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UNIVERSIDADE ESTADUAL PAULISTA – UNESP

CÂMPUS DE JABOTICABAL

PREDICTION ABILITY OF CUSTOMIZED SNP ARRAYS WITH DIFFERENT DENSITIES USING THE SINGLE-STEP GENOMIC BLUP METHOD IN A BEEF CATTLE POPULATION

Juan Diego Rodríguez Neira

Zootecnista

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TÍTULO DA TESE: PREDICTION ABILITY OF CUSTOMIZED SNP ARRAYS WITH DIFFERENT DENSITIES USING THE SINGLE-STEP GENOMIC BLUP METHOD IN A BEEF CATTLE POPULATION

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Jaboticabal, 15 de dezembro de 2021

DADOS CURRICULARES DO AUTOR

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SUMMARY

HABILIDADE DE PREDIÇÃO DE PAINÉIS DE SNP CUSTOMIZADOS COM DIFERENTES DENSIDADES USANDO O MÉTODO DE PASSO ÚNICO GENÔMICO BLUP EM UMA POPULAÇÃO DE GADO DE CORTE

RESUMO – A implementação da seleção genômica (SG) nos programas de melhoramento de bovinos de corte no Brasil tem sido suportado por o incremento do progresso genético das populações de bovinos Nelore. No entanto, um desafio de custo-benefício surge com base na quantidade e qualidade dos marcadores SNPs usados para predições acuradas dos valores genômicos (GEBVs). Portanto, o objetivo deste estudo é avaliar a habilidade de predição de marcadores SNPs em dados simulados e reais sobre características de alta e baixa herdabilidade por meio do método de passo único GBLUP, empregando painéis customizados de baixa e moderada densidade. No capítulo 2, oito réplicas de 18.000 animais genotipados foram simulados com painéis de 335k SNPs, dos quais 6.000 foram a população de validação para predizer os GEBVs. Critérios de alta (H-I) e baixa (L-I) informatividade além da localização equidistante (E-D) dos marcadores foram usados para customizar quatro densidades (35k, 16k, 4k e 2k) de painéis. Assim, em conjunto com o painel de 335k SNPs, treze cenários foram avaliados. Adicionalmente, os painéis customizados foram imputados a 335k SNPs e a acurácia da imputação foi estimada. Em geral, pelo menos 5% dos marcadores H-I ou E-D do painel de 335k SNPs alcançaram predições genômicas confiáveis e imputações acuradas. No capítulo 3, registros de 945 animais genotipados com alta densidade (HD) nascidos entre 1974 e 2018 para peso aos 210 (W210) e 450 (W450) dias de idade e o efeito materno para W210 (MW210) foram usados, dos quais 247 animais nascido despois do 2008 foram a população de validação. Cinco painéis de diferentes densidades (40k, 20k, 10k, 5k e 2k) foram customizados pelos critérios H-I e E-D e o painel HD foi usado como o cenário desejável. As predições dos GEBVs e a acurácia BIF (Beef Improvement Federation) foram obtidas com os programas da família BLUPF90. O método de regressão linear foi usado para avaliar a habilidade de predição, inflação e viés dos GEBVs para cada painel customizado. Uma superestimação da acurácia BIF foi observada quando diminuiu a densidade dos painéis. Para todas as características, a habilidade de predição apresentou aumento com altas densidades e foi similar para painéis customizados com densidades superiores a 10k SNPs, mesmo assim, a inflação foi baixa com altas densidades e o MW210 presentou as maiores inflações. O viés foi susceptível a superestimação dos GEBVs quando a densidade dos painéis customizados diminuiu. Em geral, a acurácia BIF e o nível do viés foram sensíveis aos painéis customizados de baixa densidade enquanto a habilidade de predição com pelo menos 5.000 H-I ou E-D

marcadores a partir do painel HD, apresentou predições acuradas e com menos viés. Esses resultados indicaram que o desenvolvimento de painéis customizados de baixa densidade poderia ser uma abordagem viável para SG utilizando o método ssGBLUP e com melhor custo-benefício nos programas de melhoramento de bovinos de corte.

Palavras-chave: Acurácia da predição, simulação, Acurácia da imputação, seleção genômica, bovinos de corte, inflação, MAF, peso aos 210 dias, peso aos 450 dias.

PREDICTION ABILITY OF CUSTOMIZED SNP ARRAYS WITH DIFFERENT DENSITIES USING THE SINGLE-STEP GENOMIC BLUP METHOD IN A BEEF CATTLE POPULATION

ABSTRACT - The implementation of genomic selection (GS) in Brazilian beef cattle breeding programs has been supported by the increase in genetic progress of Nellore cattle populations. However, from the fundamental principles of GS, a cost-benefit challenge arises based on the quantity and quality of SNP markers used for the prediction of reliable genomic values (GEBVs). Therefore, the objective of this study is to evaluate the prediction ability of SNP markers in simulated and real data on high and low heritability traits through of single-step GBLUP method, employing lower and moderate density customized arrays. In chapter 2, eight replicates of 18,000 genotyped animals were simulated with 335k SNPs array, of which 6,000 were the validation population to predict GEBVs. Four densities of customized SNPs arrays (35k, 16k, 4k and 2k) created from high (H-I) and low (L-I) informativeness and evenly distanced SNP markers (E-D) of SNPs, were the criteria to marker select. Thus, in conjunction with the 335k SNPs array, thirteen scenarios were evaluated. In addition, the customized arrays were imputed to 335k SNPs and the accuracy of imputation was estimated. Overall, at least 5% H-I or E-D markers from 335k array achieved reliable genomic predictions and accurate imputations. In chapter 3, records of 945 genotyped animal with high-density (HD) born between 1974 and 2018 for weight to 210 (W210) and 450 (W450) days of age and maternal effect of W210 (MW210) were used, of which 247 animals born after 2008 were the validation population. Five density arrays were customized (40k, 20k, 10k, 5k and 2k) by H-I and E-D criteria and the HD array was used as desirable scenario. The GEBV predictions and accuracy BIF (beef improvement federation) were obtained with BLUPF90 family programs. The linear regression method was used to evaluate the prediction ability, inflation, and bias of GEBV of each customized array. An overestimation of BIF accuracy was observed when the density arrays decreased. For all traits, the prediction ability increased with higher densities and was similar for customized arrays above 10k, as well, the inflation was low with higher densities and the MW210 effect displayed the higher inflations. The bias was susceptible to overestimation of GEBVs when the density customized arrays decrease. Overall, the BIF accuracy and the level of bias were sensible to of low-density customized arrays while the prediction ability at least 5,000 H-I or E-D markers from HD array, displayed accurate and less biased predictions. These results indicated that the development of low-density customized arrays might be an approach feasible to GS under ssGBLUP method and cost-effective in beef cattle breeding programs.

Keywords: Prediction accuracy, simulation, accuracy of imputation, genomic selection, beef cattle, inflation, MAF, weight at 210 days, weight at 450 days.

CHAPTER 1 – General considerations

INTRODUCTION

In the middle of the last century, Brazil begun to incursionary in the selection of representative animals of the Nellore breed, with the importation of the founders' individuals of the current population (Ferreira de Oliveira et al., 2002) and, after three decades the first Nellore breeding programs was structured (Ferraz and Fries, 2004; Fries and Ferraz, 2006). The genetic evaluation in Brazil involved independent groups formed by universities, research institutes, consultant geneticists and quantitative geneticist service companies (Berry et al., 2016; Albuquerque et al., 2017). These programs reflect differences in the strategies to improvement based in the propped conditions of each group, thus is expected variations and diversity in the current populations of Nellore cattle (Carvalheiro, 2014). However, the high correlation between growth traits and the potential of mature of individuals achieved a common interest among the genetic programs to be included in genetic evaluations for selection purposes (Laureano et al., 2011). Subsequently, the progress of Nellore genetic evaluations from structured programs allowed the incorporation of complex traits as female fertility and the inclusion maternal effects (Lôbo et al., 2010).

The advances in molecular technologies and the employed of them in genetic evaluations impacted strongly the genetic progress of cattle populations. In 2010, Brazil began with the genomic evaluation of Nellore and achieved a notable increase of science in the application of genomic technologies in Brazilian beef breeding programs has occurred (Berry et al., 2016). The inclusion of genome-wide association (GWAS) procedure to identify genomic regions associated with economic importance traits, increased the accuracy of breeding values and the genetic progress (Albuquerque et al., 2017). Additionally, the genomic selection (GS) approach through of prediction of the breeding values of young animals or animals without phenotype information, based on GWAS performed on training populations to estimate marker effects (Montaldo et al., 2012) helped to

complement and accelerate the genetic evaluations and obtain reliable genetic values (Carvalheiro, 2014).

Since early decades of implementation of the genetic improvement programs, only the animal's own records and records of its closest relatives and eventually all relatives were considered (VanRaden, 2020). However, in order to improve the genetic progress of the traits of economic importance, Smith, (1967), claim that consider the information coming from DNA could improvement the estimates of breeding values. Around 80's, Stam, (1980), derivate and demonstrated the distribution of the genome fraction identical by descending and Soller and Beckmann, (1983), proposed structure a genomic relationship more precise employing DNA markers that subsequently improvement the parentage determination and identification of QTL.

In 2001, (Meuwissen et al., 2001), introduced the genomic selection approach that use the genomic information through of inclusion of arrays composted by molecular markers of single-nucleotide polymorphism (SNP) distributed into whole genome to predictions of genomic breeding values (GEBVs). The GS allows more parentage control by capture more precise DNA inheritance (VanRaden, 2020), increase accuracy of models, identified higher proportion of additive genetic variances, increase the genetic gain by decrease generational interval and displays advantage on complex traits (VanRaden, 2008). The genomic prediction arises from the estimation of effects for each SNPs include in the analysis (Meuwissen, 2009), through of non-parametric (Meuwissen et al., 2001) and parametric methods (Misztal et al., 2009; VanRaden, 2008). The single-step Genomic BLUP (ssGBLUP) is a parametric method that combines information from genotyped and non-genotyped animals in a unique analysis (Aguilar et al., 2010) and has been relevant to be use in genomic improvement programs by display less bias and improve the accuracy of genomic predictions (Mäntysaari et al., 2020).

The GS through of estimation of marker effects allow estimate the independent chromosome segments (ICS) and knowing the shared alleles of genotyped animals, and indirectly the effective population size (Ne) (Misztal et al.,

2020). Thus, the optimal density of markers to detected QTLs is relate directly with Ne (Lee et al., 2017). The farm animals present a small Ne due that were originated from a narrow genetic basis thus the number of marker and ICS to estimate is lower to obtain accurate genomic predictions (Misztal et al., 2020). In Nellore cattle, few studies have been development to knowing the Ne; however, Cardoso et al. (2018) achieved identified a diverse and structured population from Ne above of 100 when the selection is implemented. Therefore, to achieve accurate predictions in GS, it's possible the use of low and moderate density arrays varying of 10k to 50k SNPs (Georges et al., 2019).

Commonly the large number of arrays to cattle protected by intellectual property and built principally to Taurus cattle are frequently employed in Indicus cattle, being that both species no segregate the same markers (Boddhireddy et al., 2014). The advances in genotyping techniques in the last decade, the genotyping cost decreased approximately 80%, promoting customize and standardize low, as well as, moderate density arrays to carry out in genomic evaluations (VanRaden, 2020).

The use of a lower number of markers for genomic predictions has been showed accurate predictions and slightly different in contrast whit the use of more dense arrays, highlining the LD, MAF and position of SNPS into the genome as criteria to select markers (Barjasteh et al., 2010; Boddhireddy et al., 2014; Su et al., 2012; Wu et al., 2016). Likewise, the incorporation of approaches to imputation of genotypes in genomic predictions from low and moderate customized arrays has displayed reliable imputation with low imputed allele errors (Aliloo et al., 2018; H. Aliloo et al., 2018; Barjasteh et al., 2010; Lopez et al., 2020; Mulder et al., 2012; Shashkova et al., 2021). Therefore, the development of customized arrays is a great chose for genomic predictions due could reduce the cost of implementation of genetic improve programs as well as the use in other approaches such the imputations of genotypes.

CONCLUSION

The results of this study revealed that genomic selection with low-density customized arrays could be feasible and cost-effective in Nellore beef cattle. Therefore, there is an important margin to reduce high or moderate to low-density SNPs arrays without compromising the predictive capacity of the genomic information using the ssGBLUP method. This fact opens the opportunity for indicine beef cattle breeding programs develop *in-silico* SNPs markers arrays for GEBVs predictions, minimizing the number of SNPs to be imputed. At least 10,000 informative SNPs obtained from the Illumina BovineHD BeadChip SNPs are necessary to adequately predict the GEBVs for growth and maternal related traits of young candidates with the ssGBLUP method. Additionally, the criteria to select the SNPs to customize the arrays is non-essential if the markers are properly distributed in the genome and highly informative.

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