Original Article

Evaluation of Breeding Values and Variance Components of Birth and Weaning Weights in the Holstein Cows Herd Based on Genetic Information

Hamad Senkal, R[1] *, Al-Jubori, O. S[1], Al-Waith, H. K[1]

1. Department of Animal Production, College of Agricultural Engineering Sciences, University of Baghdad, Baghdad, Iraq

Abstract

Birth weights, weaning, and daily weight gain of calves before weaning vary according to farm animals' environment, production, and breeding systems. It is expected that these traits will be affected by direct genetic influences and the genetic effects of the mother. Therefore, this study was designed and conducted on 50 Holstein cows herds to estimate breeding value (after estimating the mean of allele effect and the mean of allele replacement effect of the DRB3 gene), as well as the variance components of the birth and weaning weight traits, depending on the variance resulting from the inherited polymorphism of the DBR3 gene. The results of this study showed a preference for the wild allele A based on its mutant counterpart B was the mean allele-effect value and the mean allele substitution value, corresponding to the preference for the A allele in both traits, the individuals with the AA genotype outperformed the homozygotes and mutants in the educational value (a value that is estimated based on what the individuals carry from the genotypes). The genetic variance of weaning weight was higher than the genetic variance of birth weight, and this may be due to the preference of allele A and the AA structure over the other two components in positively affecting birth and weaning weights, indicating the importance of this genetic structure of the DBR3 gene in selection within the genetic improvement programs for the color characteristic of Holstein cows.

Keywords: Breeding value, Variance component, Birth weight, weaning weight, Holstein Cows

1. Introduction

Birth weights, weaning, and daily weight gain of calves before weaning vary according to farm animals' environment, production, and breeding systems. It is expected that these traits will be affected by direct genetic influences and the genetic effects of the mother. Therefore, it is crucial to evaluate the genetic potential of these traits to improve beef production. Also, it has great importance to understand the genetic factors and the environmental parameters that affect these variables. It is essential to know the genetic and environmental parameters associations to implement optional breeding and selection programs (1).

After the development in the field of detecting the structure of genes in farm animals and calculating the difference between the degrees of similarity between individuals within the same family, genomic information was relied upon to detect genetic variation in different genetic sites and the overlap in their effect on the variation of productive traits (2). Breeding based on selection markers and genomic information also assisted in the additive effect that plays a vital role in influencing the phylogeny and development of farm animals (3); likewise, the effect of dominance in the traits had an added value on the additional variance of the studied traits. Therefore,

many studies began to pay attention to this effect because of its critical role in the total variance of productive traits (4, 5). Therefore the study of gene maps has focused mainly on additional variability, and several studies have emphasized the importance of non-neglected contribution to the sites of quantitative traits QTL (6).

One of the essential tools in the genetic improvement of livestock species is the prediction of breeding values. Predicting breeding values depends on knowledge of relationships between individuals. Determining genetic relationships between animals allows an estimate of the proportion of the apparent variation that can be inherited. The expected variance in the total estimated breeding values, including all the effects of estimated genetic markers, does not exceed the total genetic variance (7).

The bovine lymphocyte antigen (BoLA) system is defined as the major histocompatibility complex of cattle (8, 9); the main histocompatibility complex genes encode on the cell surface glycoprotein molecules that are highly polymorphic that represent the antigenic peptide of T cells (10) and play a fundamental role in the immune response to external factors. BoLA is mapped on chromosome 23 and consists of Class I, IIa, IIb, and III regions (11); the DRB3 gene locus has received wide attention due to its polymorphism and its association with immunity and productivity in dairy cows; 130 BOLA-DRB3 alleles have been identified that contain 5 exons and 4 introns (http://www.ebi.ac .uk/ipd/MHC/bola/) (12). The multiplicity of genetic phenotypes in alleles can produce more than 20 amino acids. Each allele has an advantage in expressing the type of complex tissue compatibility. These differences are in the binding and antigen site of the peptide and thus functionally specialized to provide antigens to aid production mainly from external proteins and parasites of T cells and T cells helper, as their cells play several vital roles, including the activity of macrophages and lymphocytes, as macrophages search for external

viruses, bacteria and parts of most parasites that attack and swallow them, and thus play a significant role in the immune response of anyone as long as they are against diseases (10).

Therefore, the current study was designed to estimate the educational values and parameter variation of birth weight, weaning, and daily weight gain characteristics

2. Materials and Methods

This study was conducted on 50 Holstein cows' herds to estimate breeding value and variance component on birth and weaning weight traits depending on DRB3 gene information.

A medical syringe collected blood samples from the jugular vein in 15 ml sterile polypropylene tubes containing 0.5 ml of EDTA (0.5 M) as an anticoagulant by the phenol-chloroform extraction veterinarian at the station. The 284 bp fragment consisting (Paswan) of the 267 bp exon 2 region of the DRB3 gene and the flanking intron of 17 bp present in the genomic DNA of cattle was amplified by employing the corresponding primer pairs (forward and reverse), a program and the details of the primer sequences are as (13).

Following the completion of PCR, the polymorphism of the DRB3 gene was identified in blood samples from the cows after cutting to the required piece of the gene (284 bp) by restriction enzyme *HeaIII* from *Haemophilus aegyptius* bacteria the digestion with *Hae*III.

Equations used to calculate values were according to Calus (14) as:

1- Average allele A effect α A = q [a+d (q-p)]

2- Average allele B effect αB = q [a+d (q-p)]

Moreover, the average of substitution means the difference between the two values.

1-Breeding values

$\alpha 1$, AB= $\alpha 1$+$\alpha 2$ BB=2 $\alpha 2$ AA= 2

2- Dominance deviation

AA=-2q²d, AB=2pqd, AA=-2p²d

3- Different data:

α^2, VD=4p²q²d², VG=VA+VD VA=2pq

3. Results and Discussion

Following the completion of PCR, the polymorphism of the DRB3 gene was identified in blood samples from the cows after proceeding with the cutting to the required piece of the gene (284 bp) by restriction enzyme *HeaIII* from *Haemophilus aegyptius* bacteria. The digestion with *HaeIII* revealed four restriction sites, which resulted in three pieces:

1- AA allelic (167, 52, and 52) bp
2- AB allelic (219, 167, 52, and 52) bp
3- BB allelic (219 and 52) bp

The results showed that allele frequency for dominance allele (A) was 0.65 while the other allele (B) was 0.35, and the number and percentage of distribution ratio of DRB3 gene polymorphism for AA, AB, and BB which reached 46.00, 42, 00 & 12, 00 % for respectively (15).

Table 1 shows the superiority of the individuals carrying the homozygotes dominant genotype AA over the hybrid and mutant individuals in the educational values of the birth and weaning weight traits; as can be seen in table 1, the breeding values increased with the increase in the number of dominant alleles carried by the individual. The breeding value represents the value of the individual dependent on the alleles and genetic combinations they carry (16, 17); it is thus a true expression of the individual's genetic value and its productive viability in the absence of the environmental impact that may lead to the deviation of this value. Therefore, it is an essential basis for selecting the best individuals within the herd to be the next generation's parents (14)

In this study, dominance deviations tend to favor the homozygotes mutant genotype (Table 1), which is superior to the two dominant hybrid and homozygotes combinations. This indicates the negative allelic interaction in favor of the mutant structure. Thus the preference is in favor of the AA genotype, which came with the lowest dominant deviation (18).

Table 2 shows the positive effect of the dominant allele A of the DBR3 gene on the mean allele effect value (0.819), which came with a positive value at the expense of the recessive allele B for the birth weight and weaning traits, which are economic characteristics that represent the level of growth and weight gain of the animal (19), it is the value of the difference between the mean of individuals carrying a given allele from the general mean (16, 20).

Table 1. Breeding values, dominance deviation for DRB3 genotypes, and genetic variance and its content (Additive and dominance variance) for birth and weaning weight traits

Genotype	Trait	Breeding value	Dominance deviation	VA	VD	VG
AA		28.57	27.82			
AB	Birth Weight	27.76	28.63	0.3	0.39	0.69
BB		26.95	29.16			
genotype	Trait	Breeding value	Dominance deviation	VA	VD	VG
AA		64.04	63.2			
AB	Weaning Weight	63.23	64.49	0.29	1.03	1.32
BB		65.36	62.42			

Table 2. Breeding values, dominance deviation for DRB3 genotypes and genetic variance and its content (Additive and dominance variance) for total milk production and length of peak lactation

Allele	Trait	Average allele effect	The average effect of allele substitution
A	Birth Weight	0.2844	0.819
B		- 0.528	- 0.819
Allele	Trait	Average allele effect	The average effect of allele substitution
A	Weaning Weight	0.28	0.804
B		- 0.52	- 0.804

As for the mean effect of allele substitution, it was also in favor of the dominant allele A because of its recessive host B for the weight at birth and weaning trait. The values of the recessive allele were negative -0.528 and -0.52, respectively. The mean effect of allele substitution was also in favor of the dominant allele A on account of its recessive host B for the weight at birth and weaning trait. The values of the recessive allele were negative -0.528 and -0.52, respectively.

The mean effect of allele substitution was also in favor of the dominant allele A on account of its recessive host B for the weight at birth and weaning trait. The values of the recessive allele were negative -0.528 and -0.52, respectively. This value shows the effect of selection for one of the genes at the expense of the allele on the general mean of the studied trait.

This result is broadly consistent with the fact that birth weight and weaning weight are quantitative traits that are greatly influenced by the environment, as it was found that the inheritance of these traits was 20-30% for birth weight and 20-40% for weaning weight (21). It is affected by a large number of genes, thus reducing the individual influence of any of the studied genes, so studying more genes helps develop breeding and mating programs for dairy cows (22).

This result indicates the possibility of using this gene in animal breeding and improvement programs by selecting the studied traits to obtain a higher value of additional variance within the total variance. The recorded data showed that the AA genotype was better because of its higher reproductive value compared to other genotypes because the additional effect will be inherited on the offspring (3), and the average effect of the allele within the overall effect of all affected genes on the studied traits in order not to underestimate it (the average effect of the allele) between the value-added or lost as a result of choosing one of the alleles (20), which supports the adoption of this gene within the breeding and improvement programs. These results were attributed to the role of a complex histocompatibility gene in increasing the body's immunity against pathogens, including the bacterial causes of mastitis that affect the lactic gland in cows (23) and thus lead to improving the health of the cows and increasing the amount of feed consumed during pregnancy and after birth, which helps to produce Born in calves with good birth weights, as well as an excellent daily weight gain, as a result of the effect of this gene on the health of newborns and thus obtaining a good weaning weight also (15).

4. Conclusion

It is evident from the recorded data that it is crucial to adopt the data of this gene within the programs of improving the production of these two traits and their early prediction, as well as the importance of the selection of allele A and its actual value if it is homo or hybrid for both traits birth and weaning weight traits.

Authors' Contribution

Study concept and design:
Acquisition of data:
Analysis and interpretation of data:
Drafting of the manuscript:
Critical revision of the manuscript for important intellectual content:
Statistical analysis:
Administrative, technical, and material support:

Ethics

We hereby declare all ethical standards have been respected in preparation of the submitted article.

Conflict of Interest

The authors declare that they have no conflict of interest.

References

1. Ma L, Brautbar A, Boerwinkle E, Sing CF, Clark AG, Keinan A. Knowledge-driven analysis identifies a gene–gene interaction affecting high-density lipoprotein cholesterol levels in multi-ethnic populations. PLoS Gen. 2012;8(5):e1002714.
2. Lopes MS, Bastiaansen JW, Janss L, Knol EF, Bovenhuis H. Estimation of additive, dominance, and imprinting

genetic variance using genomic data. Genes Genom Genet. 2015;5(12):2629-37.

3. Jiang J, Shen B, O'Connell JR, VanRaden PM, Cole JB, Ma L. Dissection of additive, dominance, and imprinting effects for production and reproduction traits in Holstein cattle. BMC Genet. 2017;18(1):1-13.

4. Moore T, Haig D. Genomic imprinting in mammalian development: a parental tug-of-war. Trends Genet. 1991;7(2):45-9.

5. Wittenburg D, Melzer N, Reinsch N. Genomic additive and dominance variance of milk performance traits. J Anim Breed Genet. 2015;132(1):3-8.

6. Xiang T, Christensen OF, Vitezica ZG, Legarra A. Genomic evaluation by including dominance effects and inbreeding depression for purebred and crossbred performance with an application in pigs. Genet Sel Evol. 2016;48(1):1-14.

7. Pegolo S, Mota LFM, Bisutti V, Martinez-Castillero M, Giannuzzi D, Gallo L, et al. Genetic parameters of differential somatic cell count, milk composition, and cheese-making traits measured and predicted using spectral data in Holstein cows. J Dairy Sci. 2021;104(10):10934-49.

8. Amorena B, Stone W. Serologically defined (SD) locus in cattle. Science. 1978;201(4351):159-60.

9. Pantelić V, Sretenović L, Ostojić-Andrić D, Trivunović S, Petrović MM, Aleksić S, et al. Heritability and genetic correlation of production and reproduction traits of Simmental cows. Afr J Biotechnol. 2011;10(36):7117-21.

10. Spooner R, Levéziel H, Grosclaude F, Oliver R, Vaiman M. Evidence for a possible major histocompatibility complex (BLA) in cattle. Int J Immunogenet. 1978;5(5):335-46.

11. Vandre R, Sharma A, Gowane G, Ravi R, Shweta R, Sinha R, et al. Polymorphism and disease resistance possessions of MHC class II BoLA genes. Double Helix Res-Int J Biomed Life Sci. 2014;5(2):362-72.

12. Dibyendu C, Avtar S, Tantia M, Archana V, Chakravarty A. Genetic polymorphism of BoLA-DRB3. 2 locus in Sahiwal cattle. Anim Sci Report. 2015;9(1):33-40.

13. Paswan C, Bhushan B, Patra B, Kumar P, Sharma A, Dandapat S, et al. Characterization of MHC DRB3. 2 alleles of crossbred cattle by polymerase chain reaction-restriction fragment length polymorphism. Asian-Australas J Anim Sci. 2005;18(9):1226-30.

14. Calus MP. Genomic breeding value prediction: methods and procedures. Animal. 2010;4(2):157-64.

15. Al-Waith K, AL-Anbari N, Mohamed T. Relationship of the DRB3 gen polymorphism with productive performance in Holstein cows. J Entomol Zool Stud. 2018;6(2):2363-6.

16. Falconer DS. Early selection experiments. Annu Rev Genet. 1992;26(1):1-16.

17. Schaeffer L. Strategy for applying genome-wide selection in dairy cattle. J Anim Breed Genet. 2006;123(4):218-23.

18. Visscher P, Woolliams J, Smith D, Williams J. Estimation of pedigree errors in the UK dairy population using microsatellite markers and the impact on selection. J Dairy Sci. 2002;85(9):2368-75.

19. El-Saied U, De la Fuente L, Rodríguez R, San Primitivo F. Genetic parameter estimates for birth and weaning weights, pre-weaning daily weight gain and three type traits for Charolais beef cattle in Spain. Span J Agric Res. 2006;4(2):146-55.

20. Falconer DS. Introduction to Quantitative Genetics: Pearson Education; 1996.

21. Montaldo HH, López CT, Lizana C. Genetic parameters for milk yield and reproduction traits in the Chilean Dairy Overo Colorado cattle breed. Cienc Investig Agrar. 2017;44(1):24-34.

22. Yaser ML, Senkal RH. Effect of mutation site of k-casein gene on protein quantity, composition, and other milk constituents in Holstein cows. J Pharm Sci Res. 2019;11(2):398-401.

23. Behl JD, Verma N, Tyagi N, Mishra P, Behl R, Joshi B. The major histocompatibility complex in bovines: a review. Int Sch Res Notices. 2012;2012.