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ESTIMATION OF BREEDING VALUES AND GENETIC VARIANCE DEPENDING ON LACTOFERRIN GENE POLYMORPHISM IN IRAQI GOAT BREED

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Abstract

Data were made available of 50 native does reared in Ruminants Research Station belong to the ministry of Agriculture, Iraq to determine the breeding values and genetic variance depending on Lactoferrin gene polymorphism in Iraqi goat breed. Results showed that the single nucleotide polymorphism (SNP) was detected as substitution of nitrogen base C to T, which lead to two alleles, first was the wild allele (A) which contain of two pieces (264 and 166 bp) while second was the mutant allele (B) which contain of complete piece (430 bp).Allele frequency was 0.77 and 0.23 for A and B respectively and the genotypes frequency was 0.62, 0.30 and 0.08 for AA, AB and BB respectively. the average effect of allele A was - 0.0007 compared with average of effect B, which was 0.0023 for milk protein rate. Average effect of allele A was – 1.953 kg while the average effect of allele B was 6.539 kg of milk yield as a deviation from mean. Average gene substitution A instead of B was – 0.003 while average substitution B instead of A was 0.003 for protein rate. Milk yield was increased about 8.493 kg by substitution B allele instead of A allele. Breeding values were differed according to genotypes for milk yield namely, -3.906, 4.586 and 13.078 for AA, AB and BB genotypes respectively and the genetic deviations were 0.337, -1.126 and 3.771 for the three genotypes, respectively.

Key words : Lactoferrin gene, breeding value, Iraqi goats.

Introduction

Goat is a widespread animal and more than 850 million goat around the world and the economic value of this animal is different from country to other and determined through the productive and reproductive efficiency (Hermiz, 2005; AL-Barzinji, 2012). The native goat in Iraq is distributed all over the country and reared with the sheep as a mixed flock and the Iraqi goat breeds characterized with undertake to live in harsh conditions of poor pastures and high resistance of diseases (Elia *et al*., 2005; Ishak *et al*., 2005). The latest statistic reported that the goat population was about 1.4 million (Ministry of Planning, 2008). The major aim of goat rearing is for meat and milk production while the hair production is still a secondary aim. Many attempts were done to improve the native goat performance through exploiting the progress in genetic and biological sciences and determining many of genetic markers, which related strongly with the phenotype variance of important traits such as milk , meat production, reproduction traits and behavioral performance (Haradecka *et al*., 2008; Mirkana *et al*., 2010). One of the genetic markers, which used in this field is lactoferrin gene which different in location and size in mammalian species, the gene located on chromosome 3 in human, on chromosome 9 in rat and on chromosome 22 for both goat and cow and contains of 17 exon with 16 intron (Teng, 2002).

Lactoferrin gene is responsible for oligo protein coding and the protein is correlated strongly with Ferineand transport it. Lactoferrin protein is secreted from the extract glands like mammary gland and sweat glands and it play a crucial role in many biological functions (Cheng *et al*., 2008). Kanyshkova *et al*. (2003) reported that lactoferrin protein behave like enzyme similar with

amylase, DNAse and RNAse, while Legrand *et al*. (2005) reported that the lactoferrin effect significantly on microbial pathogens inhibition especially Gram negative bacteria.

The major aim of the current study is to determine the breeding values and genetic variance in one locus (additive and dominant variance) through analysis of the polymorphism resulted from single nucleotide (SNP) in this gene and exploit it as a guideline to improve the local animal in Iraq.

Materials and Methods

Data were made available of 50 native does reared in Ruminants Research Station belong to the ministry of Agriculture, Iraq. The flock is reared in semi open sheds (35% open – 65% closed). Feeding is varied according season and the diet is mainly contained of concentrate feed about 500gm head/day and increased during reproduction season. Green feed was also supplied while the roughage feed was free (*add-libitum*).

Blood samples were withdrawn about 5ml from each animal from jugular vein by using vacuum tubes needles contain anti-coagulant (EDTA).

DNA was extracted by using special kit manufactured by Genead company and polymerase chain reaction (PCR) and restriction fragments length polymorphism (RFLP) method were used for detection the genotypes of region that studded (430 bp), which located in exon 4 of lactoferrin gene by restriction enzyme *NIaII* and special primer as : Forward 5-TGTCCCTGGGCTCTTTAG-3 and Reverse 5-CCGAAGTGGCTTGTGAA-3 (Akisa, 2012).

Milk samples were collected by using plastic tubes and send in the same day to the lab to determine the milk components by milkoscan system.

Average gene effect was calculated according to Falconer and Macay (1996) : Average effect of allele (A) $\alpha A = q[a+d(q-p)]$.

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

Average of gene substitution is the difference between αA and αB.

Breeding values were estimated as: $AB = \alpha 1+\alpha 2$, $BB = 2\ \alpha 2$, $AA = 2\ \alpha 1$.

Genetic dominant deviations were estimated: $BB = -2q^2d$, $AB = 2pqd$, $AA = -2p^2d$.

Total genetic variance (GV), Dominant variance (DV) and Additive variance (AV) were determined as: $GV=AV+DV$, $DV =4p^2q^2d^2$ and $AV=2pq\ \alpha^2$, respectively.

Statistical analysis

Data were analyzed by SAS (2012) and general linear model (GLM) method was used to study the lactoferrin genotypes.

Results

Results showed that the extraction of region that studded from lactoferrin gene (430 bp), which located on exon 4 by PCR-RFLP and special primer by special tubes (Mastermix PCRtube). Recognition site was recognized by *NIaII* restriction enzyme and the single nucleotide polymorphism (SNP) was detected as substitution of nitrogen base C to T, which lead to two alleles, first was the wild allele (A), which contain of two pieces (264 and 166 bp) while second was the mutant allele (B), which contain of complete piece (430 bp). The results are agreed with the results of Akisa (2012), but not agreed with those of Kang (2010).

Results showed that the allele frequency was 0.77 and 0.23 for A and B, respectively and the genotypes frequency was 0.62, 0.30 and 0.08 for AA, AB and BB, respectively.

Results represented in table 1 showed that the average effect of allele A was -0.0007 compared with average of effect B, which was 0.0023 for milk protein rate. Average effect of allele A was –1.953 kg while the average effect of allele B was 6.539 kg of milk yield as a deviation from mean. Average gene substitution A instead of B was –0.003, while average substitution B instead of A was 0.003 for protein rate. Milk yield was increased about 8.493 kg by substitution B allele instead of A allele.

Results showed that the breeding values (BV) of protein rate were 0.0014, 0.0016 and 0.0046 for AA, AB and BB genotypes respectively and the dominant deviations were 0.019, - 0.063 and 0.213 for the genotypes, respectively.

Genetic, dominant and additive variance were 0.007763, 0073 and 0.000032 for milk protein according to AA, AB and BB genotypes (table 2). Breeding values were differed according to genotypes for milk yield namely, -3.906, 4.586 and 13.078 for AA, AB and BB genotypes respectively and the genetic deviations were 0.337, -1.126 and 3.771 for the three genotypes, respectively. Total genetic variance , dominance and additive variance of milk yield was 25.4841, 0.0041 and 25.458 for AA,AB and BB genotypes, respectively.

Discussion

Depending on the results of the current study, we can notice a clear effect of alleles resulted from

Table 1 : Effect of average allele and average allele substitution on milk protein and milk yield.

Allele	Average allele effect	Average allele substitution
Protein rate		
A	-0.0007	-0.003
B	0.0023	0.003
Total milk yield		
A	-1.953	-8.493
B	6.539	8.493

Table 2 : Breeding values and genetic variances of protein rate and milk yield depending on lactoferrin genotypes.

Genotype	Breeding value	Dominant deviation	Additive variance	Dominant variance	Genetic variance
Protein rate					
AA	-0.0014	0.019	0.000032	0.00773	0.007763
AB	0.0016	-0.063			
BB	0.0046	0.213			
Total milk yield					
AA	-3.906	0.337	25.458	0.0041	25.4841
AB	4.586	-1.126			
BB	13.078	3.771			

nucleotides substitution on milk protein content and milk yield in Iraqi native does, this results support the past studies which referred to the importance of allele effect substitution on breeding value or genetic deviation in most of quantitative traits. In this study, the substitution of nucleotide C to T was enhance the milk yield therefore the does with BB genotypes were the highest breeding value compared with the other genotypes (AA and AB). In addition, the group with BB genotype was the highest additive variance compared with the other groups. The wide differences among groups make the genetic selection more easy and accurate especially in case of high additive variance because the additive variance is transfer completely to the next generations (Jicai, 2017).

Ma *et al*. (2012) reported that the determination of dominant variance is still difficult because the weakness of statistical tests, which used to detect non additive effects in quantitative traits. The past studies were not concordant with regard to the input of non additive variance in the phenotypic variance, Hill and Goddard (2008) referred to a limited effect of these factors on the phenotypic variance of economical traits while VanRaden (2016) noted to the importance of factors and considered it as a good source or indicators for prediction. Breeding values are effect significantly on selection activity because the relative response is proportional to accuracy of the breeding but the estimation of breeding value for traits such as milk yield requires a large data (Ronnegart *et al*., 2012). As a conclusion, the current study through a light on the possibility for using the polymorphism which resulted from SNPs that occur in lactoferrin gene as an efficient tool to divide the herd into sub genetic groups and calculate the breeding values or genetic variance . although the method, which used in this study looks like a good method for proceeding selection but further studies are needed to prove this assumption.

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