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IMPLEMENTING GENOMIC SELECTION IN THE IMB: CHALLENGES AND OPPORTUNITIES

Implementando la selección genómica en el búfalo mediterráneo italiano: desafíos y oportunidades

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ABSTRACT

Single-step genomic best linear unbiased predictor (ssGBLUP) is a method for jointly estimating breeding values (BV) for genotyped and non-genotyped animals. Genomic information in the Italian Mediterranean Buffalo (IMB) is now available. Its inclusion in the genetic evaluation system could increase both the accuracy and genetic progress of the traits of interest of the breed. The study aimed to test the feasibility of ssGBLUP and show the first results of implementing a genomic evaluation for production and type traits in the IMB. Phenotypic information on production (270-day milk, mozzarella yield (MY), protein and fat kg and %, respectively) and morphology: feet and legs (FL) and mammary system (MS) were used for this study. Production records included 743,904 lactations from 276,451 buffalo cows born from 1984 to 2019. Morphological traits were from 91,966 buffalo cows from 2004 to 2022. Regarding the genotypes, 2,017 buffalo cows and 133 bulls were used. Data were analyzed fitting two multi-trait animal models, a 6-trait model for production data and a 2-trait model for morphology data. According to the relationship matrix used, two models were fitted: (i) the BLUP with the numerator relationship matrix (A) and (ii) the ssGBLUP where A and the genomic relationship matrix (G) are blended into H. BVs were estimated with BLUP and ssGBLUP models. The cutoff year used to create the partial data set was 2012. The correlation, accuracy, dispersion, and bias statistics were calculated (LR method). Both bulls (N=49) and cows (N=1288) were used for validations. On average, the correlation between EBVs from partial and whole datasets estimated with BLUP and ssGBLUP increased from 6 to 49% and from 14 to 17% for production and type traits, respectively. Among the traits analyzed, the most affected by the change were protein/fat content, MY, and AM. The accuracy increase for these traits was above 20% when using the ssGBLUP. All LR statistics also improved for non-genotyped females. These results showed that implementing ssGBLUP in the breeding program can generate more accurate predictions for essential traits in dairy IMB than traditional BLUP.

Keywords: genomics, Italian Mediterranean buffalo, selection.

RESUMEN

El mejor predictor lineal insesgado genómico de un solo paso (ssGBLUP) es un método para estimar conjuntamente los valores genéticos (BV) para animales genotipados y no genotipados. La información genómica del búfalo mediterráneo italiano (IMB) ya está disponible. Su inclusión en el sistema de evaluación genética podría incrementar tanto la precisión como el progreso genético de los rasgos de interés de la raza. El estudio tuvo como objetivo probar la viabilidad de ssGBLUP y mostrar los primeros resultados de la implementación de una evaluación genómica para rasgos de producción y tipo en el IMB. Para este estudio se utilizó información fenotípica sobre producción (leche a 270 días, rendimiento de kg de mozzarella (MY), % y kg de proteína y grasa, respectivamente) y morfología: pies y piernas (FL) y sistema mamario (MS). Los registros de producción incluyeron 743.904 lactancias de 276.451 vacas búfalas nacidas de 1984 a 2019. Los rasgos morfológicos fueron de 91.966 vacas búfalas de 2004 a 2022. En cuanto a los genotipos, se utilizaron 2.017 vacas búfalas y 133 toros. Los datos se analizaron ajustando dos modelos animales con múltiples rasgos, un modelo de 6 rasgos para datos de producción y un modelo de 2 rasgos para datos de morfología. De acuerdo con la matriz de relaciones utilizada, se ajustaron dos modelos: (i) el BLUP con la matriz de relaciones del numerador (A) y (ii) el ssGBLUP donde A y la matriz de relaciones genómicas (G) se mezclan en H. Los BV se estimaron con Modelos BLUP y ssGBLUP. El año de corte utilizado para crear el conjunto de datos parcial fue 2012. Se calcularon las estadísticas de correlación, precisión, dispersión y sesgo (método LR). Para las validaciones se utilizaron toros (N=49) y vacas (N=1288). En promedio, la correlación entre los EBV de conjuntos de datos parciales y completos estimados con BLUP y ssGBLUP aumentó del 6 al 49 % y del 14 al 17 % para los rasgos de producción y tipo, respectivamente. Entre los rasgos analizados, los más afectados por el cambio fueron el contenido de proteína/grasa, MY y AM. El aumento de precisión para estos rasgos fue superior al 20 % cuando se utilizó ssGBLUP. Todas las estadísticas de LR también mejoraron para las hembras no genotipadas. Estos resultados mostraron que la implementación de ssGBLUP en el programa de mejoramiento puede generar predicciones más precisas para rasgos esenciales en el IMB lechero que el BLUP tradicional.

Palabras clave: genómica, búfalo mediterráneo italiano, selección.

INTRODUCTION

The current breeding goal for the Italian Mediterranean Buffalo (IMB) centers on enhancing production and functional traits. Genetic selection in buffaloes has faced obstacles due to the absence of genealogical data, challenges in implementing data collection, and poor reproductive performance. Consequently, the full potential of the buffalo has yet to be actualized. Nevertheless, the Italian Mediterranean buffalo stands out as the sole breed globally, with a well-established genetic program that has been in operation for over two decades.

The advent of genomics has significantly transformed the genetic selection of livestock, although its implementation varies across species. This discrepancy arises from factors such as population structure, the extensive use of artificial insemination, and the accessibility of precise phenotypic data. Initially, methodological approaches restricted genomics application to large populations, but algorithms now cater to highly heterogeneous situations. Among these approaches is the Single-step Genomic BLUP (ssGBLUP) method. This method has replaced the multiphase process initially utilized for genomic evaluations in various farm animal species. The ssGBLUP method employs the inverse of a relationship matrix H-1 [1], merging the traditional additive relatedness matrix (A) with the genomic relatedness matrix (G). Despite earlier challenges related to unknown parental groups (UPG) and computational costs, recent studies have demonstrated the efficacy of this method in estimating Estimated Breeding Values (EBV) across diverse livestock species, including dairy animals [2, 3, 4], beef cattle [5], goats [6], sheep [7, 8], and buffaloes [9, 10].

The enhancement of buffalo genetics holds significant importance in Italian breeding. Italy ranks sixth globally in buffalo milk production and sixteenth in livestock numbers. Consequently, this study assesses the efficacy of genomic models in predicting breeding values for production traits in Italian Mediterranean buffalo.

MATERIALS AND METHODS

Ethics Statement

Animal welfare and use committee approval was unnecessary for this study as datasets were obtained from pre-existing databases based on routine animal recording procedures.

Data

The National Association of Italian Buffalo Breeders (ANASB) provided data for the present study and regarded productive, morphological and pedigree information. Production records included 743,904 lactations from 276,451 buffalo cows born from 1984 to 2019. Morphological traits were from 91,966 buffalo cows from 2004 to 2022. Regarding the genotypes, a total of 2,250 animals were used.

Analysis

Data were analysed fitting two multi-trait animal models, a 6-trait model for production data and a 2-trait model for morphology data. According to the relationship matrix used, two models were fitted: (i) the BLUP with the numerator relationship matrix (A) and (ii) the ssGBLUP where A and the genomic relationship matrix (G) are blended into H. Breeding values were estimated with BLUP and ssGBLUP models. The genetic values were estimated twice to evaluate the models: in the first test, the candidate animals had their phenotypes available (complete data), while in the second, they had their phenotypes masked (partial data). The cutoff year used to create the partial data set was set at 2012. Therefore, the reduced data set corresponded to buffaloes with fine calving in 2012. The following statistics were calculated to evaluate the models: dispersion, precision, correlation and bias.

RESULTS AND DISCUSSION

The correlation between the two methods was larger than 90% for production and between 87 and 91% for morphology. Regarding average reliability, the ssGBLUP method showed a higher value than to the classic method. As seen in TABLE I, the increase was between 6 and 41%, depending on the trait. However, differences are observed between traits, and this is because they have diverse heritabilities, and this causes the snps to have a different impact on each trait.

The validation of the results through the LR method [11] has the purpose of verifying the impact of the snp on the estimation and its predictive capacity when an animal does not have a phenotype. This method is widely used to validate the transition from genetics to genomics in different livestock species, such as cattle [5, 4], ovine [8], chicken [12] e buffalo [10, 13]. In theory, the dispersion, correlation and precision should be close to 1, and the results show how the ssGBLUP method tends to predict better than the classical method. While, the Bias indicates the error that we are making in the estimate. Overall, ssGBLUP results were better than BLUP's (TABLE II). There was a moderate increase (18%) in the minimum prediction accuracy with ssGBLUP. This result further confirms the benefits of including genomic information in the genetic evaluation for production and morphological traits.

When we talk about genetic selection, the precision of our estimate is essential to guarantee the genetic progress of our population. The data's reliability increase is achieved with the permanent inclusion of information, the validation of the pedigree, and the meticulous implementation of quality control measures [14]. Regarding genotypes, various studies have confirmed that it is beneficial to genotype females; in fact, including female genotypes is becoming more attractive lately [15]. In the IMB this aspect is fundamental, since it has a low number of bulls authorized for artificial fertilization. Therefore, the genotyping of females is essential. Current data show that of the total available genotypes, 10% correspond to males and 90% to females. Increasing precision with the inclusion of females has also been reported in small and large populations [16]. For example, it was concluded that a less biased and more reliable GEBV was obtained in Nordic Jersey cattle by including genotypes from unselected females [17].

The correlation between the total dataset and the partial dataset (Table II) indicated that the use of genomic information leads to greater stability of the evaluation for the selection candidates (ssGBLUP, 0.51-0.60), which means that the genomic model predicts better genetic values when the animal does not have its phenotype. Similar results were shown by Cesarani et al. [15] in the Italian Simmental cattle, with the ssGBLUP method obtaining an increase in the correlation of 14%.

With the ssGBLUP, we create a new matrix of combined relationships that turns out to be more efficient than what we had with the BLUP method and also perform an adjustment of the kinship relationships between genotyped and non-genotyped individuals. This adjustment is crucial role in reducing bias when calculating breeding values from animals with no phenotypic data available [18].

TABLE I

INCREASED ACCURACY, SSGBLUP VS BLUP

Trait	Method	Increased (%)
Milk	ssGBLUP vs BLUP	10.39
Fat %	ssGBLUP vs BLUP	11.84
Protein %	ssGBLUP vs BLUP	10.39
Fat Kg	ssGBLUP vs BLUP	10.67
Protein Kg	ssGBLUP vs BLUP	9.09
Yield	ssGBLUP vs BLUP	40.68
Feet and legs	ssGBLUP vs BLUP	6.56
Under teat	ssGBLUP vs BLUP	7.46

TABLE II

MINIMUM AND MAXIMUM VALUE OBTAINED BY THE BLUP AND SSGBLUP METHOD

Statistics LR	BLUP	ssGBLUP
Dispersion	0.64 -1.15	0.80 - 1.06
Correlation	0.37 - 0.57	0.51 - 0.60
Accuracy	0.38 - 0.51	0.45 - 0.52
Bias	-0.57 - 0.06	-0.18 - 0.43

CONCLUSION

These results obtained by inserting the genotypes into the calculation of the genetic values move in the expected direction. These results indicate that ssGBLUP can be implemented in the routine genetic evaluation of Italian Mediterranean Buffalo. This implementation will be beneficial, especially for those traits with low heritability. It is advisable to continue increasing the number of genotyped animals more significant to obtain greater precision increases.

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