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## Estimation of genetic variance using data of prolactin gene in Turkish Awassi sheep

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### Abstract

This study analyzed the single nucleotide polymorphism (SNP) of 118 Turkish Awassi sheep. It was aimed to estimate the breeding value, additive, dominant variance and allele substitution of prolactin gene and their effect on milk production. Three genotypes were found, AA, AB and BB, using PCR-RFLP technique and *HeaIII* restriction enzyme (intron2). Breeding values of these genotypes were -1.9082, 0.8168 and 3.5438 respectively and dominant deviation were -0.2989, 0.455 and -1.0309 respectively, the values of genetic variance (VG), additive variance (VA) and dominant variance (VD) were: 8.11943; 3.8113 and 0.30813 respectively, the substitution effect mean of A and B alleles were 2.726 and -2.726. Whereas, the average gene effect of A and B alleles was 1.7719 and -0.9541 respectively. It can be concluded that selection of A allele and its actual value as one or two copies in individuals improve the milk production of Turkish Awassi sheep.

**Keywords:** Breeding value, dominant variance, alleles substitute, prolactin gene

### 1. Introduction

Prolactin gene is located on chromosome 20 and consists of five expression regions<sup>[1]</sup>. It encodes for prolactin enzyme which plays lots of roles in the development of mammary gland and the milking secretion<sup>[2]</sup>. Prolactin gene stimulates development of mammary gland and it is the main responsible of protean production and lactose in milk<sup>[3]</sup> as well as it works to increase perseverance in production<sup>[4,2]</sup>, so many studies were linked between genetic variation in this gene and phenotypic variation in milk production<sup>[2, 5, 6, 7]</sup> after a great development in livestock genotype detection, genomic information was become source for genetic variance detection and interaction between allelic and non-allelic genes and their effects on production variance traits instead of the resemblance between individual within the same family<sup>[8]</sup>. Genetic improvement which depends on selection programs based on genetic information focuses primarily on the dominant, additive and epistasis between allele and non-allele genes have a significant impact on livestock performance<sup>[9]</sup>. As to that the dominance effect has an added value to the additive effect within the variance of the studied trait so many studies focused on this effect because it has an important role in the overall variation of complex and production traits<sup>[10, 11, 12]</sup>.

It is important to analyze the genetic variance component to estimate the breeding value and the interaction between alleles which represented by additive and dominant values respectively<sup>[13]</sup>.

Many studies of genomic maps focused on additive variance but some studies insisted on non-additive effects on quantitative traits loci (QTL)<sup>[14]</sup>.

This study aimed to estimate of breeding value, additive, dominant variance and allele substitutes effects of prolactin gene and their effects on milk production and components in Turkish Awassi sheep and use the results as a guideline for improving the performance of livestock's.

### 2. Materials and methods

118 Turkish Awassi ewes aged from 1-6 years and 55-70 kg weights selected from the flock reared in ruminants' station research/ ministry of agriculture (20 km west of Baghdad).

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## 2.1 DNA extraction

Blood samples from each ewe was collected at the same time (10 ml from jugular vein) to determine the polymorphism of prolactin gene (Intron2) according to the procedure of Vincent and Rothschild [15]:

F: 5' - ACCTCTCTTCGGAAATGTTCA -3'

R: 5' - CTGTTGGGCTTGCTCTTTGTC -3'

The amplification reaction was carried out in the following conditions: an initial denaturation step at 92°C for 2 min followed by 35 cycles of denaturation at 92°C for 45 sec, annealing at 56°C for 45 sec and extension at 72°C for 3 min, and a final extension of 72°C for 5 min. the PCR-RFLP technique and *HeaIII* restriction enzyme was used to determine SNP in intron 2 of the prolactin gene.

## 2.2 Statistical Analysis

The genotypic frequencies, allelic frequencies, were analyzed with SAS program. The genotype distributions in this breed were tested for Hardy- Weinberg equilibrium using the appropriate chi-square ( $\chi^2$ ) test.

Equations used to calculate values were according to Falconer and Mackay [13].

1- Average allele effect, ( $\alpha_A = q[a+d(q-p)]$ ,  $\alpha_B = -p[a+d(q-p)]$ )

2-breeding values ( $AA= 2 \alpha_1$ ,  $AB= \alpha_1+\alpha_2$ ,  $BB=2 \alpha_2$ )

3- Dominants deviations

( $AA=-2q^2d$ ,  $AB=2pqr$ ,  $BB =-2p^2d$ )

4- The variances( $\alpha^2$ ,  $VD=4p^2q^2d^2$ ,  $VG=VA+VD$   $VA=2pq$ )

## 3. Results and Discussion

PCR-RFLP technique showed the existence of three genotypes for prolactin gene in Awassi sheep, AA and AB and BB (Figure 1), proportions of genotypes 23.73, 22.03 and 54.24 % respectively, and the frequency of alleles A and B 0.35 and 0.65, respectively sheep with genotype AA Registered the highest rate of milk production compared to AB, BB (114.09, 112.95 and 109.37 respectively). AA genotype recorded the highest breeding value, which consistent with the fact that this genotype is the highest milk production and it is also a less dominance deviation from another genotypes (AB AND BB) (Table 1).

Depending on the values of additive variance, we can select the AA genotype because it related to the highest value which will reduce the generation interval, increase genetic accuracy, low cost [16]. The accuracy of the use of genetic markers to estimate the breeding value is depends on the heritability, available data of phenotypes and their relationship with markers and the method used to assess the impact of genetic markers, and the low correlation between genetic markers and quantitative traits [17].

The dominance effect is the interaction of gene alleles which is important to understand the mechanism of variation in hybrid individuals [18]. In a study on Chinese local cows additive effect was negative for two of the sites of the gene Tf(-229.6, -132.9) While positive in another location (17.1). However, the identification of the non-additive effect

including the dominance effect is still difficult in the study of human and animal genetic maps and this is based on the weakening of the statistical tests in determining the non-additive effect of genetic loci [19]. The lack of full brothers (full-sibs) in the study reduces the estimates of non-additive effect because the full-sibs are the main source of the estimates of non-additive effect [9].

The emergence of the additive variance when a genetic analysis of any quantitative status does not mean that genes operate through the addendum only (in the sense that it showed no dominance or epistasis) the additive variance exist for genes, whatever the degree of its dominance and the degree of its epistasis [13].

In any case, there is at least one economic influence these components of genetic traits, but there is still debate about the contribution of these components in the economic traits and whether it can be used to predict the genetic characteristics [19]. Many studies indicated that mating systems using the additive and non-additive variance measurements in the selection programs were lead to increase the final genetic outcome (genetic gain) [20].

The average gene effect of allele A and B was 1.7719 and -0.9541 respectively (Table 2) the presence of the allele A led to production improvement, while the B allele led to decrease milk production, added value results from the selection of the best allele [13].

The average effect of gene substitution of allele A and B was 2.726 and -2.726, respectively (Table 2). Note that this value indicates the gene and not to genotype value associated with the genes carried by the individual transmits to their progeny and this will lead to the possibility of identifying the breeding value of the traits [13].

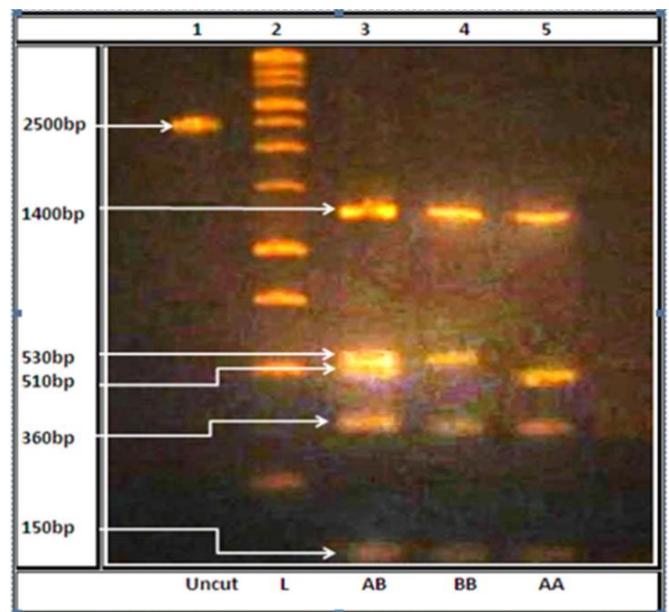


Fig 1: Genotypes of intron three in prolactin gene

Table 1: Breeding value and dominance deviation of genotype in prolactin gene for milk production

Genotype	Number	(A-TMP)	BV	DD	AV	DV	GV
BB	64	109.37	-1.9082	-0.2989	3.8113	0.30813	4.11943
AB	26	112.95	0.8178	0.455			
AA	28	114.09	3.5438	-1.0309			

A-TMP: Average of total milk production, BV: Breeding value, DD: The dominance deviation  
AV: Additive variance, DV: Dominance variance, GV: Genetic variance.

**Table 2:** The average gene effect and the average effect of gene substitution of allele

allele	average gene effect	average effect of gene substitution
A	1.7719	2.726
B	-0.9541	-2.726

#### 4. Conclusion

The AA genotype represented greatest breeding value, greater milk production and lesser dominant variation for Awassi Sheep.

#### 5. Acknowledgment

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