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Comparing Machine Learning Algorithms and Linear Model for Detecting Significant SNPs for Genomic Evaluation of Growth Traits in F_2 Chickens

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ABSTRACT

High-density Single Nucleotide Polymorphisms (SNPs) panels are expensive, especially in developing countries. However, methods have been developed to detect critical SNPs from these panels and design low-density chips for genomic evaluation at lower cost. This study aimed to determine the efficiency of Random Forest (RF) and Gradient Boosting Machine (GBM) algorithms, and Linear Model (LM) in identification of SNPs subsets to predict Genomic Estimated Breeding Values (GEBVs) for Body Weights at 6 (BW6) and 9 (BW9) weeks in broiler chickens and compare the predicted GEBVs with those obtained by the 60K SNP panel. The data were collected on 312 F_2 chickens that genotyped with 60K Illumina SNP BeadChip. After applying quality control, the remaining 45,512 SNPs were ranked based on p-values, mean square error percentage, and relative influence, obtained by LM, RF and GBM methods, respectively. Then, subsets of top 400, 1,000, 3,000 and 5,000 SNPs, selected by each method, were employed to construct genomic relationship matrices for the prediction of GEBVs with genomic best linear unbiased prediction model. Results indicated that predicted accuracies by RF and GBM were generally higher than LM. A Subset of 1,000 SNPs selected by RF and GBM algorithms compared to the total SNPs increased accuracy from 0.38 to 0.64 and 0.66 for BW6, and from 0.42 to 0.60 and 0.66 for BW9, respectively. The findings of the present study provide that machine learning methods, especially GBM, can perform better than LM in selecting important SNPs and increasing the accuracy of genomic prediction in broiler chickens.

Keywords: Broilers chickens, Chickens body weight, Genomic prediction, Single nucleotide polymorphisms.

INTRODUCTION

Single Nucleotide Polymorphisms (SNPs) have been widely utilized in biological research, cancer research, parentage testing, mapping of quantitative trait loci, and evaluation of genomic selection due to their effectiveness as genetic markers. High-Density (HD) SNP panels are now accessible for many species due to advancements in high-throughput sequencing technology (Unterseer *et al*., 2014). One of the important factors in using high-density SNPs is the cost, which is a big limiting factor in utilizing it, especially in developing countries (Mrode *et al*., 2018). High-density SNP panels used for genomic evaluations have a large number of SNPs that have little to no effect on the traits and could decrease prediction accuracy (Ye *et al*., 2019). Therefore, various strategies have

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been performed to select SNPs with large effect from high-density SNP chips, such as selecting SNP evenly spaced across the genome (Habier *et al* ., 2009) and based on allelic frequency (Abdollahi *et al*., 2014).

It has been reported that detected subset of SNPs through conventional Genome-Wide Association Study (GWAS) increased the accuracy of genomic selection (Liu *et al*., 2020). On the contrary, Lu *et al*. (2020) indicated that pre-selecting SNPs based on estimates of variance contributed using weighted single-step Genomic Best Linear Unbiased Prediction (ssGBLUP) or p-values using single-SNP GWAS did not increase accuracy of genomic predictions substantially in Japanese flounders. In conventional GWAS, a univariate phenotype is regressed on each SNP independently, due to small number of observations and large number of SNPs and LD between SNPs is not considered. Since SNPs are often correlated via Linkage Disequilibrium (LD), the most significant individual SNPs selected by linear regression may not be an optimal set for creating low-density chips. The undesirable statistical properties of the least squares prediction method for selection of SNPs has also been proposed by Wray *et al*. (2013).

Machine Learning (ML) techniques have been used in GWASs (Mokry *et al*., 2013). In the context of genome-enabled prediction of phenotypes, ML classification procedure was used by Long *et al*. (2007) in selection of SNPs for prediction of mortality traits in poultry. Random Forest (RF) (Breiman, 2001) has been applied to GWASs to identify SNP associated with phenotypes and to map QTL on the genomic regions (Minozzi *et al*., 2014). Gradient Boosting Machine (GBM) is another popular method of ML algorithm that has gained attention recently (Friedman, 2001). Piles *et al*. (2021) showed that, compared to parametric methods, the best prediction quality in terms of accuracy and stability was obtained with the GBM method for selecting SNPs in order to create low-density SNP chips. The RF and GBM algorithms are suitable alternative to other methods used for genomic evaluations at the expense of lower interpretability of results (González-Recio *et al*., 2010) and are the most appealing alternatives to analyze complex traits using dense genomic markers information (González-Recio and Forni, 2011).

Several ML algorithms have been used to detect subsets of important SNPs from high-density SNP chips in pig breeds (Schiavo *et al*., 2020), tropical Brahman cattle (Li *et al*., 2018) and purebred and commercial Korean native chickens (Seo *et al*., 2021). Different results have been reported in these studies either in the size of subsets of SNPs or in the outcomes of the methods. To the best of our knowledge, this approach has not been demonstrated in broiler chickens yet and will serve poultry industry with better insight on utilization of ML techniques in pre-selection of SNPs to enhance the accuracy of genomic selection. Therefore, the present study aimed to evaluate the efficiency of two ML algorithms, namely, RF and GBM, in identifying a subset of SNPs affecting growth traits using a crossbreed chicken population for the genomic selection purpose. Also, we aimed to compare the accuracy of genomic breeding values predicted by subsets of SNPs selected by ML algorithms with conventional GWAS and all available SNP set.

MATERIALS AND METHODS

Experimental Population, Phenotypic and Genotypic Data

A population of F_2 crosses between the fast-growing Arian line (AA) and the slow-growing Urmia Iranian indigenous chickens (NN) was used in this study. The F_1 birds were generated from the mating of AA ♂×NN ♀ and NN ♂×AA ♀ birds and reared for 12 weeks in poultry research farm of Tarbiat Modares University, Tehran, Iran. Then, F_1 males from each reciprocal cross were mated each to 4–8 females from other

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families, and F_2 chickens were produced and raised individually in cages equipped with water nipples and feeders for 12 weeks under the same environmental conditions and ration. Individual weekly weight was collected throughout the growing period. A total of 312 birds from six different hatches were available. For the present study, body weights recorded at 6 (BW6) and 9 (BW9) weeks were used. More information about these traits can be found in Emrani *et al*. (2017). Before implication of ML, a multiple linear regression of observations on sex and hatch was used to adjust the body weight data (Brown and Reverter, 2002).

Genomic DNA was extracted from 312 blood samples using salting out method and stored at -20°C. After extraction, spectrophotometry and agarose gel electrophoresis methods were used to determine the quantity and quality of DNA. These DNA samples were genotyped with the Illumina Chicken 60K SNP BeadChip, in cooperation with Cobb-Vantress Inc., and the Aarhus University, Denmark. Quality control steps were applied to the original data with PLINK 1.9 software (Purcell *et al*., 2007). SNPs with call rate of < 95%, minor allele frequency of < 5%, a Hardy–Weinberg equilibrium test p-value < 1×10^{-6} were deleted (Emrani *et al*., 2017). After quality control, 45,512 of SNPs for twenty-eight autosome chromosomes and 300 birds remained for final analysis.

Methods for Selecting Markers

The linear model for conventional GWAS was as follows:

$$y = 1\mu + Zq + e$$

Where, y= vector of corrected phenotypic values for BW6 and BW9, 1= an n-vector of ones, μ= population mean, q= effect of the marker in the model, which is treated as a fixed regression of observation on genotype, Z= a vector containing genotypes of the marker with 0, 1 and 2 for A_1A_1, A_1A_2 and A_2A_2, respectively, e= vector of random residual effects, assuming $e\sim N(0, I\sigma_e^2)$, where σ_e^2 is the residual variance and I is the identity matrix.

The genetic association tests were conducted using the '--Linear' command in PLINK v1.9 (Purcell *et al*., 2007). The SNPs were selected based on the p-values from GWAS results.

In the RF algorithm, which contains several decision trees, a bootstrap sample of original training data is used to grow each tree. The RF algorithm predicts the outcome by averaging the outputs obtained from all the trees in the forest (Breiman, 2001). When making bootstrap samples to grow each tree, approximately 34 percent of records will not be selected, which is called Out Of Bag (OOB) records. To calculate the importance of each SNP, OOB error was calculated by predicting the outcome of OOB samples via the corresponding tree. Then, the values of each predictor were permuted (shuffled) and prediction error of OOB samples were calculated again. The Mean Square Error Percentage (MSEP) difference between permuted and non-permuted samples (averaged over all the trees in the forest) indicated the importance or predictive ability of that particular predictor. The 'randomForest' package was used to perform this analysis in R software (Breiman, 2013).

In the GBM algorithm, the basic functions are weak learners such as a decision trees. The purpose of the boosting algorithm is to enhance ensemble of weak learners into a strong learner. In this method, a basic learner such as a decision trees are added sequentially to the residuals of the previous tree. Thus, it is expected that, by focusing on the incorrectly predicted data in the previous tree, error rate in the next tree will be lessened and as long as the error rate is decreasing, the boosting algorithm will continue (Friedman, 2001). In the present study, important markers in the GBM method are identified by Relative Influence (RI), which is the average of reduction in MSEP over all the trees when that particular SNP to be split in the data (Friedman, 2001). The 'GBM' package was

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used to perform this algorithm in R software (Greenwell *et al*., 2019). For GBM and RF methods, hyper-parameters tuning performed via nested grid search within a 3-fold cross-validation on the 75 percent randomly selected subset of the data.

Genome-Wide Screening for Top Ranking SNPs

All SNPs were ranked from the most to the least important SNP by criteria values of RF (increase in MSEP), GBM (RI), and LM (P-value) using 'dplyr' package implemented in R (Wickham *et al*., 2023). For the 5,000 number of important SNPs, obtained from LM, RF and GBM, venn diagrams were drawn by the 'VennDiagram' package (Chen and Boutros, 2011). Top 400, 1,000, 3,000, and 5,000 SNPs with the above-mentioned criteria were used to create genomic relationship matrices.

Genomic Estimated Breeding Value

Genomic Estimated Breeding Values (GEBV) were derived using Genomic Best Linear Unbiased Prediction (GBLUP) model. The statistical model of GBLUP is written as follows (Gianola *et al*., 2006):

$$y = \mu + g + e$$

where y is corrected phenotypes, μ is the population mean, g is a vector of random additive genomic values with $g \sim N(0, G\sigma_g^2$, where G is the additive genomic relationship matrix between genotyped individuals and σ_g^2 is the additive genomic variance, and e is the vector of random residual effects with $e \sim N(0, \mathbf{I}\sigma_e^2)$,, where σ_e^2 is the residual variance, and $\mathbf{I}$ is the identity matrix. The additive genomic relationship matrix (G) is constructed as $\frac{ZZ'}{m}$, where Z is the matrix of centered and standardized genotypes for all individuals and m is the number of markers. Kernel Hilbert space regression method was used to implement the GBLUP approach and the genomic heritability in the selected subsets, and all markers were estimated using the Bayesian Generalized Linear Regression (BGLR) package (Pérez-Rodríguez and de Los Campos, 2022) in R software. The Gibbs sampler was run for 50,000 iterations, with a 10,000 burn-in period and a thinning interval of 5 iterations, i.e., 10,000 samples were used for inference.

Cross-Validation for the Accuracy of Genomic Breeding Values

Accuracy of genomic prediction was calculated on 5-fold cross-validation base as follows (Li *et al*., 2018):

$$\text{Accuracy} = \frac{r_{GEBV,phen}}{\sqrt{h^2}}$$

Where, $r_{GEBV,phen}$ is correlation coefficient between the predicted GEBVs of the birds in the test fold and the corrected phenotypes (phen) and h^2 is estimated heritability of the trait.

Unbiasedness of genomic prediction was calculated on 5-fold cross-validation base as follows:

$$b_{GEBV,phen} = r_{GEBV,phen}(S_{phen}/S_{GEBV})$$

Where, $bGEBV, Phen$ is regression coefficient of corrected phenotypes on GEBV that show unbiasedness of the GEBV, $r_{GEBV,phen}$ is correlation coefficient between the predicted GEBVs of the birds in the test fold and the corrected phenotypes, S_{phen} is the standard deviation of corrected phenotypes, and S_{GEBV} is the standard deviation of predicted GEBVs. Finally, the Tukey HSD (Honestly Significant Difference) test was used to compare the significant differences between the best subsets of SNPs, which had the highest increase in genomic prediction accuracy with each other and the all SNPs.

RESULTS AND DISCUSSION

The rank of SNPs from the most to the least important for BW6 and BW9 are

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shown in Figure 1. Based on LM method, the 5,000 pre-selected SNPs had a p-values range from 1.01×10^{-5} to 7.60×10^{-2} and 7.57×10^{-6} to 8.09×10^{-2} for BW6 and BW9, respectively. For RF method, the importance of SNPs changes from positive to negative values. The highest positive value in RF indicates an increase in the MSEP when the SNP is randomly permuted compared to the prediction error before SNP permutation. In this model, 47, 7, and 46% of SNPs for BW6 and 47, 9 and 44% of SNPs for BW9 had positive, zero, and negative effects, respectively. About 5% of

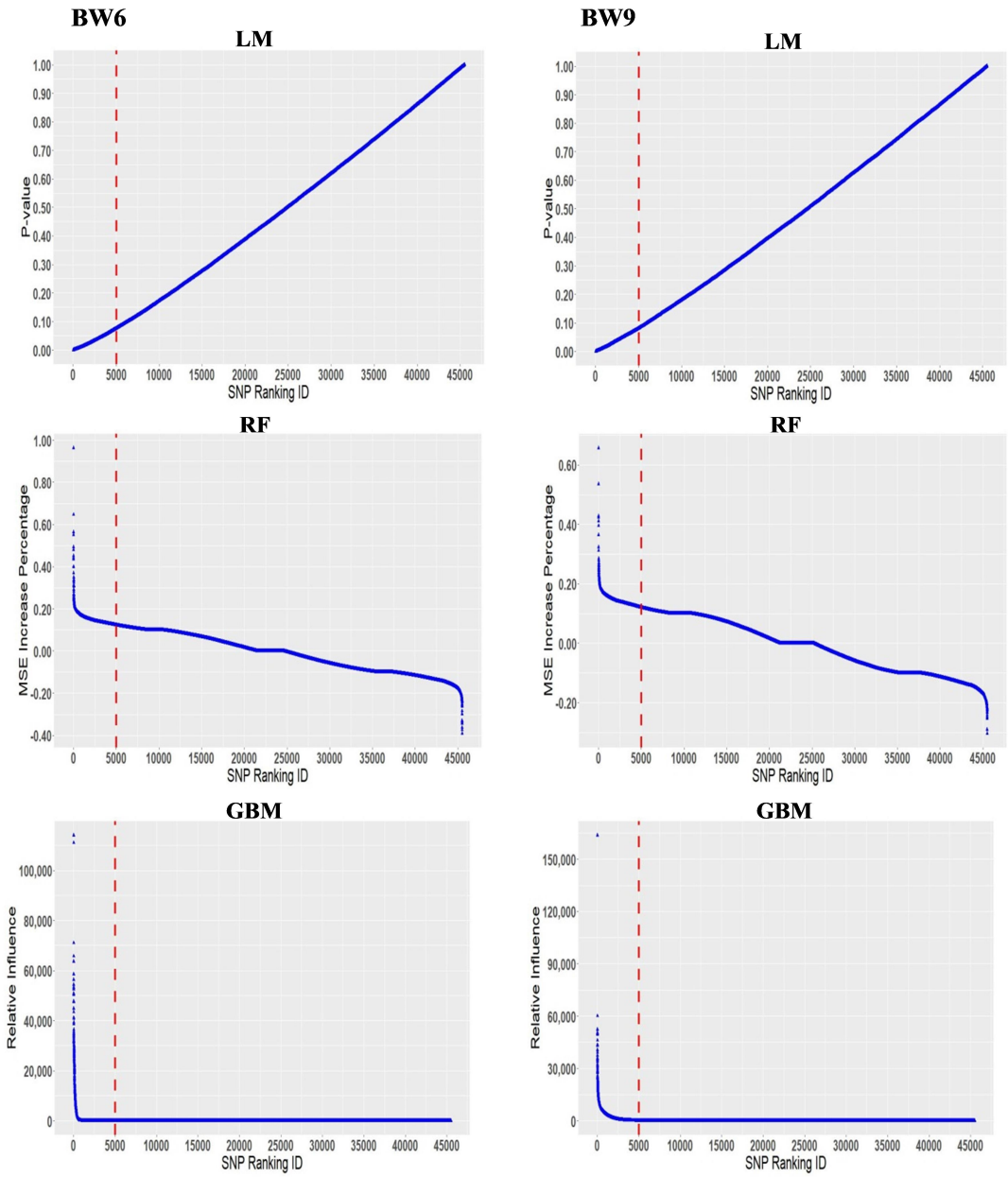

Figure 1. The distribution of ranked SNP for BW6 and BW9 from LM, RF and GBM methods.

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SNPs for BW6 and 2.8% for BW9 (5,000 pre-selected SNPs) had a MSEP increase more than 0.2, respectively. In the GBM method, 26 and 16% of SNPs had larger than zero effect for BW6 and BW9, respectively. In 5,000 pre-selected SNPs with GBM method, none of the SNPs had a zero RI, however, 65.3% of SNPs for BW6 had a RI less than one and close to zero. For BW9, the amount of RI for last SNP of the 5,000 pre-selected SNPs was 58.1, and 52.52% of SNPs had a RI less than 1,000. Based on this method, about 3.6% of SNPs for BW6 and 5.1% for BW9 (5,000 pre-selected SNPs) had a RI more than 10000.

For the top 5,000 SNPs, the total number of common SNPs between the three methods are shown by Venn diagrams in Figure 2. A total of 924 and 1100 SNPs was common across three methods for BW6 and BW9, respectively. The results indicated that the similarity between RF and GBM method was higher than that observed between LM with RF and GBM. The estimates of genomic heritability for body weight traits using the genomic relationships matrix consisting of all or subsets of selected SNPs for three methods are presented in Figure 3. Genomic heritability for BW6 and BW9 consisting of all SNPs was estimated to be 0.28 and 0.30, respectively. These estimates were consistent with the studies of Demeure *et al*. (2013) and Abdollahi *et al*. (2014), who fitted all SNPs and reported a moderate estimates of 0.22 and 0.30, respectively, for growth traits in chickens. Genomic heritability estimation was increased when the matrix of genomic relationships was constructed by subsets of SNPs pre-selected by any of the three proposed methods in the present study. Pre-selected subsets of SNPs by GBM showed the highest rate of increase in genomic heritability in comparison with LM and RF.

The highest estimates of heritability for BW6 with pre-selected SNPs by LM, RF, and GBM methods were, 0.42, 0.39 and 0.48, respectively, in subsets of 5000 SNPs (in LM) and 1,000 SNPs (in RF and GBM). For BW9, the highest heritability was 0.43, 0.46 and 0.58 in subsets of 5,000 SNPs (in LM), 1,000 SNPs (in RF) and 3,000 SNPs (in GBM), respectively. In comparison to all 45,512 SNPs, the heritability estimates were increased from 0.28 to 0.35 and from 0.30 to 0.46 through preselection of 5,000 SNPs using LM model for BW6 and BW9, respectively. By using 1,000 pre-selected SNPs, the increases in the heritability estimates were ranged from 0.28 to 0.37 for BW6 and 0.30 to 0.43 for BW9 with RF model and from 0.28 to 0.48 for BW6 and 0.30 to 0.54 for BW9 with GBM model. Ren *et al*. (2022) indicated that high-density SNP

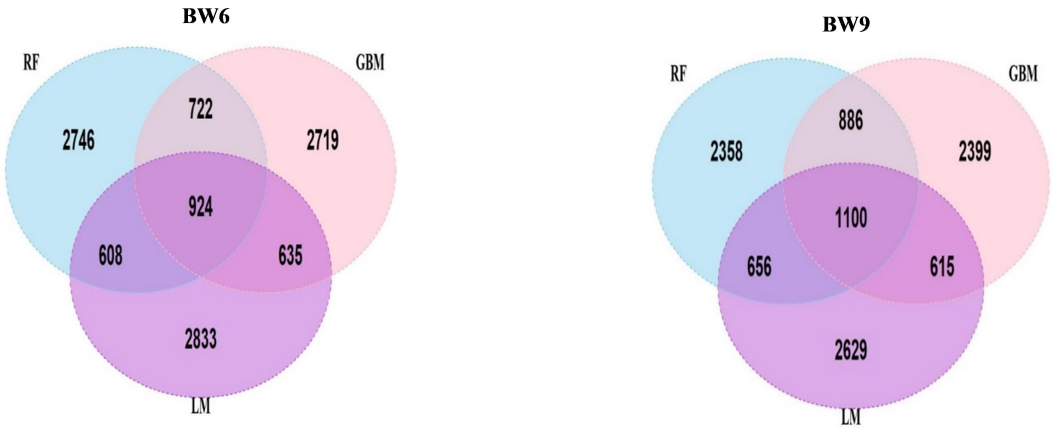

Figure 2. Venn diagram showing the 5,000 number of important SNPs from RF, GBM, and LM methods. Circle represents the number of identified SNPs and the intersection areas represent the number of overlapping SNPs.

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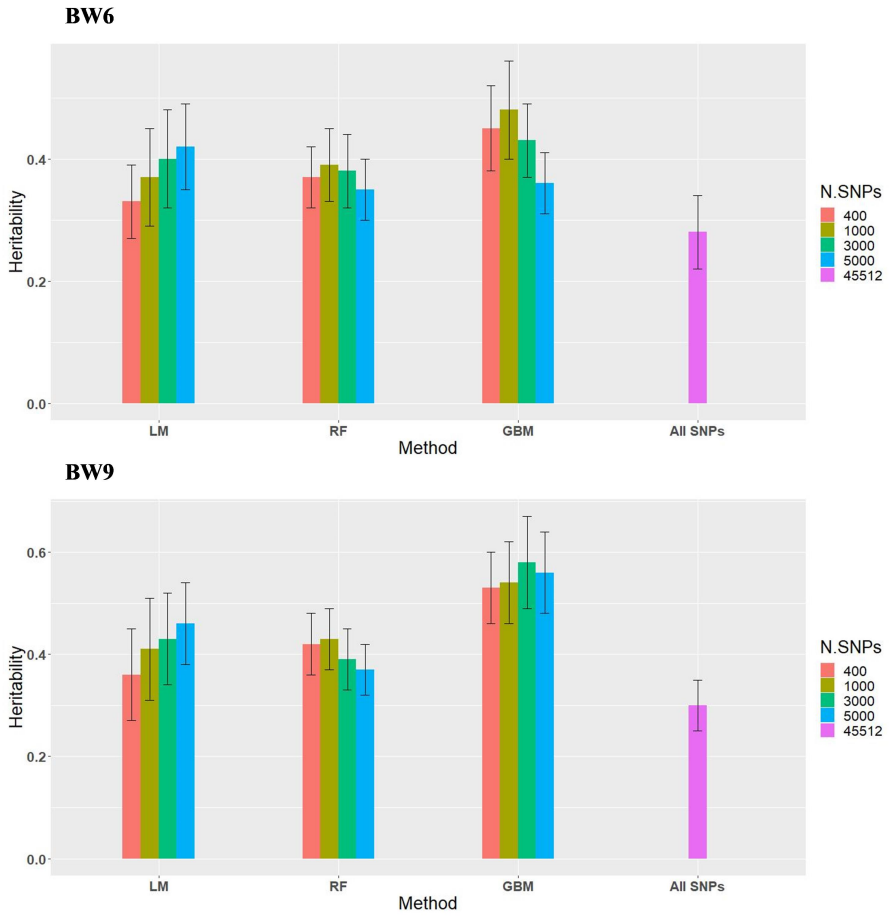

Figure 3. Genomic heritability of all SNPs for BW6 and BW9 from LM, RF and GBM methods.

data provide more information for genomic evaluation compared to medium-density SNP data, but they do not confer any advantage for heritability estimation. Literature studies reported that the estimates of genomic heritability were very sensitive to differences in LD between SNPs, suggesting that genomic heritability is overestimated in region with high LD and underestimated in region with low LD (Speed *et al*., 2012). The stronger LD of the remaining SNPs and the removal of the imperfect LD between the causal mutations may improve the genomic relationships between individuals and increase the heritability of the trait (Abdollahi *et al*., 2014; Ye *et al*., 2019). Abdollahi *et al*. (2014) estimated genomic heritability for body weight at 6 weeks in broilers chickens using the genomic relationship matrix consisting of all SNPs and a subset of selected SNPs and reported that the genomic heritability with the selected SNP (0.59) is expected to be overestimated in comparison to all SNPs (0.30). However, the subsets of SNPs could increase the GEBV accuracy. The increase in the accuracy of GEBV has been reported by Luo *et al*, (2021) who proposed a strategy for genomic selection in aquaculture using a subset of markers selected by the p-value of GWAS and indicated that the prediction accuracy of a subset of top SNPs was higher than using total SNPs. Li *et al*. (2018) reported that ML

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methods could consider complex and nonlinear relationships. Therefore, they can produce a smaller error variance and increase genetic variance and heritability. These authors estimated the heritability of a subset of 3,000 SNPs with GBM method to be higher than all of 38,082 SNPs for body weight in Brahman cattle.

Figures 4 and 5 show the mean accuracy and regression coefficient (as a measurement of unbiasedness) of genomic breeding value for BW6 and BW9 traits using SNP subsets in a 5-fold cross-validation scheme, respectively. Accuracy of genomic prediction for BW6 and BW9 using all SNPs was estimated to be 0.38 and 0.42, respectively, which was lower than the genomic prediction accuracy obtained from the subsets of selected SNPs (400, 1,000, 3,000 and 5,000 selected with three methods). Average accuracy of genomic breeding value (±standard error) with top 400, 1,000, 3,000, and 5,000 SNP subsets selected by LM, RF and GBM methods were estimated to be 0.56 (±0.02), 0.61 (±0.04), 0.52 (±0.02) and 0.47 (±0.02) for BW6, and 0.58 (±0.02), 0.61 (±0.02), 0.55 (±0.02) and 0.51 (±0.01) for BW9, respectively. Mean regression coefficient of genomic prediction on phenotype using total SNPs for BW6 and BW9 were estimated to be 0.76 and 0.90, respectively. With top 400, 1,000, 3,000, and 5,000 SNP subsets selected by the three methods, mean regression coefficient (± standard error) were 0.94 (±0.05), 0.97 (±0.04), 0.94 (±0.02) and 0.95 (± 0.01) for

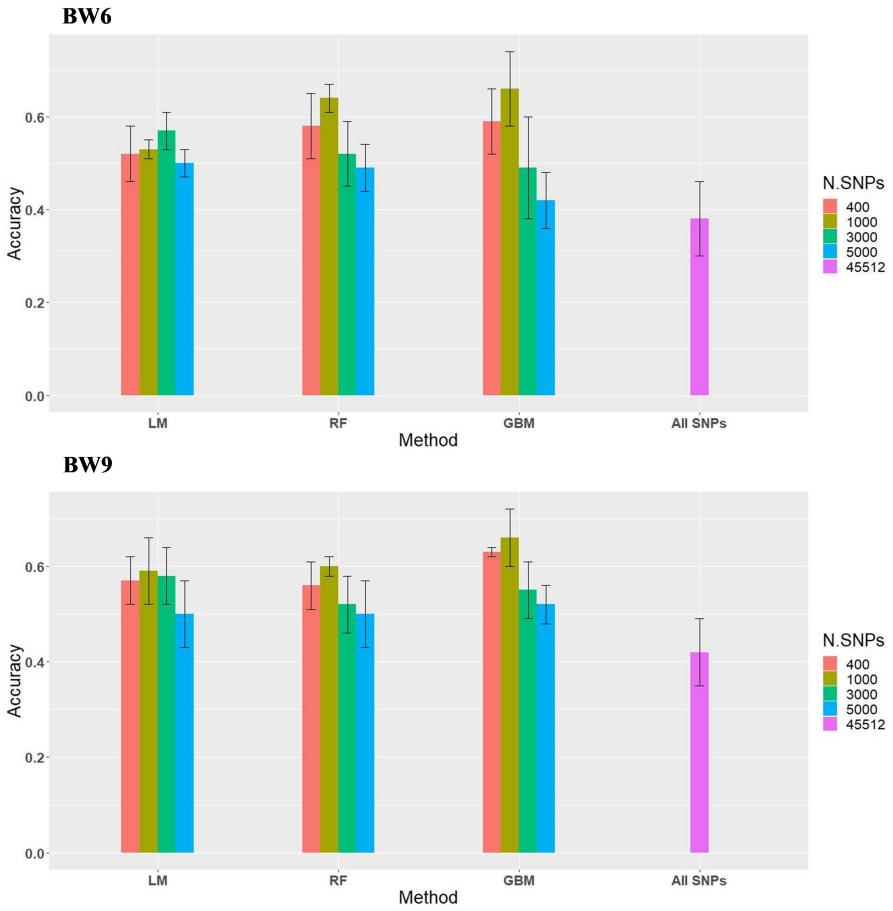

Figure 4. Accuracy of genomic prediction of all SNPs and different subsets of using a 5-fold cross-validation approach for BW6 and BW9 from LM, RF and GBM methods.

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BW6, and 1.06 (±0.01), 1.03 (±0.02), 1.05 (±0.04) and 1.06 (±0.05) for BW9, respectively. The best average accuracy of genomic breeding value and regression coefficient provided by 1,000 SNP subset was 0.61 (±0.04) and 0.97 (±0.04) for BW6 and 0.61 (±0.02) and 1.03 (±0.02) for BW9, respectively. In the study of Liu *et al*. (2020), the highest accuracy of genomic breeding value by a subset of 817 SNPs selected from high-density SNP panels was 0.60 for body weight at the age of 12 weeks, and by a subset of 354 SNPs, it was 0.45 for feed conversion ratio in broilers. Furthermore, several studies indicated a direct relationship between effective population size and the accuracy of GEBVs. The significant impact of smaller effective population size on the prediction accuracy of GBLUP was revealed by Daetwyler *et al*. (2010), which is a reflection of strong linkage disequilibrium between variants due to close genetic relatedness between individuals (Jang *et al*., 2023; Calus *et al*., 2008).

Significant differences between genomic prediction accuracy of the best subsets of SNPs (which had the highest increase in genomic prediction accuracy) with each other and all SNPs are presented in Table 1. The results showed that, in the present study, 1,000 SNPs selected by ML algorithms was the best pre-selected SNPs for estimating genomic breeding value in broiler chickens for body weight traits. In BW6, there was no significant difference between RF and GBM algorithms in the best subsets (1,000 SNPs) of the selected SNPs, and they were superior to linear model with the best subset (3,000 SNPs). However, in BW9, GBM was superior to the other methods. These findings are consistent with the results of Kriaridou *et al*. (2020), who used different subsets of SNPs in four aquaculture datasets, ranging from 100 to 9,000 SNPs, and observed that SNP densities between 1,000 and 2000 SNPs had a very similar accuracy of genomic evaluation to high-density genotyping. Ye *et al*. (2019) used selected markers from whole-genome sequencing data based on the p-value obtained from GWAS, and showed that the use of pre-selected markers for most traits did not increase the genomic prediction accuracy in broilers and even increased the bias. One of the possible reasons is the difficulty of discovering causative variants using GWAS due to the large number of variants (600k) and high LD between variants. On the contrary, Li *et al*. (2018) indicated an increase in the accuracy of genomic prediction by selecting a subset of significant SNPs from high-density SNP panel (651,253) using RF method. One of the advantages of ML method is its ability to analyze data with a high dimension, however, factors such as linkage disequilibrium and minor allele frequency can affect the performance of ML algorithms for selecting important markers (Zhou and Troyanskaya, 2015). Decision trees are known to have low bias and high variance in prediction, but RF overcomes this issue by forming many trees on each bootstrap sample, to minimize prediction errors by lowering the variance of prediction. In the GBM, both bias and variance are expected to be reduced due to the boosting process which is the assembling multiple weak learners sequentially and using the weighted average of each tree for prediction (Li *et al*., 2018). Hence ML can be superior to linear models for selecting SNPs from high-density SNP panels.

Literature results on improving accurate prediction of breeding values using high-density SNP genotype, even with implementation of a specific model, are inconsistent. Several studies indicated that selecting markers from high-density genomic data can result in a small improvement in genomic accuracy (Lopez *et al*., 2020). Our strategy for screening SNPs in two growth traits improved estimation of genomic breeding value accuracies. A subset of 1,000 SNPs selected by the RF and GBM methods compared to the total SNPs increased the accuracy of genomic prediction from 0.38 to 0.64 and 0.66 for BW6 and from 0.42 to 0.60 and 0.66 for

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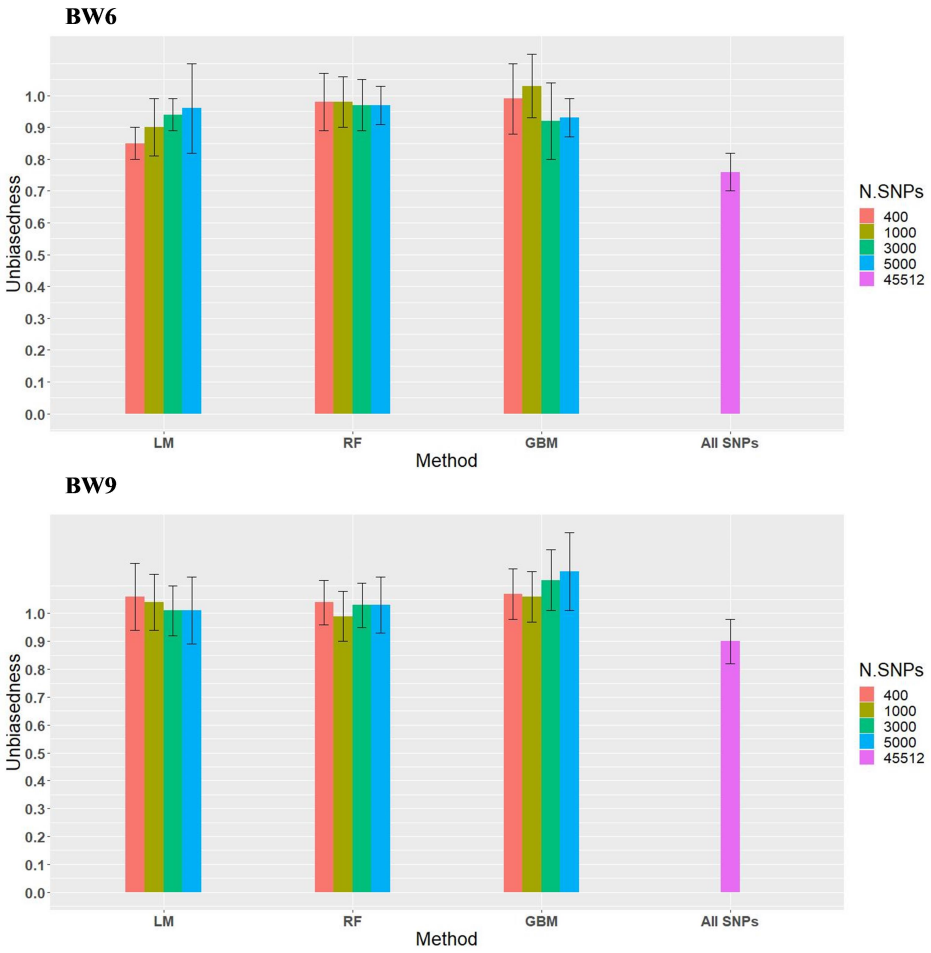

Figure 5. Unbiasedness of genomic prediction of all SNPs, and deferent subsets of using a 5-fold cross-validation approach for BW6 and BW9 from LM, RF and GBM methods.

Table 1. The Tukey HSD test for accuracy of genomic prediction for body weights using pre-selected markers with the best subsets of SNPs.

Method	BW6	BW9
All SNP	0.38[a]	0.42[a]
LM1,000	0.53[b]	0.59[b]
LM3,000	0.57[c]	0.58[bc]
RF400	0.58[c]	0.56[c]
RF1,000	0.64[d]	0.60[b]
GBM400	0.59[c]	0.62[d]
GBM1,000	0.66[d]	0.66[e]

BW6= 6 weeks Body Weight; BW9= 9 weeks Body Weight; LM= Linear Model; RF = Random Forests; GBM= Gradient Boosting Machine.

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BW9, respectively. Liu *et al*. (2020) improved genomic prediction accuracy for body weight traits in broiler chickens by selecting a subsets of SNPs based on p-values obtained from GWAS, revealing that high prediction accuracy for growth traits may be achieved even with a small number of markers. SNPs that are not close to causal mutations may have a negative impact on genomic prediction. Also, many SNPs may not tag any causative mutations when the number of markers is too large. Therefore, if only effective SNPs that tag any causative mutations are included in the model, the ability of the model to predict genomic breeding value may be increased and the model error is decreased by removing the unrelated markers. Druet *et al*. (2014) showed that the accuracy of genomic prediction depends largely on the coverage of key genes affecting the target traits by genotyping platforms.

CONCLUSIONS

The genomic selection has become one of the main techniques for animal breeding programs. High costs of genotyping has limited the use of genomic selection in poultry due to the large number of selection candidate, especially in developing countries. Therefore, selecting effective SNPs is useful in designing low-density panels that could provide broad potential and applicability in genomic evaluation. In the present study, the accuracy of GEBV for BW6 and BW9 obtained from a subset of pre-selected 1,000 SNPs by RF and GBM performed better than the subset selected by LM, indicating that ML algorithms can be used as a selection tools to find significant markers for designing and developing low-density SNP marker panels. However, due to the small population size of the current study, further studies with more data, different methods, and a wide range of different SNP subsets are needed to find optimum and reliable set of subsets.

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مقایسه الگوریتم‌های یادگیری ماشین در شناسایی SNP های تاثیرگذار برای ارزیابی ژنومی صفات رشد در جوجه های F_2

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چکیده

استفاد از تراشه‌های چندشکلی‌های تک‌نوکلئوتیدی (SNP) با چگالی بالا به‌خصوص در کشورهای درحال توسعه بسیار هزینه‌بر هستند، اما روش‌هایی برای شناسایی SNPهای تاثیرگذار از این تراشه‌ها و طراحی تراشه‌های با چگالی کم برای ارزیابی ژنومی با هزینه کمتر توسعه یافته است. هدف از مطالعه حاضر، تعیین کارآیی الگوریتم‌های جنگل تصادفی (RF)، گرادیان بوستینگ (GBM) و مدل خطی (LM) در شناسایی زیرمجموعه‌های SNPها از یک تراشهK ۶۰ برای پیش‌بینی ارزش‌های اصلاحی و ژنومی (GEBVs) وزن بدن در سن ۶ (BW6) و ۹ (BW9) هفتگی جوجه‌های گوشتی و مقایسه GEBVs پیش بینی شده از زیر مجموعه‌ها با کل SNPهای تراشه ۶۰K است. داده‌های ۳۱۲ جوجه F_2 جمع‌آوری شده با تراشه 60K ایلومینا تعیین ژنوتیپ شدند. پس از اعمال کنترل کیفیت، ٤٥٥١٢ SNPهای باقیمانده براساس مقادیرp (p-values)، افزایش درصد خطای میانگین (increase in mean square error percentage) و تأثیر نسبی (relative influence) به‌دست‌آمده به ترتیب از روش‌های LM، RF و GBM رتبه‌بندی شدند. سپس زیرمجموعه‌هایی از ۴۰۰، ۱۰۰۰، ۳۰۰۰ و ۵۰۰۰ SNP برتر به دست آمده از هر روش برای ایجاد ماتریس‌های روابط ژنومی برای پیش‌بینی GEBVs با روش بهترین پیش بینی نااریب خطی ژنومی استفاده شدند. نتایج نشان داد که دقت GEBVهای پیش‌بینی شده توسط RF و GBM به طور کلی بیشتر از مدل خطی بود. زیر مجموعه‌ای از ۱۰۰۰ SNP انتخاب شده توسط الگوریتم‌های RF و GBM در مقایسه با کل SNPها، دقت GEBVها را به ترتیب از ۰/۳۸ به ۰/۶۴ و ۰/۶۶ برای BW6 و از ۰/۴۲ به ۰/۶۰ و ۰/۶۶ برای BW9 افزایش داد. یافته‌های مطالعه حاضر نشان داد که روش‌های یادگیری ماشین، به‌ویژه GBM، می‌توانند بهتر از روش خطی معمولی در انتخاب SNPهای مهم عمل کنند و دقت پیش‌بینی ژنومی را در جوجه‌های گوشتی افزایش دهند.

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