



# ESTIMATION OF GENETIC VARIANCE USING DATA OF STEAROYL-CoA DESATURASE (SCD1) GENE IN HOLSTEIN CATTLE

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## Abstract

This study analyzed the single nucleotide polymorphism (SNP) of 35 Holstein cattle. It was aimed to estimate the breeding value, additive, dominant variance and allele substitution of (SCD1) gene (exon 5) and their effect on milk production. Three genotypes were found, CC, CT and TT, using PCR-SNP. Breeding value of these genotypes were 0.05, -0.108 and -0.266 respectively and dominant deviation were 0.006, 0.032 and 0.169 respectively the values of genetic variance (VG), additive variance (VA) and dominants variance (VD) were: 0.004, 0.003 and 0.001 respectively, the average gene effect of C and T alleles was 0.025 and -0.133 respectively. It can be concluded that selection of C allele and its actual value as one or two copies in individuals improve the milk production of Holstein cattle.

**Key words:** Breeding value, dominates variance, alleles substitute, (SCD1) gene.

## Introduction

Stearoyl-CoA desaturase (SCD1) is one of the endoplasmic reticulum enzymes that are involved in converting saturated fatty acids that are considered harmful to the body into single-chain polyunsaturated fatty acids (MUFA) by means of a double sphincter (Kgwatalala *et al.*, 2009), the effect of this gene is found in cows on chromosome 26 It produces a double cis type between the 9 and 10 carbon atoms of fatty acids (Schennink *et al.*, 2008), Also the (SCD1) gene significant relationships between the polymorphisms in exon 5 of the SCD locus and the FA profile of carcass fat (Taniguchi *et al.*, 2004) and, more recently, of milk fat (Mele *et al.*, 2007; Moiola *et al.*, 2007) have been reported for cattle. In particular, an effect of the SCD genotype on monounsaturated FA content and in the desaturase activity of the SCD enzyme has been detected in Italian Holsteins (Mele *et al.*, 2007).

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 (Jicai *et al.*, 2017) 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 (Moore

and Haig, 1991; Wittenburg *et al.*, 2017; Xaing *et al.*, 2016).

It is important analyze the genetic variance component to estimate the breeding value and the interaction between alleles which represented by additive and dominant values respectively (Falconer and Mackay, 1996).

This study aimed to estimate of breeding value, additive, dominants variance and alleles substitutes effects of SCD1 gene and their effects on milk production and components in Holstein cattle and use the results as a guideline for improving the performance of livestock's.

## Materials and methods

### Experimental animals

The study was carried out in southern Iraq at the Taj Al-Nahrain tributaries belonging to Taj Al-Nahrain, located within the administrative boundaries of Diwaniyah Governorate (180 km south of Baghdad) for the period from 1/2/2019 to 1/4/2020, on a sample of 35 cows from the Holstein-Friesian cattle imported from Germany. The birth sequences were heterogeneous.

### DNA extraction

DNA was extracted from the blood samples of the cows (10 ml of udder vein) for the purpose of conducting the molecular examination of the studied gene (SCD1) in the scientific progress laboratory located in Baghdad/

Harthiya for the period in order to separate the genetic material and determine the genetics of the SCD1 gene ,The studied gene was made up of 400 pb and analyzed by analyzing the polymorphism of the single nucleotide (SNP) in the Exon5 region of the (SCD1) gene located on chromosome (26).

The amplification reaction was carried out in the following conditions: an initial denaturation step at 95°C for 5 min followed by 1 cycles of denaturation at 95°C for 30 sec, annealing at 56.7°C for 30 sec and extension at 72°C for 30 sec. followed by 30 cycles, and a final extension of 72°C for 7 min., and hold 10°C followed by 1 cycles, the PCR technique was used to determine SNP in exon 5 of the SCD1 gene.

**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 test (Chi-square-  $\chi^2$ ), Equations used to calculate values were according to Falconer and Mackay (1996).

- 1- Average allele C effect,  $\alpha_1 = \alpha_C : q[a+d(q-p)]$
- 2- Average allele T effect,  $\alpha_2 = \alpha_T : -p[a+d(q-p)]$
- 3- Average effect of gene substitution  $\alpha = \alpha_1 - \alpha_2$
- 4- Breeding values  $CC = 2x \alpha_1$ ,  $CT = \alpha_1 + \alpha_2$ ,  $TT = 2x \alpha_2$

5- Dominants deviations  $CC = -2q^2d$ ,  $CT = 2pqd$ ,  $TT = -2p^2d$

6- The variances  $AV = 2pq \alpha^2$ ,  $DV = 4p^2q^2d^2$ ,  $GV = VA + VD$

**Results and Discussion**

The results showed the number and percentage of SCD gene in the studied sample, there were high significant differences ( $P < 0.01$ ) between the ratios of the different genotypes, which amounted to (71.43, 25.71 and 2.86) in succession of the genotypes (CC, CT and TT) where The results showed a clear superiority of the genotypes of the pure individuals carrying the genotype (CC) followed by the hybrid (CT) with a low recessive genotype (TT) ratio in the studied sample table 2 and the mechanical frequency was within (0.84 and 0.16) for alleles C and T Sequentially and observed through the

**Table 1:** Primers sequence used in the study.

Primer Name	Sequences	Amplicon size(bp)	Annealing temp °C
SCD ex5-F	5'-CCCATTCGCTCTTGTCTGT-3'	400	56.7
SCD ex5-R	5'-CGTGGTCTTGCTGTGGACT-3'		

**Table 2:** The number and percentages of genotypes and the Repetition Alleles of a gene SCD1.

Genotype	Nu.	Percentage (%)
CC	25	71.43
CT	9	25.71
TT	1	2.86
total	35	100%
Chi-square- $\chi^2$	---	41.171**
Alleles		Repetition
C		0.84
T		0.16
** (P<0.01)		

**Table 3:** Average allele and Average effect of gene substitution.

Allele	Average allele	Average effect of gene substitution
C	0.025	0.158
T	-0.133	-0.158

**Table 4:** Breeding value and dominance deviation of genotype in (SCD1) gene for milk production.

Genotype	Number	(A-TMP)	BV	DD	AV	DV	GV
CC	25	4092.27	0.05	0.006			
CT	9	3632.14	-0.108	0.032	0.003	0.001	0.004
TT	1	2640	-0.266	0.169			

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

current results when compared with previous studies and on the same region of the gene (SCD) was found mostly Turkish issued B Hybrid and hereditary genotypes (CT and CC) and sometimes recessive structure (TT) and this is similar to part of our current results and sometimes contradictory, and this can be explained by the difference in the sample size and study area (Conte *et al.*, 2006 and Macciotta *et al.*, 2008 and Alim *et al.*, 2012).

The results showed that the mean effect of allele substitution (C) at alleles (T) in this study is 0.158, and the average allele substitution (T) at alleles (C) is -0.158 table 3 which means the importance of selection towards the allele (C) and its actual value In the event that there are several copies of it for the characteristic of milk production, and through the results of the current study it can be concluded that estimating the educational value by using the genetic markers will increase the genetic yield, which leads to reducing the range of the generation, increasing the genetic accuracy and reducing the cost,

and the accuracy of using the genetic markers in the educational value It depends on the amount of the genetic equivalent of the traits and the size of the data provided An abundance of phenotypic characteristics and their relationship

to genetic markers and consequently the use of these markers as an effective selection method for improving animal performance on farms (Falconer and Mackay, 1996).

Individuals with a genotype CC recorded the highest milk production rate compared to the CT and TT combinations (4092.27, 3632.14 and 2640, respectively). The genotype CC recorded the highest educational value, where this composition recorded the highest milk production and the lowest DD compared to the other two combinations table 4. Through these results, it indicates that the genotype CC and the fact that the AV is high compared to (DV), the choice of genotype CC is useful and good because (AV) will be inherited for future generations (Jicai *et al.*, 2017).

### Conclusion

The CC genotype represented greatest breeding value, greater milk production and lesser dominant variation for Holstein cattle.

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