Estimation of breeding value, genetic variation of reproductive performance by genotyping of DRB3 gene in Holstein cows

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Abstract

This study was carried out in Al-salam station for Dairy cattle, from January/11/2016 to January/11/2017, on 50 Holsein cows to study the effect of DRB3 gene information and estimate gene substitution, breeding value, dominance deviation which leads to genetic variation for services per conception and days open depending on DRB3 gene information. the results show a significant impact ($p<0.05$) of gene polymorphism on both traits, cows with AA genotype were better than cows with AB, BB respectively, also cows with AA genotype were better than cows with AB, BB genotype in breeding value for both traits, the variance value tended to additive variance at the expense of dominance variance for both traits, the effect was positive for the genetic replacement of the A allele compared to the B allele for both traits. This supports the selection of the A allele when it is present in homozygotes or heterozygotes for genetic data used in breeding programs and its importance for both traits.

Keywords: DRB3 gene information, Breeding value, Reproductive traits, Holstein cows.

Introduction

Dairy cow's products are considered one of the main lines of the agricultural sector, and milk is the main animal product in most countries of the world, for many years, governments have collected statistics on the productive, reproductive and milk quality characteristics of Holstein cows(25).

Reproductive performance is the main concern of the modern cattle breeding industry worldwide by determining the profits of milk production and processing (17). Poor reproductive performance is one of the reasons for excluding cows from the herd, because it affects the amount of milk produced per cow per day and affects the longevity of the cow and the period of her stay in the herd and indirectly affects the costs of replacing the herd and the costs of breeding (31).

By calculating the revenues of milk production and processing, reproductive performance is the primary issue of the current cow breeding business globally (17). One of the reasons for excluding cows from the herd is poor reproductive performance because it affects the amount of milk produced per cow per day, the longevity of the cow and the time she spends in the herd, and it indirectly affects the costs of breeding and replacing the herd (2, 31).

By relying on genome information to reveal genetic variation in different traits sites and overlapping in their effect on the variation for reproductive traits after calculating differences depending on the degree of similarity between individuals of the same family (16), the effect of dominance also had an added value on the additional variability of changing the studies traits. Therefore, many studies began to study this effect due to the variation of the dominant role in the total variance of the quantitative traits in which more than one pair of genes contributed (4; 10). Although the study of gene maps has largely focused on additional variability, several studies have emphasized the importance of the non-neglected contribution of QTL sites on the genome that are considered as genetic markers for these traits.(21). Using the DRB3 genes information, we can estimate the breeding value, variance and impact of estimated gene substitution on some reproductive traits in Holstein cows (24). After determining the differences based on the degree of similarity between family members, it is possible to use genome information to reveal the genetic variation in the various genetics lactations and the overlap in their impact on the variation of reproductive characteristics.

The bovine lymphocyte antigen (BoLA) system is known as the major compatibility complex in cattle (3,5and 6). Major compatibility complex (MHC) genes encode glycoprotein molecules on the cell surface of the multitude of hereditary phenotypes, which re-send the antigen peptide to T cells (23; 26), thus they play a major and fundamental role in the immune response to foreign effects, harmful and pathogenic factors. The main histocompatibility complex gene is located on chromosome 23 and consist of regions I, IIa, IIb and III.(9), the DRB3 gene site has received wide attention due to its

polymorphism and its association with reproductive traits in dairy cattle (22), 130 BOLA-DRB3 alleles had been identified which contained 5 exons and 4 introns (http:/www.ebi.ac.uk/ipd/mhc/bola/) (18).

And that polymorphism in alleles can produce more than 20 amino acids, that each allele has an advantage in expressing the type of complex compatibility of tissue and that these differences are in the location of binding peptide and antigen and thus specialized functionally to provide antigens for the production mainly from external proteins and parasites of T cells helps T cells, as their cells play several important roles, including the effeteness of phagocytes and lymphocytes. The phagocytic cell look out and swallow external viruses, bacteria and parts of most of the parasites attacking and thus play a large role in the immune response anybody as long against diseases (20), so the aimed of this study was to estimated breeding value, total genetic variance and its content from additive variance and dominance variance and gene substitution effect for milk production and length of peak lactation traits.

Materials and Methods

this study was to conducted in Al-Salam station for Dairy Cattle / Private Sector, (Al-Latifia district 25 km south of Baghdad), for the period from 1-11-2016 to 1-11-2017, on 50 Holstein cows to estimate breeding value, dominance deviation, which made genetic variation for milk production and length of peak lactation depending on DRB3 gene information and estimate gene substitution effect of the gene, milk production was recorded twice daily in the morning and evening and recording the total milk production and length of peak lactation for lactation season 20116-2017.

Blood was collected by a medical syringe from the jugular vein in a 15 ml sterile polypropylene tubes containing 0.5 ml of EDTA (0.5M) as an anticoagulant by the phenol chloroform extraction by the veterinarian at the station. The 284 bp fragment consisting (28) of the 267 bp exon 2 regions 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) as a program in table(1).

Table 1. The procedure for amplifying DRB3 gene segment.

Reaction stage	Temperature (c̊)	Time	Cycles
Initial denaturation	49	4 min.	30
Denaturation	94	60 sec.	
Annealing	60	45 sec.	
Elongation	72	45 sec.	
Final elongation	72	5 min.	

(Paswan et al., 2005)

After the polymerase reaction was finished, the polymorphism of the DRB3 gene were identified in blood samples from cows after proceed the cutting to required piece of gene (284 bp) by e restriction enzyme HeaIII from Haemophilus aegyptius bacteria the digestion with HeaIII .

Equations used to calculate values were according to (13) as:

Average allele A effect $\alpha A = q [a+d (q-p)]$.

Average allele B effect $\alpha B = p [a+d (q-p)]$.

And average of substitution means the difference between the two values.

1-Breeding values.

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

2- Dominance deviation

$AA=-2q^2d$, $AB=2pqd$, $AA=-2p^2d$

3- Different data:

α^2, $VD=4p^2q^2d^2$, $VG=VA+VD$ $VA=2pq$

Results and Discussion

Following the completion of the polymerase reaction, the DRB3 gene polymorphism was detected in blood samples from cows after the restriction enzyme *HeaIII* from bacteria was used to cut the appropriate section of the gene (284 bp) out. Four restriction sites were discovered by the *HaeIII* digestion, resulting in three fragments:

1- AA genotype (167, 52 and 52) bp

2- AB genotype (219, 167, 52 and 52) bp

3- BB genotype (219 and 52) bp

The study findings indicate that the frequency of the dominant allele (A) was 0.65, with the other allele (B) accounting for 0.35. Additionally, the distribution ratio of DRB3 gene polymorphism was 46.00% for AA, 42.00% for AB, and 12.00% for BB.

It is clear from Table (2) that the dominant allele A of the DBR3 gene positively affects the trait of services per consumption, as it reduces by -0.066 from the general average for this trait, and thus it is more effective than the mutant allele B, the decrease in services per consumption necessary for fertilization reflects positively on the period between two calving's and thus the total number of heirs during the productive life of the cow (7; 12 and 30).

The individuals carrying the dominant allele came with the least number of days open, and this indicates that the A allele supports, in one way or another, the return of the uterus to its normal state during a shorter period than the individuals carrying the mutant allele B, as the decrease of this period it requires the return of the uterus to its normal state in order for fertilization to succeed (20).

The value of the mean effect of an allele is a very important value in the field of genetic improvement of herds through generations because it represents the value that is transmitted from parents to offspring (13).

The value of substituting the A allele for the two traits was negative (-0.1875 and -6.0965, respectively) (Table 2), and it represents a decrease in the aforementioned values compared to its

counterparts that carry the mutant allele B. These values reflect the expected change in the general average. When selecting for the A allele against the mutant allele (14).

Table 2. The average effect of the allele and allele substitution of DBR3 gene on services per consumption and days open

Allele	Trait	Average of allele effect	Average of allele substitution
A	Services per consumption	-0.066	-0.1875
B		0.1219	0.1875
Allele	Trait	Average of allele effect	Average of allele substitution
A	Days open	-2.134	-6.0965
B		3.9627	6.0965

Table (3) showed that individuals with genotype AA came with the lowest educational value for the characteristic of the number of inseminations needed for fertilization (1.47563), and then followed by group AB, and group BB came with the highest value. Therefore, preference is given to the genotype AA, since the characteristic of the services per consumption is opposite, meaning that the fewer number is the better number (19, 15). The same applies to the period from birth to fruitful pollination, as the group with composition AA came with the lowest value, which is therefore the best

The breeding value expresses the value of the individual calculated on the basis of the difference between the average of its birth from the general average of the herd, meaning that individuals are evaluated on the basis of the value of their births (13, 27), which is an important value in the field of genetic improvement.

The values of the dominance deviations are higher than the educational values for the two studied traits, that the dominance deviations express the allelic interaction in one site and it is a value that is not inherited (8, 29), that the high value of the dominance deviations with the increase in the number of copies of the mutant allele gives precedence in the selection in favor of the pious dominant genotype.

Additive variance of this gene is higher than the dominance variance, and since the assemblage variance is the variance that will be inherited (11), this shows that the additive effect of this gene affecting the studied traits has a good effect ratio within the total cumulative effect of the effector genes (1).

Among the candidate genes (candidate genes), which are the genes with a direct and high effect on the trait studied, and thus the DBR3 gene can be considered among these genes in the selection

programs for services per consumption needed for fertilization and days open.

Table 3. Breeding values, dominance deviation for DRB3 genotypes and genetic variance and its content (Additive and dominance variance) for services per consumption and days open

genotype	Trait	Mean	Breeding value	Dominance deviation	VA	VD	VG
AA	Services per consumption	1.48	1.47563	1.585438	0.015996	0.0063401	0.022336
AB		1.79	1.6631	1.6865			
BB		1.75	1.85063	1.75475			
genotype	Trait	Mean	Breeding value	Dominance deviation	VA	VD	VG
AA	Days open	81.5	80.798	80.55041	16.91113	3.6606212	20.57175
AB		90.5	86.894	86.9788			
BB		91.1	92.991	88.6188			

As we show in table (3) genotype AA individuals had the lowest breeding value for the necessary number of fertilization attempts (1.47563), followed by groups AB and BB, who had the next highest value. Therefore, genotype AA is preferred because it has the opposite characteristic of the number of inseminations, which means that the lower the number, the better. The group with composition AA had the lowest value for the time from fertilization to fruitful pollination, making it the best.

The result indicates that this gene could be useful in selective programs for improving the studied traits. The AA genotype was found to have a higher breeding value and thus be more advantageous than other genotypes due to a higher value of additive variance within the total variance. This is because the additive effect can be passed down to offspring, as noted by (17). Moreover, the average allele the adoption of this gene within selective breeding programs is supported by an effect within overall effect for all affected genes on examined characteristics not to underestimate it (Average of Allele Effect) between gained or lost value as a consequence of the selection of one of the alleles (14).

Conclusion

Based on the information presented, it is clear that incorporating the data on this gene is crucial for enhancing the reproduction of these two traits and accurately predicting them early on. Additionally, it is important to consider the significance of selecting allele A and determining its purity or hybridity for the services related to both traits, such as service per consumption and days open.

Conflict of interest

The authors declare no conflict of interest.

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