mais precisos usando **A** para a VCE. Foi possível obter alta acurácia dos GEBV para W450 e SC450 usando **H** na VCE e descartando registros anteriores à GS. É possível excluir registros anteriores à

implementação da GS sem aumentar o viés e dispersão das predições. No caso do gado Brahman, o segundo objetivo específico foi estimar os componentes de variância e os parâmetros genéticos para PL e avaliar a sua correlação genética com características de crescimento e reprodutivas avaliadas em um programa de comercial de melhoramento genético, comparando o uso das matrizes **A** e **H**. Para isso, registros de PL de três ordens de gravidez (novilhas, vacas primíparas e vacas múltiparas) foram coletados para dois rebanhos na Bolívia. Modelos de limiar uni-variados e multivariados foram ajustados para PL nas três ordens de gravidez, também se ajustaram modelos multivariados entre PL e características tradicionais como pesos ajustados aos 450 (W450) e 550 (W550) dias de idade, circunferência escrotal ajustada aos 450 (SC450) e 550 (SC550), produtividade acumulada da vaca (ACP), idade ao primeiro parto (AFC) e permanência (STAY). As matrizes **A** e **H** foram testadas em todos os modelos. A herdabilidade para PL foi baixa nas três ordens, mas o uso da matriz **H** aumentou a herdabilidade em novilhas. Observou-se alta correlação genética entre PL nas ordens de gravidez. Usar a matriz **H** reduziu o desvio padrão posterior das correlações genéticas entre PL e as demais características. A correlação genética entre PL em novilhas e STAY aumentou com o uso da matriz **H**. Correlações genéticas moderadas a altas e positivas foram observadas entre PL e STAY em vacas primíparas e múltiparas. Correlações genéticas altas e médias e positivas foram observadas para AFC e PL. Correlação genética negativa foi observada entre PL e SC450 ou SC550. A correlação genética entre PL e ACP em geral foi média a alta e negativa, com maior mudança em novilhas quando usada a matriz **H**. Sempre foi observada correlação genética média ou baixa entre PL e W450 ou W550. Incluir informações genômicas aumentou a herdabilidade para PL em novilhas e melhorou a precisão das estimativas de correlação genética entre PL e características normalmente avaliadas. O terceiro objetivo específico foi testar o uso de um modelo de norma de reação (RNM) para identificar GxE que afeta a PL no gado Brahman, avaliando a inclusão de informações genômicas sobre as VCE, a habilidade de predição e a acurácia dos GEBV. Os registros de PL em novilhas foram usados junto com dados meteorológicos coletados do NASAPOWER. O índice de temperatura e umidade (THI) diário foi calculado e a data de confirmação da prenhez foi usada para associar os registros de PL com o THI acumulado 30 dias antes e depois da confirmação. RNM de limiar foram ajustados para PL usando as matrizes **A** e **H**. O uso da matriz **H** aumentou a herdabilidade do intercepto da regressão. A herdabilidade média para PL no gradiente de THI acumulado foi semelhante usando a matriz **A** ou matriz **H**. GxE afetando a PL foi confirmada pela correlação genética negativa entre os coeficientes e entre valores extremos de THI acumulado. Uma importante reclassificação entre níveis de THI foi observada como consequência da GxE. VCE e parâmetros genéticos mudaram com o uso da matriz **H**, embora nenhuma vantagem clara tenha sido observada. No entanto, o uso da matriz **H** permitiu GEBVs mais acurados e robustos para coeficientes aleatórios. Há evidências de GxE que afeta a resposta genética para PL em gado Brahman sob condições tropicais.

Palavras-chave:

Seleção genômica, bovinos de corte, acurácia, variância genética

CHAPTER 1 – General considerations

Introduction

For the year 2023, world bovine meat production reached 76 million tons (FAO, 2023a). Approximately 60% of this production comes from countries with tropical and subtropical areas, which are responsible for nearly 80% of the world's cattle population (Cooke et al., 2020; FAOSTAT, 2023). Zebu (*Bos indicus*) and *Bos indicus*-crossbred cattle predominate in tropical and subtropical regions due to their adaptative capacity (Montaldo et al., 2012). Zebu cattle is characterized by the presence of a hump, abundant dewlap, pigmented and loose skin, and short and thin hair, which gives them thermoregulatory ability and parasite resistance (Burrow, 2012; Cardoso et al., 2015). Moreover, a low metabolic rate with reduced heat production and energy requirements often implies scarce intramuscular adipocyte volume and lower growth and production rates than *Bos taurus* but also facilitates heat dissipation and grants thermotolerance (Cooke et al., 2020; Rubio Lozano et al., 2021).

Thanks to these attributes, Zebu cattle has been adopted in many production systems in the American continent, which produces 48.9% of the cattle meat on the planet. Even Brazil is the second largest producer in the world, with 10.35 million tons in 2022 from an industry based on Zebu cattle (FAO, 2023; FAOSTAT, 2023). For this reason, it is not surprising that Brazil is a leader in animal breeding programs for Zebu cattle. Several breeding programs started in the country around the 1980s, focusing on breeds such as Nellore and Brahman (Ferraz and Fries, 2004). These initial breeding programs performed genetic evaluations using phenotypic and pedigree information to compute the estimated breeding values (EBV).

The advances in molecular biology allowed the inclusion of direct DNA information in genetic evaluation models. Meuwissen and Hayes (2001) showed that it was possible to use molecular markers of single-nucleotide polymorphism (SNP) distributed in the whole genome to performed genetic evaluations. Including this third type of information enables computing the genomic breeding value (GEBV) and has

led to the development of what is now known as genomic selection (GS) (VanRaden, 2008; VanRaden, 2020).

In the decade of the 2010s, genomic selection models began to be tested and implemented in Brazil, mainly focusing on Nelore cattle (Berry et al., 2016; Carvalheiro, 2014). Initially, many groups worked independently in genomic selection research but established successful partnerships between universities, research institutes, private companies, and farmer associations (Carvalheiro, 2014). Currently, many of these groups have joint efforts and have implemented GS in commercial Nelore breeding programs, increasing in 50% the prediction accuracy for young animals EBVs compared with traditional pedigree-based test, which allowed intensified use of young bulls and maximized genetic gains (Albuquerque et al., 2017). Other research and farmers associations as National Association of Breeders and Researchers (ANCP) have incorporated data from other countries like Paraguay, Colombia, and Bolivia and have extended genomic selection to other zebu breeds such as Brahman and Guzera (ANCP, 2024).

Nelore is Brazil's most important beef cattle breed, with the largest number of records available for genetic evaluation. Traditionally, the selection index for Nelore cattle includes growth traits and scrotal circumference. Therefore, it is unsurprising that these are among the most studied traits for developing genomic association models in this breed (Fernandes Júnior et al., 2022). Both kind of traits show a similar prediction accuracy (0.27 to 0.72) for young animals when using genomic information; this does not happen with the traditional pedigree-based selection since reproductive traits have low heritability estimates, limiting their prediction accuracy in traditional genetic evaluations (Neves et al., 2014; Fernandes Júnior et al., 2022).

Several models have been tested for applying GS in Zebu cattle; however, there is currently higher interest in single-step GBLUP (ssGBLUP) in commercial breeding programs. The great advantage of ssGBLUP is that it combines pedigree and phenotypic information from genotyped and non-genotyped individuals; therefore, it allows the computation of GEBV for all animals (Misztal et al., 2009). The ssGBLUP has been tested in Nelore cattle for traditional growth and

reproduction traits, both for estimating variance components and for genomic prediction (Kluska et al., 2018; Watanabe et al., 2021).

In cases such as those of traditional traits of Nellore cattle, using ssGBLUP often involves mixing information from the old pedigree-based selection program (PedS) with current information from GS. This is controversial because in GS commercial programs, selection decisions are based on genomic information, and only subsets of potential parents are genotyped, this is an additional selection step that has been named selective genotyping (Jensen, 2016; Gowane et al., 2019). This contradicts the assumptions for traditional variance components estimation in PedS since the estimates were assumed unbiased because they depend on tracing the pedigree relationships to the conceptual base population, removing bias by considering all selection steps and information. Therefore, using just pedigree records for a population undergoing GS would produce biased variance components estimates (Jensen, 2016).

Vitezica et al., (2011a) pointed out that an advantage of ssGBLUP is creating a unified framework that accounts for bias by considering all selection information and referencing genomic and pedigree-based relationships to the base population. Nevertheless, the possible bias in variance components estimation is concerning because it can lead to bias in GEBV even using ssGBLUP (Wang et al., 2020). For example, selective genotyping can increase genetic additive variance estimates reflecting GEBV bias (Gowane et al., 2019; Wang et al., 2020). Moreover, changes in variance components can occur due to GS implementation, stating that it is not adequate mixing records from both phases of the breeding programs (Cesarani et al., 2020b; Hidalgo et al., 2020).

From these considerations, it is essential to continue researching the application of ssGBLUP in Nelore cattle's traditional growth and reproduction traits since this approach can help to decide if data from PedS should be discarded for variance components estimation, and it is interesting to test how the single-step approach can influence these estimates. Moreover, Legarra and Reverter (2018) proposed a practical method for genomic prediction validation, which could help

establish what datasets and variance component estimation methodology allows for obtaining the most robust GEBV.

Another application of ssGBLUP in zebu cattle is to improve genomic selection programs for breeds with fewer records, as in the case of Brahman cattle. Montaldo et al., (2012) highlight that Brahman cattle is among the most important breeds for beef production in the tropics. Some reports have shown the importance of Brahman cattle for genomic-crossbreeding programs that seek animals with adaptability to the tropics and with productive aptitudes of Boss Taurus (Bolormaa et al., 2011; Elzo et al., 2017; Raidan et al., 2018). Nevertheless, Brahman cattle records are often less abundant than in Nellore. Genomic selection becomes even more interesting when low heritability traits are considered since the most significant gains in accuracy expected for this trait, as is the case of reproduction traits in zebu cattle (Albuquerque et al., 2017; Meuwissen and Hayes, 2001).

The Brahman breed is one of the most important Zebu cattle breeds in the Americas, and it is present in countries such as the United States, Colombia, Venezuela, Brazil, and Bolivia, among others. The latest genetic evaluation published by the Colombian Association of Zebu Cattle Breeders (ASOCEBU) for the year 2023 (<https://www.asocebu.com/evaluaciongenetica/eg2023.pdf>) considered 56,538 phenotypes with 5,631 bulls for weaning weight and 43,269 phenotypes with 4,766 bulls for 18-month adjusted weight. Meanwhile, the Brazilian Association of Zebu Cattle Breeders (ABCZ) reported that as of 2020, there were 224,481 registered animals (<https://www.abcz.org.br/a-abcz/racas-zebuinas/raca/2/brahman>). The Brahman breeding program of the ANCP includes 229,430 animals, with 48% located in Brazil and 37.4% in Bolivia. These numbers demonstrate the importance of Brahman cattle in South American beef production, thanks to the adaptation to tropical production systems.

Some of ANCP's associate producers in Bolivia have farms located in the Beni and Santa Cruz de la Sierra departments. These departments are characterized by a humid tropical climate (relative humidity between 60-80%) and an average temperature varying between 22 and 28°C, which can reach up to 35°C and can suddenly fall to 16-18°C when cold winds from the south reach the territory. The

region's annual precipitation is between 1000 and 4000 mm; the rainiest season occurs between the months of December and March, when floods are common and coincide with high temperatures and relative humidity (Instituto Nacional de Estadística, 2023). These climatic challenges hinder the reproductive performance of the animals and present an interesting case to test the use of genomic information through ssGBLUP to select heifers with less tendency to gestational loss. This novel trait has low heritability and environmental sensitivity, so in this kind of trait, genomic selection should allow a faster and more accurate evaluation of young animals (Fernandes Júnior et al., 2022; Sigdel et al., 2022).

Environmental adversity in the tropics and increasing temperatures due to climate change make selecting animals with adaptive capacity necessary, and reaction norm models (RNM) are great tools to identify these animals (Pegolo et al., 2011). The RNM allows the genotype-environment interaction (G x E) to be included in the genetic evaluation equations, enabling the selection of animals with better performance in specific environments. Furthermore, it has been shown that combining RNM with genomic information increases the reliability of animal performance predictions in different environments (Oliveira et al., 2018; Mota et al., 2020).

Therefore, to reduce pregnancy losses in Brahman cattle raised in challenging environments, it is proposed to apply genomic RNM that uses environmental variables to describe the G x E in productive and reproductive traits, assessing the effect of the inclusion of genomic information on the breeding values precision and their ability to predict future performance in adverse environments.

Conclusion

Changes in (co)variance component estimates and genetic parameters are evidence of genotypes by environmental interaction that affect the genetic response for pregnancy loss in Brahman cattle under tropical conditions. The accumulated THI influences the pregnancy loss in Brahman cattle and can be used as a weather covariate to select animals with higher environmental adaptability. Using genomic information improved the prediction ability and increased accuracy of reaction norm models.

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