

ARTICLE / INVESTIGACIÓN

Genetic analysis of milk production and lactation period in Holstein cows according to BTN1A1 Gene Polymorphism

Riyadh Senekal, Hussien Al-Waith, Nasar Al-Anbari, Wafa'a Al-Samarai

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University of Baghdad, Iraq.

Corresponding author: riyadh.senkal@coagri.uobaghdad.edu.iq.

Abstract: The results showed that the Holstein BTN1A1 gene has two alleles (A allele) which is superior to the second allele (B allele) in the two values of the substitution effect and the average effect of the allele, and the homo genotype AA over the hetero genotype AB was successful in the breeding value of the two traits. It was also revealed through the new equations that the gene is responsible for the characteristic of milk production of the total output and the amount of 37725 Iraqi dinars of the full value of the milk price, and it also affects by ± 7.24 days of the length of the milking season, which is estimated at 3583.8 Iraqi dinars. It is responsible for the inheritance of 70.09 kg of total milk production for 6.35 days/season length, reflecting the product's price value. The possibility of adopting the BTN1A1 gene within the selection programs to improve some productive traits, as well as the possibility of conducting a comparison between genes on the basis of the new equations, determining their contribution to the studied traits, and choosing the most influential gene to be an effective marker in the selection of quantitative traits.

Key words: Genetic analysis, Milk production, length of lactation, Holstein cows, BTN1A1 gene.

Introduction

Heritability is defined as the ratio of the genetic variance to the total variance, which means that it is the product of dividing the part of the variance due to the inheritance (numerator) by the total variance of the trait (denominator). It gives an idea of the extent of the effect of heritage on a specific quantitative quality; for example, the heritability of a milk production trait is 25%. This percentage shows the total impact of the total of genes affecting the feature, meaning that it is a function of the estimation of the increase or decrease in the genetic variation resulting from the selection of parents and mothers that are transmitted to the next generation without knowing the contribution of each gene to this ratio^{1,2}, which is shown by the new equation (that is, the proportion of each gene's contribution to the variance of the studied quantitative trait).

The most critical traditional methods for calculating the heritability of any characteristic are full-sib, half-sib, regression on one parent, regression on average parents, and third-generation declines over the first generation, and all of these methods require information for at least two generations. Therefore, the environment is different between the two generations, which leaves a certain percentage of error in estimation, and the result of these equations represents the sum of the effect of genes affecting the studied trait entirely without specifying the development of each gene separately, and the new equation dealt with the two previous points³.

Calculating the heritability of the trait based on the gene's contribution to the total genetic variance does not need information about the ancestors of the current generation (you do not need the knowledge of the previous generation), as the equation is more accurate than its predecessors because it studies the effect of genetics and the environment

in one time and not between two different times, which in turn causes the addition of a ratio. It needs to be corrected in heritability, through which it is possible to compare the other genes that affect the studied trait and choose the gene most influencing the selection processes in what is known as marker-assisted selection.

It estimates the value of the quantitative and price effect of the gene (in the studied herd) using the root of the total variance since the variance is the square of the sum of the deviations of the values from the general average. This value and dividing the result by the number of individuals will dictate the extent of the effect of the studied gene (\pm) on the studied trait, such as grams of weight or minutes of height and according to the type of the studied trait. The studied gene per kilogram of milk, which is an essential value because the number of units (such as the number of kilograms) differs between individuals, as the general average of the trait represents the contribution of all genes affecting the studied feature without discrimination of the practical value of each gene, which can be identified through the equation. It is possible to use the same equations to predict the gene's contribution to the same traits studied in the next generation, and this is done by replacing the genetic variance with the clustering variance since the clustering two is the one that will be inherited to the next generation.

Butyrophyllin (BTN) belongs to the immunoglobulin family of membrane proteins⁴; the bovine Butyrophyllin (BTN) gene is present in the long arm of chromosome 23, consisting of 8 exons and 7 introns^{5,6}.

Genetic variation in the bovine BTN1A1 gene has been studied as a genetic marker to control milk production and lipid content at the QTL. It affects economically essential traits in milk animals because it is expressed explicitly in

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lactating milk tissues, and the BTN1A1 gene product may act in the secretion of milk fat⁷.

Therefore, this study aims to devise new equations to analyze the genetic information of the studied gene to facilitate understanding the genetic contribution in quantitative units (grams, centimeters) of the studied traits.

Materials and methods

This study was conducted in Al-Salam station for Dairy cattle /private sector (Al-Latifia district 25 km southern Baghdad) on 50 Holstein cows, genetic analysis of the BTN1A1 gene was carried out according to the characteristics of milk production and the length of lactation to devise modern equations to calculate the genetic equivalent in the broad sense and limited and the amount of the gene's contribution to the amount of total milk produced as well as The contribution of the gene to the length of lactation as well as its final effect on the milking price in days. Based on the genetic information, DNA samples of good quality, purity and concentration were used for further analysis; the polymerase chain reaction (PCR) technique for BTN1A1 typing is based upon the extensive polymorphism that is present in an 893 region of exon 8 of the butyrophyllin gene was amplified by using primers as^{8,9}.

-Inferred equations:

1- Heritability of a gene effect (in the broad sense):

$$H^2G = 2pq\alpha^2 + 4p^2q^2d^2/6^2$$

P: repetition of the dominant allele, q: repetition of the recessive allele, α : the average effect of allele substitution, d: repeat the hybrid composition, δ : variance

The numerator in this equation is the sum of the covariance $A=2pq\alpha^2$ and $D=4p^2q^2d^2$; as for the denominator, it represents the total variance of the trait and can be obtained from one of the following two equations:

$$A - \delta^2 = \sum x^2 - (\sum x)^2 / n$$

$$B - SST = \sum Y_{ij}^2 - CF$$

2- Heritability of a gene effect (in the narrow sense):

$$h^2G = 2pq\alpha^2 / \delta^2$$

3- Quantitative effect of a gene:

4- The calorific value of the gene effect:

$$\sqrt{(vA+vD/n)} \times \text{Price} \quad (1)$$

Since the previous value represents the estimate of the increase and decrease in the units of the quantitative trait, multiplying it by the value of one unit price will represent the price value of the gene effect.

5- The ratio of the quantitative effect of a gene:

$$\sqrt{(vA+vD/n)} / M \quad (2)$$

Dividing the quantitative effect value by the average of the trait will show the extent of the gene's contribution to one unit of the quality (for example, the effect of the studied gene in every kilogram of milk), which is an essential value because the number of units (such as the number of kilograms) differs between individuals, as the general average of the trait is It represents the contribution of all genes affecting the studied trait without discrimination of the practical value of each gene, which can be identified through the current equation.

6- The percentage of the gene's economic contribution to the price value of the studied trait.

$$\sqrt{(vA+vD/n)} / M \times \text{price} \quad (3)$$

It represents the percentage of the gene's contribution to the unit price of the studied quantitative trait.

7- Prediction of the quantitative and price contribution of the fetus in the next generation:

$$\sqrt{(vA/n)} \quad (4)$$

- Quantitative effect of a gene in the offspring:

The clustering variance is the part inherited from the genetic variance of the individual, which is a fair value because it is part of the variance value, which in turn is a fair value for deviations from the general mean of the trait. In the offspring of the current herd.

a- Calorific value of the quantitative effect of a gene in the offspring:

$$\sqrt{(vA/n)} \times \text{Price} \quad (5)$$

Multiplying the previous value (the quantitative effect) by the price of one unit of the quantitative trait indicates the price value of the effect of the gene on the offspring.

b- The percentage of the quantitative effect of a gene in the offspring:

$$\sqrt{(vA/n)} / M \quad (6)$$

The division of the value of the quantitative effect of the gene in the offspring by the average of the quantitative trait in the progeny shows the ratio of this effect, which is an essential value because the number of units differs from one individual to another, which gives a specific value for each individual if this value is multiplied by the number of units of the quantitative trait that the individual possesses.

c- The price value of the ratio of the quantitative effect of a gene in the offspring:

$$\sqrt{(vA/n)} / M \times \text{Price} \quad (7)$$

Multiplying the previous equation with the price of one unit of the studied quantitative trait shows the extent of the gene's contribution to the cost of this unit and its reflection on the price of the animal as a whole.

Results

The AA genotype recorded the highest educational value, and it is consistent with the fact that this combination is the highest in milk production and lactation period, as well as the least deviating dominantly compared to the genotype (AB) (Table 1), that this result indicates that the AA genotype is the best. And because the additive variance (VA) is high compared to the dominant variance (VD), so choosing the best genotype (AA) will be feasible because the clustering effect will be inherited for the following generations^{4,10}. It was understanding the variation mechanism in hybrid individuals¹¹.

The average effect of the A allele of BTN1A1 was the highest compared to that of the B allele, and it is expected that the presence of the allele A added an increase in the

total milk production and lactation period and the average substitution effect of allele A was positive because it contributed to the total milk production and lactation period (Table 2), which shows the value Added or missing as a result of selection for one of the alleles³, these results give an absolute preference to allele A of the BTN1A1 gene over the mutant B allele, which indicates the importance of selection in favor of this allele

Table 2. Average of allele effect and the average of allele substitution for total milk production and lactation period traits.

The equations extracted in this research found that the heritability in its broad and narrow sense amounted to 0.26 and 0.22, respectively, for the milk production trait is within the logical range of the trait^{12,13}.

Also, the quantitative effect of the gene is 75.45 kg (Table 3) of milk within the total milk production, meaning that the AA genotype adds this amount. Still, the mutant structure causes a loss of the same amount, which gives clear pictures of the quantitative contribution of this gene within the total quantitative effect of all genes affecting the production trait. Milk is a quantitative trait that is affected by a large number of genes¹⁴, and the effect of the gene on each kilogram of milk reached 0.04 kg (Table 3). If we assume that the price of milk is 500 Iraqi dinars, it affects the price value of milk by an amount of 37725 and 200 dinars in the value of Total milk produced and price per kilogram, respectively; on the other hand, the value of what this gene inherits to the next generation in the case of the AA composition is approximately 70 kg of milk per season and 0.037 kg per kilogram of milk per person (Table 3) if these values are calculated based on the cumulative variance of the gene, which is the value that is inherited to the next generation. Suppose the price value of the inherited values is calculated. In that case, it becomes evident that this gene is responsible for the value of 35 thousand and 18.5 dinars of the

total milk price and each kilogram in the next generation.

These values are understandable for educators and economists, which enhances their understanding of the importance of marker-assisted selection programs and facilitates comparison between different genes, relying on candidate genes within the selection programs.

The equations extracted in this research found that the genetic equivalent in its broad and narrow sense amounted to 0.11 and 0.09, respectively, for the lactation period (Table 4), which is within the logical range of the trait^{15,16}.

The gene's quantitative effect on the lactation period's characteristic was 7.24 days (Table 4). It shows that the pure, wild composition of the gene increases the production season by seven days (Table 4), which is very close to the price value of the gene calculated through the total production of milk, which is 37725 (Table 3), which supports the accuracy of the equations that the researcher devised in this research. And it supports the adoption of this method with other genes affecting the characteristic of milk production and lactation period, considering that this characteristic is A quantitative characteristic that is affected by a large number of genes, as it can be seen from the table that the value of the effect of this gene per day ranges from 0.037 per day, meaning its weight of 18 Iraqi dinars (Table 4).

As for the amount of this gene inherited, it increases the number of days of the production season for the offspring by about 6.35 days, with a price value of 3143.25 and 0.03 dinars for the season and one day, respectively.

That the price value of the gene matches when measured by season length and total production indicates the importance of adopting these equations to clarify the percentage of genes participation accurately and naturally in the studied traits as well as facilitate the task for breeders and economists in adopting genetic improvement programs, which enhances the improvement of the studied traits and increases the support of researchers in this field.

Genotype	Traits	Mean	Adjusted average	Breeding value	Dominance deviation	VA	VD	VG
AA	Total milk production	1992.24	1910.874	2347.978	1872.462	245647.91	39025.15	284673.06
AB		1486.07		1567.4358	2108.42			
BB		0		786.894	2418.85			
Genotype	Trait	Mean		Breeding value	Dominance deviation	VA	VD	VG
AA	lactation period	195.35	192.6224	232.274	187.8349	2021.46	606.21	2627.68
AB		158.74		161.46759	217.244			
BB		0		90.6612	255.935			

Table 1. Mean, adjusted average, Breeding value, Dominance deviation and variance components of milk production and lactation period.

Allele	Trait	Average of allele effect	Average of allele substitution
A	Total milk production	218.55176	780.542
B		-561.9902	-780.542
A	lactation period	19.825792	70.8064
B		-50.98061	-70.8064

Table 2. Average of allele effect and the average of allele substitution for total milk production and lactation period traits.

Measurements of the actual and relative values of gene	Values (total milk production)
Heritability (broad)	0.26
Heritability (Narrow) based on VA	0.22
Measurements based on genetic variance (current values)	
The value of the actual (real) effect of a gene (or quantitative effect)	75.45 Kg / total weight
The price effect or total (price value)	37.725 Iraqi dinars *
Percentage of the true effect of the gene(Kg)	0.04 / day
The price effect of the gene (Kg)	200 Iraqi dinars
Measurements based on clustering variance (predicted genetics)	
The actual inherited collective effect (Kg)	70.09 Kg/ weight
Inherited calorific value (total)	35.045 Iraqi dinars
Percentage of the true aggregate effect of inheritance (Kg) ¹	0.037 Kg
The inherited calorific value ratio(Kg)	18.5 Iraqi dinars

¹ 1 Kg of milk = 500 Iraqi dinars

Table 3. Measurements of the actual and relative values of genes for total milk production trait.

Conclusions

We conclude from this study the possibility of adopting these equations in calculating the effect of individual genes affecting the quantitative traits studied, mainly after it was found in this research that the gene obtained the same value after studying its effect using these equations through two characteristics separately. The BTN1A1 gene can be adopted in milk production trait genetic improvement programs (AA genotype).

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Measurements of the actual and relative values of gene	Values (lactation period)
Heritability (broad)	0.11
Heritability (Narrow) based on VA	0.09
Average milk production per day	9.95 Kg ¹
Measurements based on genetic variance (current values)	
The value of the actual (real) effect of a gene (or quantitative effect)	7.24 Kg / total weight
The price effect or total (price value)	35.838 Iraqi dinars ²
Percentage of the true effect of the gene(Kg)	0.037 / day
The price effect of the gene (Kg)	18.29 Iraqi dinars
Measurements based on clustering variance (predicted genetics)	
The actual inherited collective effect (Kg)	6.35 Kg/ weight
Inherited calorific value (total)	31.432 Iraqi dinars
Percentage of the true aggregate effect of inheritance (Kg)	0.03 Kg
The inherited calorific value ratio(Kg)	14.85 Iraqi dinars

¹ Price (4950 Iraqi dinars)

² 1 Kg of milk = 500 Iraqi dinars

Table 4. Measurements of the actual and relative values of the gene for the lactation period trait.

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