J. Agric. Sci. Technol. (2024) Vol. 26 (2): 299-312

Genomic Evaluation of Average Daily Gain Traits in a Mixture of Arian Line and Urmia Iranian Native Chickens

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ABSTRACT

The aims of this investigation were to compare the accuracy and bias of prediction of Estimated Breeding Values (EBV) for Average Daily Gain (ADG) at 2-4 weeks old by employing pedigree-based BLUP and single-step Genomic BLUP (ssGBLUP) techniques. Additionally, the study aimed to identify the optimal minor allele frequencies (MAF) threshold for pre-selecting SNPs for genetic prediction. The present investigation utilized a total of 488 F2 broiler chickens, which were derived from the crossbreeding of fast-growing Arian chickens and slow-growing native chickens from Urmia, Iran. These chickens were between 2-4 weeks old at the time of the study. Samples were genotyped using the Illumina 60K chicken Beadchip. In order to examine the impact of MAF on prediction accuracy, a total of 48,379 quality-controlled SNPs were categorized into five subgroups based on their MAF values: 0.05-0.1, 0.1-0.2, 0.2-0.3, 0.3-0.4, and 0.4-0.5. The findings substantiated the dominance of ssGBLUP over conventional BLUP techniques. The average accuracy of GP improved by 1.96, 3.87, and 2.12% using ssGBLUP compared to BLUP method for ADG at 2-4 weeks of age, respectively. Using a specific MAF bin and a subset of SNPs based on age group significantly enhanced the accuracy of genomic prediction for ADG traits. Current results highlighted that the pre-selection of SNPs based on allele frequency may provide a reasonable compromise between accuracy of results, number of independent variables to be considered and computing requirements.

Keywords: BLUP, Estimated breeding value, Minor allele frequencies, SNP, ssGBLUP.

INTRODUCTION

The breeding program faces a significant constraint in the form of uncertainty surrounding the actual genetic value of breeding animals. Consequently, investments in breeding programs are frequently directed towards trait measurement, genetic evaluation methodology, and technologies aimed at enhancing reproductive performance. By ensuring a reliable measurement system and employing a more accurate genetic evaluation methodology, it becomes possible to effectively identify genetically superior animals, thereby enabling more accurate selection and ultimately achieving higher genetic gain (Goddard and Hayes, 2007). The availability of high-density SNP panel and the implementation of Genomic Selection (GS) present an exceptional opportunity to unravel the underlying genetic factors of complex traits. This is particularly advantageous for traits that are challenging or costly to measure, as well as those with low heritability (Meuwissen *et al*., 2001). Various studies have utilized the single-step Genomic Best Linear Unbiased Prediction (ssGBLUP) method to Estimate

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[DOI: 10.22034/JAST.26.2.299]

Genomic Breeding Values (GEBV) for livestock (Salek Ardestani *et al*., 2021; Legarra *et al*., 2009). By combining the pedigree-based relationship matrix (A) with the Genomic relationship matrix (G) into a Hybrid matrix (H), ssGBLUP enhances the accuracy and minimizes the prediction bias of GEBVs compared to multi-step genomic predictions (Christensen *et al*., 2012; Simeone *et al*., 2012; Li *et al*., 2014; Song *et al*., 2017).

In theory, the probability of finding Linkage Disequilibrium (LD) between Single Nucleotide Polymorphisms (SNPs) and Quantitative Trait Loci (QTL) is enhanced with the use of higher density SNP panels (Meuwissen *et al*., 2016). Nevertheless, the utilization of High Density (HD) SNP panels for constructing a G matrix has not resulted in substantial enhancements in the accuracy of the estimates (Misztal *et al*., 2013). Using a high density SNP panel can result in a significant statistical and computational problem. Additionally, the expense of genotyping animals with medium to high density SNP panels can be a burden in numerous livestock and poultry breeding programs. Therefore, employing preselection and utilizing a subset of SNPs may offer a practical solution that balances result accuracy, the number of independent variables to be taken into account, computing demands, and genotyping expenses (Meuwissen and Goddard, 2010; Druet *et al*., 2014).

Although Average Daily Gain (ADG) is one of the main objective traits in poultry breeding due to their economic implications, the best age for conducting genomic evaluation for ADG has not been well determined. In the current study, we aimed to predict Genomic Breeding Values (GEBV) using ssGBLUP methodology for average daily gain at 2-4 weeks of age on a set of 488 F_2 broiler chicken by using whole SNPs data and 5 different subsets of SNPs based on different MAF bins (0.05-0.1, 0.1-0.2, 0.2-0.3, 0.3-0.4 and 0.4-0.5). Also, GEBVs were compared with BVs estimated from a traditional BLUP method.

MATERIALS AND METHODS

Experimental Population

To investigate ADG traits at the age of 2-4 weeks, the F_1 population was generated by applying reciprocal crosses between a commercial fast-growing broiler strain (Arian line, **A**) and a slow-growing indigenous population (Urmia Iranian native chickens, **N**). Each F_1 male, resulted from a reciprocal cross and, mated with four to eight females from the other families. Finally, 488 F_2 chickens from eight half-sib families were generated in five different hatches. Day-old F2 chickens were initially weighed and raised on the floor for a duration of 7 days, with continuous exposure to 24-hour lighting and a brooding temperature of 33°C. However, on the 7th day, the temperature was reduced to 30°C. Subsequently, on the 8th day, the birds were weighed again and transferred to individual cages with a temperature of 30°C. Over time, the temperature gradually decreased until it reached a final temperature of 22°C. Additionally, throughout the entire experimental period, the chickens were subjected to a light and dark cycle of 22 and 2 hours, respectively.

Genotyping and Population S tructure

DNA was extracted from 312 blood samples by the standard salting-out procedure. All samples were genotyped at Aarhus University, Denmark, using the Illumina Chicken 60K BeadChip provided by Cobb Vantress. Quality control was performed by using PLINK (v1.9) (Chang *et al*., 2015; Purcell *et al*., 2007). SNPs that had a Minor Allele Frequency (MAF) below 5% and a call rate below 95% were eliminated. Additionally, a Hardy-Weinberg equilibrium threshold of 1×10^{-6} was applied. Furthermore, samples with a high rate of

[DOI: 10.22034/JAST.26.2.299]

missing genotypes (< 99.9%) were excluded. Following the quality control process, the final dataset consisted of 48,379 SNPs and 308 birds, comprising 170 males and 138 females. Numbers of SNPs before and after quality control, as well as the average distance between adjacent SNPs on each chromosome, determined using synbreed (Wimmer *et al*., 2012), are shown in Table 1. The normality of the data after quality control was assessed and confirmed using a QQ-plot in R. In order to examine the correlation between allele frequencies and predictive abilities, a total of 48,379 SNPs were divided into 5 subsets based on different MAF bins. These subsets included 6,731 SNPs in the 0.05-0.1 range, 8,884 SNPs in the 0.1-0.2 range, 10,148 SNPs in the 0.2-0.3 range, 11,128 SNPs in the 0.3-0.4 range, and 11,488 SNPs in the 0.4-0.5 range. The software tools PLINK (v1.09) (Purcell *et al*., 2007) and GCTA (Yang *et al*., 2013) were utilized for this analysis. The population structure was assessed through Multi-Dimensional Scaling (MDS) analysis using PLINK (v1.09) (Chang *et al*., 2015). To obtain independent SNPs for all autosomes, the independence-pairwise option was employed with a window size of 30 SNPs, a step of five SNPs, and an r^2 threshold of 0.2, as recommended by Wang *et al*. (2009). Next, the pairwise Identity-By-State (IBS) relationship between all individuals was estimated using independent SNPs, as described by Liu *et al*. (2015). The MDS components were then obtained by utilizing the MDS-plot option, which was based on the IBS matrix as outlined by Sun *et al*. (2013). To perform cluster analysis on all genotypes, the neighbor joining method was employed, and agglomerative clustering was utilized based on genetic distance, following the approach described by Luo *et al*. (2020).

Statistical Analyses

The AIREMLF90 (v1.61) module from the Blupf90 program was utilized to predict the breeding values of each animal, employing Model 1 (Misztal *et al*., 2002):

$$y = 1\mu + Xb + Za + e \quad [1]$$

Where, **y** is the vector of adjusted phenotype, **μ** is the overall mean, **X** is the incidence matrix relating fixed effects of sex–hatch–year to phenotypes, **b** is the vector of fixed effects, **Z** is the incidence matrix relating phenotypes to additive genetic effects, **a** is the vector of additive genetic effects assumed to be distributed as $\sim N(0, A\sigma_a^2)$, where $\boldsymbol{A}$ is the pedigree-based relationship matrix, $\boldsymbol{\sigma_a^2}$ is the variance of additive genetic effects and e is the vector of random residual effects *as* $\sim N(0, I\sigma_e^2)$, where $\boldsymbol{I}$ is the identity matrix, and $\boldsymbol{\sigma_e^2}$ is the residual variance. Adjusted phenotypes were calculated as sum of the animals' PBV and residual values (Lourenco *et al*., 2020). PBV's and the residuals for each animal were estimated using AIREMLf90 and Pridictf90 modules from Blupf90 program by pedigree and raw phenotype fitting in model 1.

The prediction of single-step genomic breeding values was carried out using Model 2. AIREMLF90 (v1.61) (Misztal *et al*., 2014) was employed for this purpose. The entire set of SNPs, consisting of 48,379 SNPs, was utilized in the analysis. Additionally, five subsets of SNPs were created based on different Minor Allele Frequency (MAF) bins, namely 0.05–0.1, 0.1–0.2, 0.2–0.3, 0.3–0.4, and 0.4–0.5.

$$y = 1\mu + Xb + Zg + e \quad [2]$$

Where, **y**, **μ**, **X**, **b**, and **e** are the same as Model 1, **Z** is a design matrix for the random additive genetic effects; **g** is a vector of random additive genetic effects assumed to be distributed as ~N(0, $\mathbf{H}\sigma_g^2$), where, **H** is a combination of Genomic relationship matrix (**G**) and pedigree-based relationship matrix (**A**). The H matrix inverse utilized in this research was formulated as follows:

$$H^{-1} = A^{-1} + \begin{bmatrix} 0 & 0 \\ 0 & t(\alpha G + \beta A_{22})^{-1} - \omega A_{22}{}^{-1} \end{bmatrix} \quad [3]$$

In the AIREMLF90 (v1.61) software (Misztal et al., 2014), A_{22} represents the subset of the A matrix that pertains to genotyped animals. The scaling factors, t

[DOI: 10.22034/JAST.26.2.299]

Table 1. Distribution of SNPs before and after quality control and the average distance between adjacent SNPs on each chromosome.

Chromosome	No. of SNP Markers after quality control	No. of SNP in chip	Average distance (kb)
1	7546	8303	26.5
2	5762	6355	26.7
3	4340	4739	26.3
4	3553	3872	26.5
5	2303	2542	27.1
6	1815	1995	19.6
7	1907	2089	20.1
8	1502	1636	20.1
9	1269	1366	18.8
10	1378	1553	16.1
11	1329	1531	16.4
12	1356	1559	14.4
13	1251	1371	14.6
14	1081	1179	14.3
15	1094	1222	11.8
16	20	24	21.7
17	898	994	11.8
18	930	1048	11.9
19	878	973	11.3
20	1587	1815	8.8
21	805	901	8.5
22	313	432	12.6
23	631	724	9.3
24	763	853	8.5
25	177	211	11.5
26	685	776	7.4
27	518	576	9.4
28	582	708	7.6
29	118	142	7.7
30	4	7	6.9
Z	1984	2842	37.5
Total	48379	54338	15.8

and ω, were both initially set to one as the default option. To enhance predictions and prevent singularity issues, the blending factors α and β were assigned values of 0.95 and 0.05, respectively (VanRaden, 2007; Lourenco *et al*., 2014). The correlation between Prediction Breeding Values (GEBVs/PBVs) and adjusted phenotypes of birds in the validation population was used to calculate the accuracy. The equation below was used to calculate the standard error of prediction accuracy (Salek Ardestani *et al*., 2021):

$$\text{Standard error} = \frac{1-\text{accuracy}^2}{\sqrt{\text{number of individuals}-1}} \quad \textbf{[4]}$$

The accuracy improvement was computed utilizing the subsequent formula (Salek Ardestani *et al*., 2021):

$$\text{Improvement accuracy} = \left(\frac{\text{accuracy of GEBV}-\text{accuracy of EBV}}{\text{accuracy of EBV}}\right) \times 100 \quad \textbf{[5]}$$

The prediction bias was determined by calculating the regression coefficients (r) of GEBVs on adjusted phenotype using the lm function in R (R Core Team, 2013).

[DOI: 10.22034/JAST.26.2.299]

Cross Validations for Model Assessment

In order to evaluate the predictive accuracy of various prediction models, the 5-fold Cross-Validation (CV) method was employed. Among the total of 308 birds, a random selection of 40 birds was designated as the validation population, while the remaining 268 birds constituted the reference population. This process was repeated 5 times to ensure reliability. The estimation of GEBVs in the validation set was carried out using the ssGBLUP method. Additionally, traditional breeding values were estimated using the BLUP method for different age groups. The accuracy and bias of GEBVs/EBVs were utilized to compare the predictive performance of different scenarios.

RESULTS

Summary Statistics and Population Structure

Table 2 presents the statistical measures of ADG, including the mean, standard deviation, coefficient of variation, and the minimum and maximum values, for weeks 2 to 4. In order to investigate the genetic population structure, we conducted MDS analysis (Figure 1) and neighbour-joining tree analysis (Figure 2) using 48,379 SNPs in a crossbreed population. Our analysis identified the presence of eight distinct subgroups within the population under study.

Predictive Ability

The accuracy of EBV (GEBV) for ADG at 2 to 4 weeks of age were 0.102 (0.104), 0.155 (0.161) and 0.094 (0.096), respectively (Figure 3). The highest and lowest accuracy improvement in ssGBLUP over BLUP were observed for 3 (3.87%) and 2 (1.96%) weeks of age, respectively. The lowest bias of genomic predictions (0.91) using ssGBLUP model was observed for ADG at 3 weeks of age (Table 3).

Impact of MAF bins on predictive ability

In order to assess the influence of MAF on predictive capability, we categorized SNPs into five distinct subgroups based on different MAF ranges: 0.05-0.1 (6,731 SNPs), 0.1-0.2 (8,884 SNPs), 0.2-0.3 (10,148 SNPs), 0.3-0.4 (11,128 SNPs), and 0.4-0.5 (11,488 SNPs). For ADG at week 2, the highest accuracy (0.111, 0.105) was observed for MAF bins 0.3-0.4 and 0.4-0.5, which resulted in respectively, 6.86% and 0.98% improvement compared to using all SNPs. The lowest bias of estimates (r= 0.81) was observed for MAF bin 0.4-0.5 (Table 4). However, for ADG at 3 weeks of age, using MAF bin 0.4-0.5 resulted in the highest accuracy improvement (8.38%) and the lowest bias of estimates (r= 1.02) (Table 5). For ADG at 4 weeks of age, MAF bins 0.4-0.5 (0.108) and 0.3-0.4 (0.107) showed the highest accuracy of prediction, respectively. The regression coefficient of GEBVs predicted using this two MAF bins ranges between 1.32 to 1.56 (Table 6). The

Table 2. Descriptive statistics of the Average Daily Gain (ADG) traits in chickens.[a]

Trait/g	Mean	SD	CV	Min	Max
ADG2	18.03	6.64	36.80	0.864	30.90
ADG3	28.70	7.82	27.23	7.460	58.92
ADG4	38.70	10.71	27.67	5.813	72.95

[a] ADG2 to ADG4= Average Daily Gain at 2 weeks of age to Average Daily Gain at 4 weeks of age based grams (g), SD= Standard Deviation, CV= Coefficient of Variation, Min= Minimum, Max= Maximum.

[DOI: 10.22034/JAST.26.2.299]

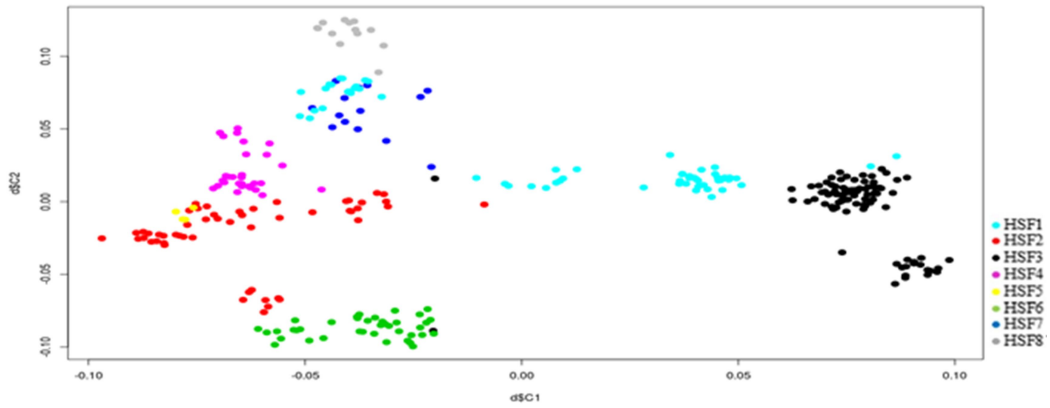

Figure 1. Population structure identification with multidimensional scaling analysis. Fullsib families are shown in the same color (HSF = half-sibling family).

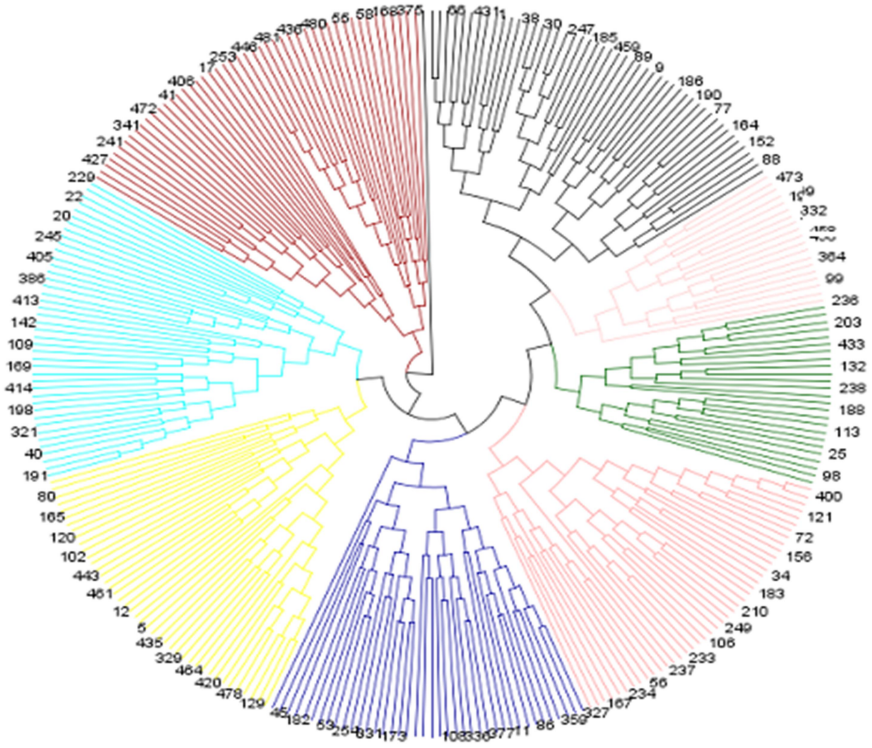

Figure 2. Genetic relationships among 8 chicken groups constructed using a neighbor-joining phylogenetic tree from shared allele distance, based on 48,379 single nucleotide polymorphisms (SNPs).

[DOI: 10.22034/JAST.26.2.299]

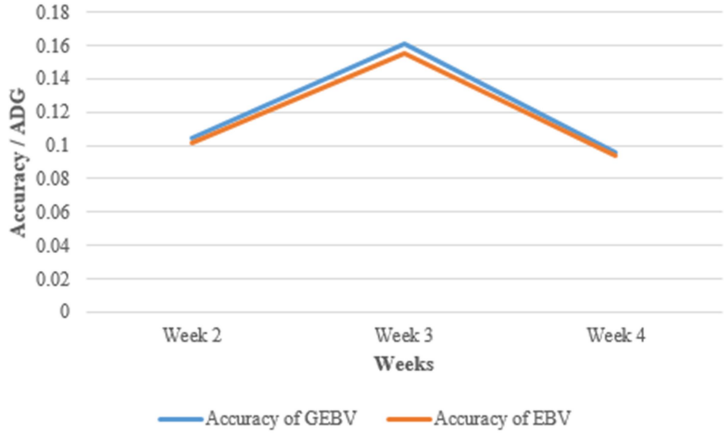

Figure 3. Comparison of BLUP and ssGBLUP accuracy in the second, third, and fourth weeks for the average daily gain (ADG) traits in F_2 chickens.

Table 3. Accuracy and bias of BLUP and ssGBLUP predictions for broiler average daily gain traits in different weeks using 5-fold cross-validation method.

Weeks	Accuracy / BLUP	Accuracy / ssGBLUP	Improvement accuracy% / ssGBLUP	Regression coefficient / ssGBLUP
2	0.102 ± 0.044	0.104 ± 0.044	1.96	0.75
3	0.155 ± 0.044	0.161 ± 0.044	3.87	0.91
4	0.094 ± 0.044	0.096 ± 0.044	2.12	1.5

Table 4. Accuracy and bias of genomic prediction of average daily gain trait using different MAF bins at two weeks of age.

MAF	Accuracy / ssGBLUP	Improvement accuracy% / ssGBLUP	Improvements for each MAF %	Regression coefficient / ssGBLUP
0.05-0.1	0.066 ± 0.045	-35.29	-37.25	0.59
0.1-0.2	0.099 ± 0.044	-2.94	-4.9	0.76
0.2-0.3	0.094 ± 0.044	-7.84	-9.8	0.66
0.3-0.4	0.111 ± 0.044	8.82	6.86	0.74
0.4-0.5	0.105 ± 0.044	2.94	0.98	0.81

accuracy based on the SNPs with MAF bin 0.3-0.4 and 0.4-0.5 across all traits was slightly increased relative to ssGBLUP (60k) (Figures 4, 5 and 6).

DISCUSSION

Developing an accurate and unbiased genomic prediction technique can prove to be a lucrative approach for genetic improvement of economic in the poultry sector (Mrode *et al*., 2019). Using a combination of pedigree and genomic information is expected to result in more accurate estimates of genetic merit compared to using pedigree information alone. In the current study, we employed the ssGBLUP technique to forecast the GEBVs for ADG traits during the 2 to 4-week age range. Subsequently, we compared the accuracy and bias of these predictions with estimates obtained through the conventional BLUP approach. Figure 3 demonstrates that ssGBLUP consistently outperforms the traditional BLUP method in terms of prediction accuracy across all age groups (Gao *et al*., 2012; Koivula *et al*., 2015). According to the findings of Silva *et al*.

[DOI: 10.22034/JAST.26.2.299]

Table 5. Accuracy and bias of genomic prediction of average daily gain trait using different MAF bins at three weeks of age.

MAF	Accuracy / ssGBLUP	Improvement accuracy % / ssGBLUP	Improvements for each MAF %	Regression coefficient / ssGBLUP
0.05-0.1	0.153 ± 0.044	-1.29	-5.16	1.02
0.1-0.2	0.160 ± 0.044	3.22	-0.65	1.08
0.2-0.3	0.142 ± 0.044	-8.38	-12.25	0.89
0.3-0.4	0.164 ± 0.044	5.80	1.93	0.85
0.4-0.5	0.174 ± 0.043	12.25	8.38	1.02

Table 6. Accuracy and bias of genomic prediction of average daily gain using different MAF bins at four weeks of age.

MAF	Accuracy / ssGBLUP	Improvement accuracy% / ssGBLUP	Improvements for each MAF %	Regression coefficient / ssGBLUP
0.05-0.1	0.066 ± 0.045	-29.78	-31.9	1.40
0.1-0.2	0.104 ± 0.044	10.63	8.51	1.82
0.2-0.3	0.099 ± 0.044	5.31	3.19	1.80
0.3-0.4	0.107 ± 0.044	13.82	11.7	1.56
0.4-0.5	0.108 ± 0.044	14.89	12.77	1.32

(2016), the utilization of ssGBLUP resulted in higher accuracy compared to the implementation of BayesCπ and GBLUP methods for evaluating residual feed intake and feed conversion ratio traits in Nelore cattle. Furthermore, in their study, Salek Ardestani *et al*. (2021) discovered that ssGBLUP exhibited the highest level of prediction accuracy when compared to BLUP, GBLUP, BayesC, and BayesCπ methods for the medium-size genotyped Canadian pig population. Similarly, Yan *et al*. (2017) reported that ssGBLUP demonstrated lower bias in estimates and higher prediction accuracy in comparison to traditional BLUP for a pure line of laying hens. Nevertheless, predictions using ssGBLUP compared to BLUP resulted in small improvement in accuracy for most of the age groups, which could be due to the small reference population size used in the current study and the architecture of the growth traits which is polygenic (Clark *et al*., 2011). The attainment of high accuracy in GEBV necessitates a substantial number of records in the reference population due to the relatively low to moderate heritability of growth traits at various weeks of age (Mebratie *et al*., 2017; Adeyinka *et al*., 2006) as highlighted by previous studies (Bermann *et al*., 2021; Goddard and Hayes, 2009). Furthermore, the occurrence of false positive errors in actual data can also contribute to a slight improvement in accuracy compared to BLUP (VanRaden *et al*., 2017). Moreover, if a limited effective population is chosen over an extended duration, the majority of the genetic variability can be elucidated by the genetic variability of SNPs owing to the interconnection among individuals (VanRaden *et al*., 2009). Consequently, substantial advancements in prediction accuracy will not be attained (MacLeod *et al*., 2014). According to the latest findings, Song *et al*. (2019) discovered a slight enhancement in accuracy (1%) when utilizing ssGBLUP instead of BLUP for growth traits in a Yorkshire population of 592 pigs. This improvement can be attributed to the limited number of animals with genotype and phenotype information, as well as the shallow pedigree depth. Additionally, Song *et al*. (2019) demonstrated that increasing the size of the reference population further improved accuracy. In a similar vein, Lourenco *et al*. (2014) observed a 3% increase in prediction

[DOI: 10.22034/JAST.26.2.299]

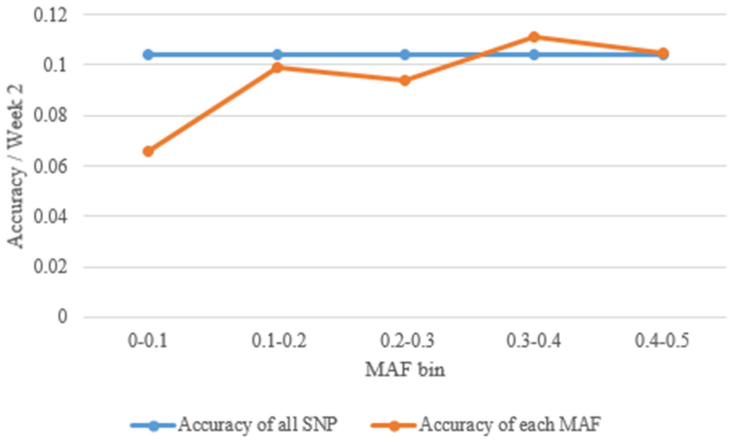

Figure 4. Comparison of the accuracy of each MAF subgroup with the accuracy of information about all markers in the second week.

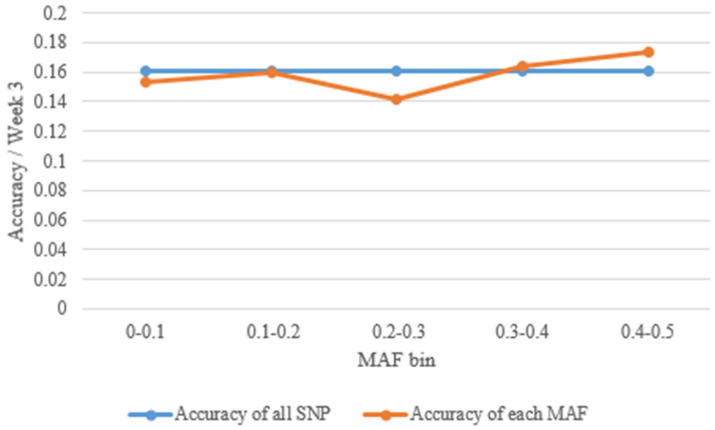

Figure 5. Comparison of the accuracy of each MAF subgroup with the accuracy of information about all markers in the third week.

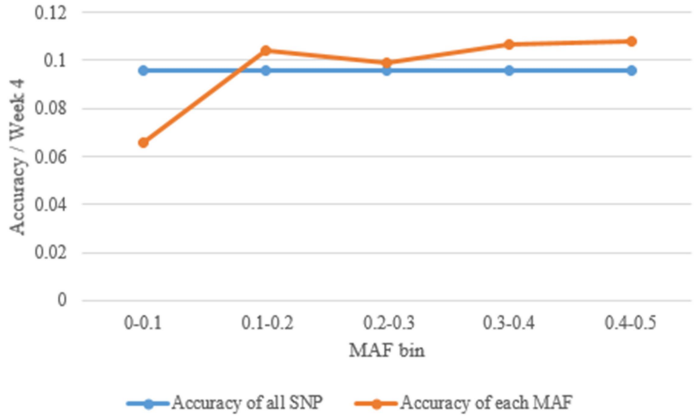

Figure 6. Comparison of the accuracy of each MAF subgroup with the accuracy of information about all markers in the fourth week.

[DOI: 10.22034/JAST.26.2.299]

accuracy for fat percentage using ssGBLUP compared to BLUP in a relatively small population of dairy cows with genotype information. In the current study, the enhancement in genomic prediction accuracy using ssGBLUP in comparison to BLUP was evident for the 3-week-old age group (3.87%). This improvement could be attributed to the higher genetic correlation observed between adjusted phenotypes and GEBVs as compared to EBVs for this specific age category. In general, a stronger genetic correlation between GEBVs and adjusted phenotypes leads to a higher level of accuracy in genomic prediction. The degree of genetic correlation between adjusted phenotype and EBVs for ADG at 3 weeks of age were increased by be 0.006 using ssGBLUP compared to BLUP method. However, small accuracy improvement was observed for ADG at 2 and 4 weeks of age, which could be due to the relatively small increase in genetic correlation between adjusted phenotypes and EBVs using ssGBLUP over BLUP (0.002 at 2 and 4 weeks of age, respectively). Based on the current results, implementation of genomic evaluation based on ssGBLUP method using whole SNPs for ADG at 3 weeks of age can result in more accurate results in populations with similar structure. Our research has yielded valuable findings regarding the implementation of genomic selection using low-density markers in the F2 cross broiler population. While it is commonly believed that a large portion of genetic diversity can be accounted for by utilizing high-density panels, it should be noted that the majority of SNPs in these panels are in Linkage Disequilibrium (LD) with causal mutations. Therefore, increasing the number of markers may not necessarily lead to a significant improvement in the accuracy of genomic evaluation for populations with a single-breed reference population (Su *et al*., 2012; Zhang *et al*., 2018). Additionally, the utilization of a high-density SNP panel may give rise to a significant statistical and computational concern. Furthermore, the genotyping of animals through medium to high-density SNP panels will incur substantial expenses in numerous livestock and poultry breeding initiatives. Therefore, employing preselection and utilizing a subset of SNPs can offer a satisfactory balance between result accuracy, the number of independent variables to be taken into account, computational demands, and genotyping expenses (Meuwissen and Goddard, 2010; MacLeod *et al*., 2014). In the present study, we constructed five subsets of SNPs based on different MAF bins for ADG at 2-4 weeks of age. The results showed that the use of SNPs with MAF bins 0.3-0.4 and 0.04-0.5 for ADG at 2, 3 and 4 weeks of age, and SNPs with MAF bins 0.1-0.2 and 0.2-0.3 for ADG at 4 weeks of age, can result in noticeable improvement of accuracy of prediction compared to using all SNPs (Figure 7). Consistent with our results, several studies showed that using the subset of SNPs can provide even better results than using of all SNPs information (Rolf *et al*., 2010; Wellmann *et al*., 2013; Ogawa *et al*., 2014; Li *et al*., 2018; Salvian *et al*., 2020).

CONCLUSIONS

In the current study, we investigated the accuracy and bias of genomic prediction across different age group, 2-4 weeks of age in the F_2 broiler population using 5-fold cross-validation method based on the ssGBLUP method. Moreover, different subset of SNPs varying minor allele frequency were used for genomic predictions using ssGBLUP method. Given the level of regression coefficient and accuracy of genomic prediction, it seems that ADG at 3 weeks of age using whole SNPs or subset of SNPs with MAF bins 0.3-0.4 and 0.4-0.5 could be used for future genomic prediction in broiler populations with population structure like the one used in the current study. Generally, SNPs with MAF bin 0.4-0.5 had higher predictive ability compared to other MAF bins for most of the age groups. However, one of the

[DOI: 10.22034/JAST.26.2.299]

limitations of the current study is that the small population size was used for genomic prediction and so further studies are needed to confirm the current results.

ACKNOWLEDGEMENTS

This work was funded by Isfahan University of Technology, Isfahan, Iran. Genotyping of the birds was supported by Aarhus University, Denmark. The authors would like to thank Dr. Just Jensen for financial support of the bird's genotyping. Access to the developed 60K SNP Illumina chicken array was kindly provided by the USDA Chicken GWMAS Consortium, Cobb Vantress, and Hendrix Genetics.

REFERENCES

1. Adeyinka, I. A., Oni, O. O., Nwagu, B. I. and Adeyinka, F. D. 2006. Genetic Parameter Estimates of Body Weights of Naked Neck Broiler Chickens. *Int. J. Poult. Sci.*, **5(6)**: 589-592.
2. Bermann, M., Legarra, A., Hollifield, M. K., Masuda, Y., Lourenco, D. and Misztal, I. 2021. Validation of Single-Step GBLUP Genomic Predictions from Threshold Models Using the Linear Regression Method: An Application in Chicken Mortality. *J. Anim. Breed. Genet.*, **138(1)**: 4-13.
3. Chang, C. C., Chow, C. C., Tellier, L. C., Vattikuti, S., Purcell, S. M. and Lee, J. J. 2015. Second-Generation PLINK: Rising to the Challenge of Larger and Richer Datasets. *Gigascience*, **4(1)**: 1-16.
4. Christensen, O. F., Madsen, P., Nielsen, B., Ostersen, T. and Su, G. 2012. Single-Step Methods for Genomic Evaluation in Pigs. *Anim.*, **6(10)**: 1565-1571.
5. Clark, S. A., Hickey, J. M. and Van der Werf, J. H. 2011. Different Models of Genetic Variation and Their Effect on Genomic Evaluation. *Genet. Sel. Evol.*, **43(1)**: 1-9.
6. Druet, T., Macleod, I. M. and Hayes, B. J. 2014. Toward Genomic Prediction from Whole-Genome Sequence Data: Impact of Sequencing Design on Genotype Imputation and Accuracy of Predictions. *Heredity*, **112(1)**: 39-47.
7. Gao, H., Christensen, O. F., Madsen, P., Nielsen, U. S., Zhang, Y., Lund, M. S. and Su, G. 2012. Comparison on Genomic Predictions Using Three GBLUP Methods and Two Single-Step Blending Methods in the Nordic Holstein Population. *Genet. Sel. Evol.*, **44(1)**: 1-8.
8. Goddard, M. E. and Hayes, B. J. 2009. Mapping Genes for Complex Traits in Domestic Animals and Their Use in Breeding Programmes. *Nat. Rev. Genet.*, **10(6)**:
9. Goddard, M.E. and Hayes, B.J. 2007. Genomic Selection. *J. Anim. Breed. Genet*., **124(6)**: 323-330.
10. Koivula, M., Strandén, I., Pösö, J., Aamand, G. P. and Mäntysaari, E. A. 2015. Single-Step Genomic Evaluation Using Multitrait Random Regression Model and Test-Day Data. *J. Dairy Sci.*, **98(4)**: 2775-2784.
11. Legarra, A., Aguilar, I. and Misztal, I. 2009. A Relationship Matrix Including Full Pedigree and Genomic Information. *J. Dairy Sci.*, **92(9)**: 4656-4663.
12. Li, B., Zhang, N., Wang, Y. G., George, A. W., Reverter, A. and Li, Y. 2018. Genomic Prediction of Breeding Values Using a Subset of SNPs Identified by Three Machine Learning Methods. *Front. Genet.*, **9**: 1-20.
13. Li, X., Wang, S., Huang, J., Li, L., Zhang, Q. and Ding, X. 2014. Improving the Accuracy of Genomic Prediction in Chinese Holstein Cattle by Using One-Step Blending. *Genet. Sel. Evol.*, **46(1)**: 1-5.
14. Liu, R., Sun, Y., Zhao, G., Wang, H., Zheng, M., Li, P., Liu, L. and Wen, J. 2015. Identification of Loci and Genes for Growth Related Traits from a Genome-Wide Association Study in a Slow-×Fast-Growing Broiler Chicken Cross. *Genes Genomics*, **37(10)**: 829-836.
15. Lourenco, D. A. L., Misztal, I., Tsuruta, S., Aguilar, I., Ezra, E., Ron, M., Shirak, A. and Weller, J. I. 2014. Methods for Genomic Evaluation of a Relatively Small Genotyped Dairy Population and Effect of Genotyped Cow Information in Multiparity Analyses. *J. Dairy Sci.*, **97(3)**: 1742-1752
16. Lourenco, D., Legarra, A., Tsuruta, S., Masuda, Y., Aguilar, I. and Misztal, I. 2020. Single-step Genomic Evaluations

[DOI: 10.22034/JAST.26.2.299]

from Theory to Practice: Using SNP Chips and Sequence Data in BLUPF90. *Genes.*, **11(7)**: 1-32.
17. Luo, W., Luo, C., Wang, M., Guo, L., Chen, X., Li, Z., Zheng, M., Folaniyi , B. S., Luo, W., Shu, D., Song, L., Fang, M., Zhang, X., Qu, H. and Nie, Q. 2020. Genome Diversity of Chinese Indigenous Chicken and the Selective Signatures in Chinese Gamecock Chicken. *Sci. Rep.*, **10(1)**: 1-14.
18. MacLeod, I. M., Hayes, B. J. and Goddard, M. E. 2014. The Effects of Demography and Long-Term Selection on the Accuracy of Genomic Prediction with Sequence Data. *Genetics*, **198(4)**: 1671-1684.
19. Mebratie, W., Shirali, M., Madsen, P., Sapp, R. L., Hawken, R. and Jensen, J. 2017. The Effect of Selection and Sex on Genetic Parameters of Body Weight at Different Ages in a Commercial Broiler Chicken Population. *Livest Sci.*, **204**: 78-87.
20. Meuwissen, T. H., Hayes, B. J. and Goddard, M. 2001. Prediction of Total Genetic Value Using Genome-Wide Dense Marker Maps. *Genetics*, **157(4)**: 1819-1829.
21. Meuwissen, T. and Goddard, M. 2010. Accurate Prediction of Genetic Values for Complex Traits by Whole-Genome Resequencing. *Genetics*, **185(2)**: 623-631.
22. Meuwissen, T., Hayes, B. and Goddard, M. 2016. Genomic Selection: A Paradigm Shift in Animal Breeding. *Anim. Front.*, **6(1)**: 6-14.
23. Misztal, I., Aggrey, S. E. and Muir, W. M. 2013. Experiences with a Single-Step Genome Evaluation. *Poult. Sci.*, **92(9)**: 2530-2534.
24. Misztal, I., Tsuruta, S., Lourenco, D., Aguilar, I., Legarra, A. and Vitezica, Z. 2014. Manual for BLUPF90 Family of Programs. University of Georgia, Athens.
25. Misztal, I., Tsuruta, S., Strabel, T., Auvray, B., Druet, T. and Lee, D. 2002. "BLUPF90 and related programs (BGF90). *In Proceedings of the 7th World Congress on Genetics Applied to Livestock Production*, Montpellier, PP. 743–744.
26. Mrode, R., Ojango, J. M., Okeyo, A. M. and Mwacharo, J. M. 2019. Genomic Selection and Use of Molecular Tools in Breeding Programs for Indigenous and Crossbred Cattle in Developing Countries: Current Status and Future Prospects. *Front. Genet.*, **9:** 1-11..
27. Ogawa, S., Matsuda, H., Taniguchi, Y., Watanabe, T., Nishimura, S., Sugimoto, Y. and Iwaisaki, H. 2014. Effects of Single Nucleotide Polymorphism Marker Density on Degree of Genetic Variance Explained and Genomic Evaluation for Carcass Traits in Japanese Black Beef Cattle. *BMC Genet.*, **15(1)**: 1-13.
28. Purcell, S., Neale, B., Todd-Brown, K., Thomas, L., Ferreira, M. A., Bender, D., Maller, J., Sklar, P., de Bakker, P. I. W., Daly, M. J. and Sham, P. C. 2007. PLINK: A Tool Set for Whole-Genome Association and Population-Based Linkage Analyses. *Am. J. Hum. Genet.*, **81(3)**: 559-575.
29. R Core Team. 2013. *R: A Language and Environment for Statistical Computing.* R Foundation for Statistical Computing, Vienna.
30. Rolf, M. M., Taylor, J. F., Schnabel, R. D., McKay, S. D., McClure, M. C., Northcutt, S. L., Kerley, M. S. and Weaber, R. L. 2010. Impact of Reduced Marker Set Estimation of Genomic Relationship Matrices on Genomic Selection for Feed Efficiency in Angus Cattle. *BMC Genet.*, **11(1)**: 1-10.
31. Salek Ardestani, S., Jafarikia, M., Sargolzaei, M., Sullivan, B. and Miar, Y. 2021. Genomic Prediction of Average Daily Gain, Back-Fat Thickness, and Loin Muscle Depth Using Different Genomic Tools in Canadian Swine Populations. *Front. Genet.*, **12**: 1-13.
32. Salvian, M., Moreira, G. C. M., Reis, Â. P., Dauria, B. D., Pilonetto, F., Gervásio, I. C., Ledur, M. C., Coutinho, L. L. Spangler, M. L. and Mourão, G. B. 2020. Estimation of Breeding Values Using Different Densities of SNP to Inform Kinship in Broiler Chickens.
33. Silva, R. M. O., Fragomeni, B. O., Lourenco, D. A. L., Magalhães, A. F. B., Irano, N., Carvalheiro, R., Canesin, R. C., Mercadante, M. E. Z., Boligon, A. A., Baldi, F. S., Misztal, I. and Albuquerque, L. G. 2016. Accuracies of Genomic Prediction of Feed Efficiency Traits Using Different Prediction and Validation Methods in an Experimental Nelore Cattle Population. *J. Anim. Sci.*, **94(9)**: 3613-3623.
34. Simeone, R., Misztal, I., Aguilar, I. and Vitezica, Z. G. 2012. Evaluation of a Multi-Line Broiler Chicken Population Using a Single-Step Genomic Evaluation Procedure. *J. Anim. Breed. Genet.*, **129(1)**: 3-10.

[DOI: 10.22034/JAST.26.2.299]

35. Song, H., Zhang, J., Jiang, Y., Gao, H., Tang, S., Mi, S., Yu, F., Meng, Q., Xiao, W., Zhang, Q. and Ding, X. 2017. Genomic Prediction for Growth and Reproduction Traits in Pig Using an Admixed Reference Population. *J. Anim. Sci.*, **95(8)**: 3415-3424.
36. Song, H., Zhang, J., Zhang, Q. and Ding, X. 2019. Using Different Single-Step Strategies to Improve the Efficiency of Genomic Prediction on Body Measurement Traits in Pig. *Front. Genet.*, **9**: 1-10.
37. Su, G., Brøndum, R. F., Ma, P., Guldbrandtsen, B., Aamand, G. P. and Lund, M. S. 2012. Comparison of Genomic Predictions Using Medium-Density (~ 54,000) and High-Density (~ 777,000) Single Nucleotide Polymorphism Marker Panels in Nordic Holstein and Red Dairy Cattle Populations. *J. Dairy Sci.*, **95(8)**: 4657-4665.
38. Sun, Y., Zhao, G., Liu, R., Zheng, M., Hu, Y., Wu, D., Zhang, L., Li, P. and Wen, J. 2013. The Identification of 14 New Genes for Meat Quality Traits in Chicken Using a Genome-Wide Association Study. *BMC Genom.*, **14(1)**: 1-11.
39. VanRaden, P. M. 2007. Efficient Estimation of Breeding Values from Dense Genomic Data. *J. Dairy Sci.*, **90**: 374-375.
40. VanRaden, P. M., Tooker, M. E., O'connell, J. R., Cole, J. B. and Bickhart, D. M. 2017. Selecting Sequence Variants to Improve Genomic Predictions for Dairy Cattle. *Genet. Sel. Evol.*, **49(1)**: 1-12. https://doi.org/10.1186/s12711-017-0307-4
41. VanRaden, P. M., Van Tassell, C. P., Wiggans, G. R., Sonstegard, T. S., Schnabel, R. D., Taylor, J. F. and Schenkel, F. S. 2009. Invited Review: Reliability of Genomic Predictions for North American Holstein Bulls. *J. Dairy Sci.*, **92(1)**: 16-24.
42. Wang, D., Sun, Y., Stang, P., Berlin, J. A., Wilcox, M. A. and Li, Q. 2009. Comparison of Methods for Correcting Population Stratification in a Genome-Wide Association Study of Rheumatoid Arthritis: Principal-Component Analysis *versus* Multidimensional Scaling. *BMC Proc.,* **3(7):** 1-6.
43. Wellmann, R., Preuß, S., Tholen, E., Heinkel, J., Wimmers, K. and Bennewitz, J. 2013. Genomic Selection Using Low Density Marker Panels with Application to a Sire Line in Pigs. *Genet. Sel. Evol.*, **45(1)**: 1-11.
44. Wimmer, V., Albrecht, T., Auinger, H. J. and Schön, C. C. 2012. Synbreed: A Framework for the Analysis of Genomic Prediction Data Using R. *Bioinformatics.*, **28(15)**: 2086-2087.
45. Yan, G., Qiao, R., Zhang, F., Xin, W., Xiao, S., Huang, T., Zhang, Z. and Huang, L. 2017. Imputation-Based Whole-Genome Sequence Association Study Rediscovered the Missing QTL for Lumbar Number in Sutai Pigs. *Sci. Rep.*, **7(1)**: 1-10.
46. Yang, J., Lee, S. H., Goddard, M. E. and Visscher, P. M. 2013. Genome-Wide Complex Trait Analysis (GCTA): Methods, Data Analyses, and Interpretations. *In: "Genome-Wide Association Studies and Genomic Prediction"*. Humana Press, Totowa, NJ, PP. 215-236.
47. Zhang, C., Kemp, R. A., Stothard, P., Wang, Z., Boddicker, N., Krivushin, K., Dekkers, J. and Plastow, G. 2018. Genomic Evaluation of Feed Efficiency Component Traits in Duroc Pigs Using 80K, 650K and Whole-Genome Sequence Variants. *Genet. Sel. Evol.*, **50(1)**: 1-13.

[DOI: 10.22034/JAST.26.2.299]

ارزیابی ژنومی صفت میانگین افزایش وزن روزانه در جمعیت حاصل از تلاقی لاین آرین و جوجه‌های بومی ارومیه ایران

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چکیده

بهبود ژنتیکی صفات رشد به دلیل پیامدهای اقتصادی و زیست‌محیطی مختلف، در صنعت طیور مورد توجه قرار گرفته است. پیش‌بینی ژنومی (GP) یک راه عملی برای افزایش بهره‌وری است. علاوه بر این، یک پیش انتخاب از نشانگرهای ژنتیکی (SNPs)، گزینه معقولی برای سرعت بخشیدن به GP خواهد بود. هدف از مطالعه اخیر مقایسه صحت و اریبي مقادیر ارزش‌هاي اصلاحي برآورد شده (EBV) با استفاده از روش‌هاي BLUP مبتني بر شجره (BLUP) و BLUP ژنومي تك‌مرحله‌اي (ssGBLUP) و همچنین تعیین بهترین سطح از فراواني آللي براي انجام ارزیابي‌هاي ژنومي در صفت ADG بود. در این مطالعه از رکوردهاي ۴۸۸ قطعه پرنده F_2 حاصل از تلاقي متقابل جوجه‌هاي سریع الرشد آرین و جوجه‌هاي بومي کند رشد ارومیه ایران در سن ۲، ۳ و ۴ هفتگي استفاده شد. نمونه‌ها با استفاده از تراشه Illumina 60K chicken Beadchip تعیین ژنوتیپ شدند. تعداد ۴۸۳۷۹ نشانگر SNP پس از عبور از مرحله کنترل کیفیت به پنج گروه با فراواني آللي مختلف (MAF) (۰/۱-۰/۰۵، ۰/۲-۰/۱، ۰/۳-۰/۲، ۰/۴-۰/۳ و ۰/۵-۰/۴) تقسیم شدند. نتایج ما برتری ssGBLUP در مقایسه باBLUP را تائید کرد. میانگین دقت GP با استفاده از ssGBLUP در مقایسه با BLUP برای ADG در سنین ۴-۲ هفتگی به ترتیب ۱.۹۶، ۳.۸۷ و ۲.۱۲ درصد بهبود یافت. بسته به گروه سنی، استفاده از زیرمجموعه‌ای از SNP ها با MAF خاص در مقایسه با اطلاعات کل SNP ها منجر به بهبود قابل توجهی در دقت GP برای صفت ADG شد. نتایج نشان داد، پیش‌انتخاب SNP ها بر اساس فراوانی آللی ممکن است شرایط مطلوبی در دقت ارزیابی‌ها و محاسبات فراهم کند.

[DOI: 10.22034/JAST.26.2.299]