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Research Article

A NOVEL MUTATION IN *PPP2CA* GENE AND ITS ASSOCIATION WITH FAT TAIL STORAGE AND CARCASS TRAITS IN SHEEP

Masoomeh Zare[1], Mostafa Sadeghi[1*], Mohammad Moradi-Shahrbabak[1],
Abbas Safari[2], Misagh Moridi[2], Mahdi Nosratjou[3]

[1]*Tehran University, College of Agricultural and Natural Sciences, Department of Animal Science, Iran*

[2]*Guilan University, Faculty of Agricultural Sciences, Iran*

[3]*Tehran University,* Bsc of Animal Science, *Iran*

**Corresponding Author:*
E-mail: sadeghimos@ut.ac.ir

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ABSTRACT. In the livestock industry, a large, fat tail becomes advantageous in sheep, and therefore, a reduction in the size of the fat tail is often beneficial. Because the difference between Iranian thin and fat tail breeds in fat-related genes are in the tail. So the aim of this study aimed to find candidate genes related to fat deposition between the Iranian thin and fat tail breeds located on chromosome 5 using bioinformatics and molecular techniques. Firstly, we investigated the region placed on chromosome 5 by Genomic Sequence Databases, including Pre Ensemble and UCSC Genome Browser. The local and global alignment of sequences for other species showed a high similarity with a region of chromosome 7 in cattle (up to 95%) is identified as an orthologous region. Additionally, the *PPP2CA* gene on bovine chromosome 7 was orthologous. Then, we investigated the relationship between the polymorphism of the *PPP2CA* gene with carcass, growth, and fat tail traits in Lori-Bakhtiari (165 heads) and Zel (140 heads) breeds using PCR-SSCP technique. These data indicated two different banding patterns (genotypes) and two mutations (synonymous and Indel). The mutations interchangeable lead to the change of nucleotide T to C, then the codon was the switch from TCT to TCC both encode serine. The second mutation was the deletion of the nucleotide T at position 2 of the second pattern, which changed the open reading frame and created the end codon in this region, changing protein function. Finally, the association between genotypes and traits of weaning weight and fat tail weight in Lori-Bakhtiari and cholesterol in Zel breeds was significant ($p < 0.05$). Also, genotypes of the exon1 position in the *PPP2CA* gene were associated with carcass traits (fat percentage of carcass and triglyceride traits) in the Zel Slaughter breed ($p < 0.05$). The results showed that one of the most distinctive traits was tail fatness and visceral organs of the body in breeds considered. This area of the *PPP2CA* gene has a significant association with mentioned traits, and can implemented in breeding programs.

Keywords: *Candidate genes, PPP2CA gene, mutations synonymous, fat tail.*

INTRODUCTION

The fat-tailed sheep breeds are famous for their distinctive large tails and hindquarters [1, 2], and approximately 25% of the sheep population in the world belongs to fat-tail sheep [3]. Indeed, in the fat-tailed sheep breeds, with good carcass quality, most of the

fat is concentrated in the tail area, and it could account for almost 4.5 kg of the weight on a 27 kg of carcass [4]. The efficiency of fat deposition in the fat tails is significantly higher than that of the other components of the carcass [5, 6]. Recently, in intensive and semi-intensive systems, a large fat tail becomes a shortcoming, and therefore, a decrease in fat tail size is often advantageous.

Several factors are affecting on carcass fat percentage, which one of the critical factors is breed [7]. The Iranian livestock industry, with almost 50 million heads, has more than 28 native breeds of sheep [8]; the sheep breeds in Iran categorized into two main groups include the fat-tailed and thin-tail. On the other hand, Zel (thin-tailed) breed is the only thin-tailed breed, and [9], In contrast, the Lori-Bakhtiari, is a fat-tailed breed in the west of Iran, which possesses a large fat tail [10].

There have been several studies on the inheritance of fat tails [11, 12], but the genes that influence fat deposition in fat tails breeds are still unknown. Investigation of the genes underlying phenotypic variation can be carried out in two different ways: from phenotype to genome and from genome to phenotype [13, 14]. Recently, the second method, from genome to phenotype, has attracted the attention of researchers.

Wang et al. [15] examined the diversity between fat-tailed Kazak- and Tibetan short-tailed sheep by the transcriptome profile of tail fat tissue, and they explained that genes *NELL1* and *FMO3* lead to differences between the two groups. Furthermore, Li et al. showed that genes associated with fat deposition include *FABP4*, *ADIPOQ*, *FABP5*, and *CD36* genes in Guangling Large-tailed and Small-tailed Han sheep [6].

Furthermore, Bakhtiarizadeh et al. [16] reported on several enriched functional terms that could contribute to fat deposition in the tail of sheep between Iranian Lori-Bakhtiari and Zel sheep breeds. Finally, Moradi et al. [8], showed that the genes related to the fat tail are located on chromosomes 7, 5, and X and exposed that homozygosity has increased on chromosomes 5 and X in the benefit of the fat tail breeds and on chromosome 7 in use of thin tail breeds.

Based on this data, we discovered target genes located on chromosome 5 associated with fat deposition in fat tails between Iranian Lori-Bakhtiari and Zel sheep breeds. Therefore, the aim of this study aimed to find candidate genes related to fat deposition between the Iranian thin and fat tail breeds located on chromosome 5 using bioinformatics and molecular techniques. In this study, we demonstrated that the *PPP2CA* gene is located on chromosome 5, and it has a high degree of homology with other species.

In the next stage, the relationship between the polymorphism of the *PPP2CA* gene with carcass, growth, and tail traits in Lori-Bakhtiari and Zel breeds were investigated by the PCR-SSCP technique. These data indicate that there are two different banding patterns (genotypes) and two single nucleotide polymorphisms (SNP) (synonymous and Indel). Finally, the association between genotypes and traits of weaning weight and fat tail weight in Lori-Bakhtiari and cholesterol in Zel breeds was significant ($p < 0.05$). Also, genotypes of the exon1 position in the *PPP2CA* gene were associated with carcass traits (fat percentage of carcass and triglyceride traits) in the Zel Slaughter breed, ($p < 0.05$). It can be concluded that one of the most distinctive trait was tail fatness and visceral organs of the body in breeds considered. This work highlights the *PPP2CA* as a common powerful gene that induces fat deposition in the Lori-Bakhtiari sheep.

MATERIALS AND METHODS

Exploring genomic regions

Genomic regions on chromosome 5 (two areas of chr5: 47146931-47175489 and chr5: 47149400-47263230) were studied using pre-Ensembl (http://www.ensemblgenomes.org) and the UCSC Genome Browser. Also, these sequences were aligned with other sequences in the NCBI databases by BLAST NCBI, and BLAT, and highly-homologous sequences were identified in other species (humans, porcine, equine, and bovine).

Finally, genes of *TCF7, PPP2CA, SKP1*, and *CDKL3* were identified as genes located on chromosome 5 of sheep. Then, genes function was determined using Online Mendelian Inheritance in Man or Animal (OMIM and OMIA), Uniprot-KB, and KEGG. We also explored two QTL databases available animal genomes to identify any overlapping of the candidate regions with published QTL in dairy, beef cattle, and sheep. Lastly, we selected the *PPP2CA* gene as a candidate gene related to fat storage in the tail.

Experimental population

Two types of Iranian sheep breed, including fat tail (Lori-Bakhtiari) and thin tail (Zel), were used in our study. The 165 unrelated Lori-Bakhtiari sheep from Shahrekod's research station and 140 unrelated Zel sheep from Gorgan's research station were randomly selected. Two breeds differ in size and living conditions. Lori-Bakhtiari is a fat tail dual-purpose sheep, large in size and primarily white in body color. The Zel is a small body size sheep, also is early maturing and primarily brown. Zel is the only thin–tail Iranian breed. Data of birth weight, weaning weight, and daily gain were measured and recorded.

Blood sample collection and DNA extraction

Blood samples (4 ml per sheep) were collected from the Jugular vein, kept in a tube containing anticoagulant EDTA. All blood samples were placed on ice and transferred to the laboratory, stored at −20 °C. The DNA extraction was performed on white blood cells by salting out [17], kept at −20 °C until used. The quantity and quality of DNA extraction were measured using agarose gel electrophoresis and spectrophotometry method with nanodrop. To evaluate the amount of triglyceride and cholesterol, the blood samples were collected from studied animals.

Primer design and polymerase chain reaction (PCR)

Specific primers were used for fragments amplification, by utilizing primer3 plus and oligo analyzer software designed for 220bp fragment of exon1 *PPP2CA* gene. The sequences of the primers were as follows: F: 5′-CCGCCAGTACCCTCACAAAT-3′ and R: 5′-CTCCCCCATCCGAGATGTA-3′. The PCR reactions were performed in a 50 µl reaction mixture including 100 ng of DNA (2 µl), 25 µl of PCR master mix, 12 pmol of each primer (2 µl) and 19.5 µl of DDW.

The PCR product was amplified in the following conditions: denaturation at 95 ^{o}C for 5 min followed by 35 cycles of 95 ^{o}C for 1 min for denaturation, 60 ^{o}C for 1 min for annealing primers, and extension at 72 ^{o}C for 1 min. A final extension at 72^{o}C for 7 min was then conducted. After PCRs for reassurance of amplification accuracy and determining extended DNA, PCR products electrophoresis was done on 2% agarose gel

in parallel with 100 bp DNA marker, in 1 × TAE buffer at a fixed voltage of 80 V for 30 min. After ethidium bromide staining, products were observed and studied by ultraviolet transillumination.

PCR-SSCP and genotype determination

The PCR-SSCP method was used to detect mutations within the amplified fragments. Amounts of 4 µl of PCR products were mixed with a 12 µl denaturing solution (99% formamide, 25 mM EDTA, 0. 25% xylene cyanol, and 0. 25% bromophenol blue), 10 min denatured at 96 °C, and immediately they chilled on ice. For observing band patterns, we used the Vertical electrophoresis tank of Bio-Rad Company with glass screens 18*20*0. 1 cm, and 12% acrylamide gel was used. Samples were run for 15 h at 200 V at 4 °C on a 12% acrylamide: bisacrylamide gel (37.5:1). Bands appeared by 0.1 percent silver nitrate and NaOH solution (containing 0.1% formaldehyde). The PCR products of different SSCP templates were sequenced from both sides. Four random samples for each pattern of *PPP2CA* gene, observed in the SSCP analysis, were sequenced by Bioneer Company (South Korea). The sequences were edited and were aligned using BioEdit and Vector NT1 software. The mutations were compared with the NCBI reference sequence, accession number of AC_000164. 1.

Statistical analysis

The MIXED procedure of SAS (SAS 9.1, 2007) was used for the association analysis. Genotypic and allelic frequencies and Hardy–Weinberg equilibriums were calculated by GenAlEx 6.41 software. Traits included were fat-tail weight using fat tail domain [18], weaning weight, six months' weight, nine months' weight, weight at age, daily gain, and Kleiber ratio. Two models were used, including model 1 for growth traits and model 2 for fat tail weight and other carcass traits. The models were as follow:

Model 1: $Y_{jklmno} = \mu + year_i + M_j + S_k + j_l + B_m + G_n + b_1(D_{ijklmn} - D) + b_2(BW_{ijklmn} - BW) + b_3(A_{ijklmn} - A) + e_{ijklmnp}$

Model 2: $Y_{ij} = \mu + S_i + G_j + b_1(BW_{ij} - BW) + b_2(A_{ij} - A) + e_{ijk}$

Y_{jklmno} are records related to each trait of growth (e.g birth weight), and i, K, L, m, n, o, are animal's birth year and month of birth, the number of lambs per birth, sex, breed, and genotype, respectively. The µ is the population mean for each trait. Year: animal birth year, M: animal birth month, S: the number of lambs per each birth, J: animal sex, B: race, G: genotype, D: maternal age, A: animal age, b: Coefficient of regression of Y on maternal age, also on maternal and animal age, and G: concerning the effect of genotype, and e concerns the residual effects.

Proteins' structure prediction

Bioinformatics, including the NCBI data bank and UniportKB, were used for retrieved the amino acids sequence of the *PPP2CA* gene. To do this, we used I-TASSER and 2PHYRE web server (http://zhanglab.ccmb.med.umich.edu/I-TASSER/) to obtain the three-dimensional structure of the PPP2CA protein. Then mutations and alignment sequences were detected by BIOEDIT 7.0 software. Afterward, they were translated to protein sequence using the vector NTI 9. 0 software, with six open reading frames, and

were compared with protein sequence in UniProtKB information sources. To study the influence of recognized mutations on protein structure and performance and designing the three-dimensional structure of the PALM, gene was used the PHyre2 software and SWISS-MODEL section available on the EXPASY website. Protein tertiary structure was predicted by PHyre2 software and SWISS-MODEL in EXPASY, which is similar to the C chain domain of the family serine/threonine phosphatase and superfamily metalophosphates in humans (PDB = 3 CW5 chain C domain 1).

RESULTS AND DISCUSSION

Allele and genotype frequencies of the PPP2CA gene

Moradi et al. [8], showed that the genes related to fat tail are located on chromosomes 7, 5, and X and exposed that homozygosity has increased on chromosome 5 and X in benefit of fat tail breeds and on chromosome 7 in use of thin tail breeds. On the other hand, as studies have shown, reducing fat storage in the tail is an advantage. Therefore, according to the study of Moradi et al. [8], We focused our investigation on chromosome 5 for found target genes located on chromosome 5 associated with fat deposition in fat tails between Iranian Lori-Bakhtiari and Zel sheep breeds by Genomic Sequence Databases including Pre Ensemble and UCSC Genome Browser.

Since no genes were recorded on sheep chromosome 5, we used homology with other species to identify genes in this area. Our results showed that the region is homolog with horse's chromosome 14 (38109000-38093028) with more than 88% similarity with negative DNA strand, human chromosome 5 DNA strand (137, 723, 906 -137 704 302) in 87.9% homologous and finally the bovine chromosome 7 with 96.3% similarity (44946294-44918101).

Also, QTL's position and synteny genes in two species have proved selecting cattle chromosome 7 is homologous with sheep chromosome 5, which containing selection signatures to fat storage. Then, the Ensemble website showed that gene synteny is protected in sheep chromosome 5 and cattle chromosome 7. Therefore, according to this result, the area on the chromosome 7 cows (44946294-44918101) was selected and explored.

In this study, we demonstrate that genes of *TCF7*, *PPP2CA*, *SKP1*, and *CDKL3* are located on chromosome 5, and it has a high degree of homology with other species. Also, these genes were identified as gene neighbors in other species (humans, porcine, equine, and bovine), then we chose the *PPP2CA* gene as candidate genes related to fat deposition.

According to Databases Genomic and metabolic pathway, *PPP2CA* gene structure involved seven exons and 24768 bp in sheep and cow, and this gene led to inactive hormone-sensitive lipase (Fig. 1).

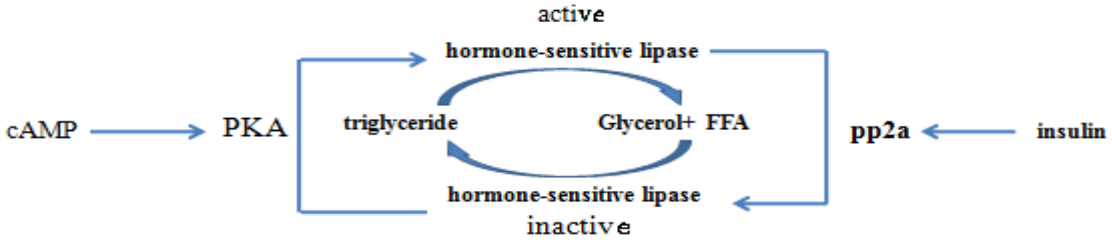

Fig. 1. *Metabolic pathway, the influence of PPP2CA gene on lipase inactivation and increased fat storage*

In the next stage, we investigated the polymorphisms of the *PPP2CA* gene by PCR-SSCP, and the results showed that the *PPP2CA* gene has two different band patterns and, in turn, has two different genotypes between samples. Also, the amplification product of the *PPP2CA* gene was 243bp in length from nucleotides 12-254 (AC_000164. 1) that involves the gene UTR5 and exon one regions (Fig. 2).

Fig. 2. *PCR-SSCP genotypes of complete exon 1 of the PPP2CA gene in Lori Bakhtiari and Zel sheep breeds*

We then investigated the nucleotide sequences of samples for each pattern of *PPP2CA* gene by Bioneer Company (South Korea). In the next stage, we used BioEdit and Vector NT1 software to study the mutation of the *PPP2CA* gene in Lori-Bakhtiari- and Zel breeds compared to the control group with the accession number of AC_000164. 1.
The data indicated that the *PPP2CA* gene could generate both SNPs, including synonymous substitution (T) and indel mutation (DEL) in Lori-Bakhtiari- and Zel breeds compared to the control group (Table 1).

Table 1.*Estimated allele and genotype frequencies in Lori-Bakhtiari and Zel sheep breeds.*

	Allele		**Genotype**	
Breeds	**Del/Del**	**T/T**	**Del/Del**	**T/T**
Lori-Bakhtiari	0. 268	0. 732	0. 260	0. 740
Zel	0. 412	0. 589	0. 300	0. 700
Slaughtered Zel	0. 280	0. 720	0. 360	0. 640

The position, allele (DEL and T), and genotype (DEL/ DEL and T/T) frequencies for each SNPs are shown in Table 1. The common allele and genotype frequencies of the two alleles (DEL and T), were calculated and showed that the T allele frequency was higher and the DEL allele frequency was lower in the Lori Bakhtiari and Zel breeds. Furthermore, the TT genotype frequency between the breeds was higher than the DEL / DEL genotype frequency (Table 1).

Association of PPP2CA gene SNPs with growth and carcass traits in Lori-Bakhtiari and Zel breed

In the first step, we hypothesized that the *PPP2CA* gene, as a candidate gene, is related to fat storage in the fat tail. So, we tested the association of the genotypes of the *PPP2CA* with the growth and carcass traits in the Lori-Bakhtiari and Zel breeds by SAS software. Our results showed that the weaning weight trait between the T/T and Del/Del genotypes was more significant than that of the other growth traits (P<0. 05), and the Del/Del genotype had the highest weaning weight (Table 2).

Table 2.*Comparison means of genotypes least squares on growth traits in the population of Lori-Bakhtiari.*

Traits	T/T	Del/ Del
Weight (kg)^{ns}	4.36 ± 0.27	4.49 ± 0.28
Weaning weight (kg)**	27.79 ± 1.46^{b}	30.67 ± 1.52^{a}
Daily gain ^{ns}	255.83 ± 9.17	251.67 ± 10.40
Kaleiber218 ratio ^{ns219}	19.97 ± 0.59	19.93 ± 0.62
Triglyceride ^{ns}	28.79 ± 0.57	30.69 ± 1.28
Cholesterol**	60.76 ± 0.94^{a}	54.26 ± 1.65^{b}

ns,*, **: non-significant and significant at 5 and 1%, respectively

Also, we tested the association of the genotype of the *PPP2CA* with blood parameters such as cholesterol and blood triglycerides traits in the Lori-Bakhtiari and Zel breeds by SAS software. This result revealed that the cholesterol blood trait in T/T genotypes significantly increased compared to Del/Del genotypes (P <0.05). But the triglycerides trait was not significant in the Lori-Bakhtiari and Zel breeds (Table 2).

In the next stage, we investigated the association of the genotype of the *PPP2CA* with the fat tail trait in the Lori-Bakhtiari, and these data indicate that, the Del/Del genotype had the highest fat tail (P <0.05) (Table 3). Finally, these results confirmed that Del/Del genotype could actively support the fat deposition in the fat tails probably by inducing the metabolic pathway of the *PPP2CA* gene, lipase enzyme inactivation, and increased fat storage.

Table 3.*Comparison means of genotypes least squares on fat tail traits in the population of Lori-Bakhtiari breed.*

Traits	TT	Del
Fat tail	3.28 ± 0.21^{b}	5.20 ± 0.21^{a}

Finally, we studied the association of the genotype with carcass trait in the *slaughtered Zel*, and our results showed that the fat carcass and triglycerides carcass traits between the T/T and Del/Del genotypes were significant than that those of the other carcass traits (P<0.05) (Table 4). Overall, these data indicate that, the Del/Del genotype had the highest fat and triglycerides traits (P<0.05).

Table 4.*Comparison means of least squares on genotypes of exons one loci PPP2CA with quantitative traits of the carcass in slaughtered Zel.*

Traits	TT	Del
Eye muscle cross-sectional area (cm) ^{ns}	14.96 ± 0.52	14.47 ± 0.76
Live weight before slaughter (kg) ^{ns}	36.24 ± 0.78	35.82 ± 1.17
Hot carcass weight (kg) ^{ns}	15.49 ± 0.45	15.42 ± 0.67
Carcass (%) ^{ns}	42.97 ± 0.27	43.12 ± 0.39
Backfat thickness (mm) ^{ns}	2.59 ± 0.21	3.15 ± 0.32
Fat (%) *	2.44 ± 0.33^{a}	3.76 ± 0.03^{b}
Protein (%) ^{ns}	20.28 ± 0.24	20.22 ± 0.33
Cholesterol (%) ^{ns}	92.83 ± 3.49	63.99 ± 4.39
Triglyceride (%) **	29.65 ± 2.76^{b}	43.97 ± 3.68^{a}
LDL (%)^{ns}	31.30 ± 2.93	26.25 ± 3.68
HDL (%)^{ns}	27.09 ± 1.96	31.72 ± 2.48

Prediction of impacts of mutations on protein structure

The amino acid sequence determines the three-dimensional structure (3D) of the protein. A change in the amino acid sequence can cause changes in the folding and stability of the protein [19].

The results of the previous section showed that the *PPP2CA* gene has two SNPs (synonymous substitution (T) and indel mutation (DEL) in Lori-Bakhtiari- and Zel breeds compared to the control group. Concerning this data, we promoted to examine impacts of mutations on protein structure, which changes in the 3D form of the PPP2CA protein lead to changes in protein function, which can lead to increased fat storage in the fat tail. To do this, we used I-TASSER and 2PHYRE web server (http://zhanglab.ccmb.med.umich.edu/I-TASSER/) to obtain the three-dimensional structure of the PPP2CA protein. Firstly, in this study, the point mutation occurred in the 198 nucleotide position, which resulted in a synonymous mutation of a codon changed from TCT to TCC (T→C), both codes belonged to the amino acid serine and did not affect the gene function (Figure 3 and 4). In addition, prediction of the 3-D structure of the protein showed that the replacement mutation did not result in a frame of the protein (Fig. 3 and 4). Indeed, Substitutions mutations are synonymous, which are affecting noncoding DNA are often considered silent mutations [20, 21, 22, 23, 24].

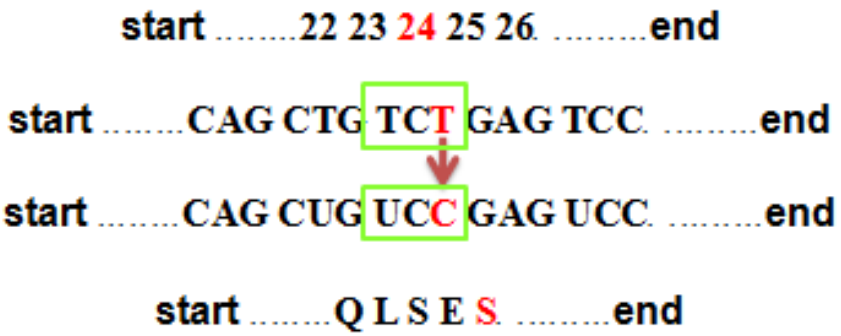

Fig. 3. *Schematic drawing of influence point mutations in the DNA and Mrna.*

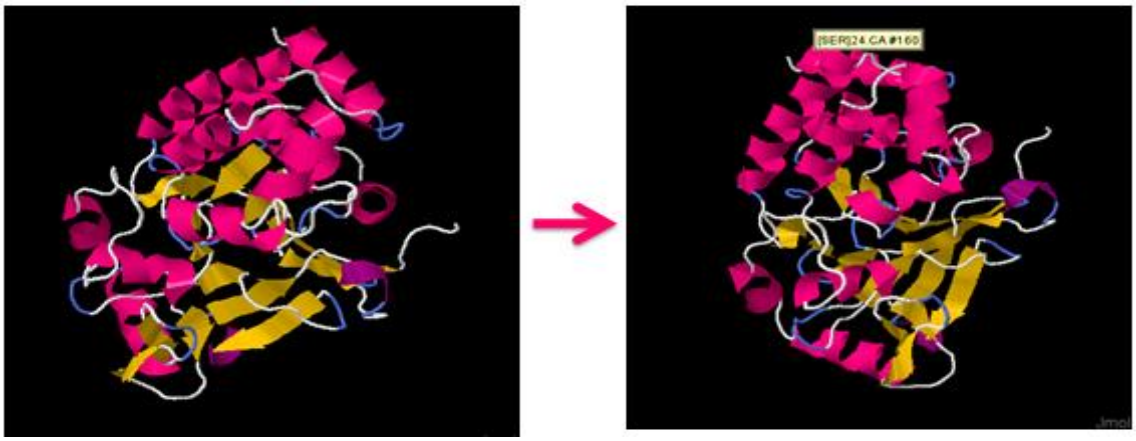

Fig. 4. *The figure left drawing protein tertiary structure and figure right point mutant effect on protein structure.*

Also, these data indicate that, the indel mutation occurred in the 210 nucleotide position with deletion T nucleotide of *PPP2CA* gene, which the indel mutation leads to the production of a truncated *PPP2CA*, due to a premature stop codon ("UAA","UGA" or "UAG") arising from a one bp deletion in the gene sequence (Fig. 5 and 6).

Fig. 5. *Schematic drawing of influence deletion mutations in the DNA and mRNA*

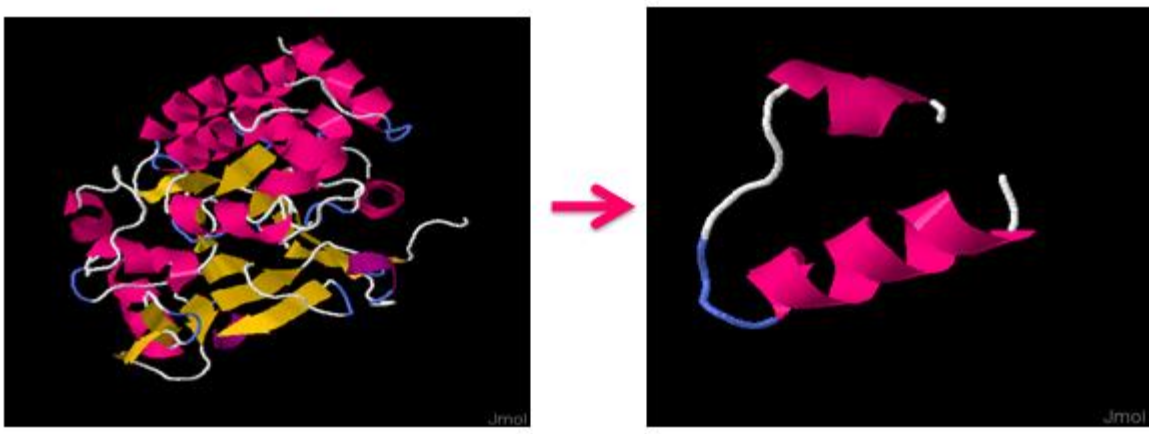

Fig. 6. *The figure left drawing protein tertiary structure and figure right deletion mutant effect on protein structure and production polypeptides too short and lacking in performance.*

The frameshift mutation also changed the codon and created the first stop codon ("UAA","UGA", or "UAG") that can be seen in the sequence (Figure 3). Since this mutation occurred at codon 28 of the protein sequence, that is, after the amino acid valine, all the protein amino acids change, finally the stop codon is found, and the translation ends (Figure 3). The polypeptide produced is uncharacteristically short and therefore has not functional.

There have been several studies of thin- and fat-tailed breeds and their inheritance of traits in different areas [7, 25, 26, 27], but it was concluded that the genomic regions or the effector genes for these traits are still unknown. In this study, we demonstrate that genes of *TCF7*, *PPP2CA*, *SKP1*, and *CDKL3* located on chromosome 5 and it has a high degree of homology with other species. Then we chose the *PPP2CA* gene as candidate gene related to fat deposition. In this research, our top priority is proving that the *PPP2CA* gene is associated with fat traits in the t fat ail in the Lori Bakhtiari and Zel breeds. Also, this research indicated that the *PPP2CA* gene has both SNPs, including synonymous substitution and indel mutation in Lori-Bakhtiari- and Zel breeds compared to the control group. The common allele and genotype frequencies showed that the T allele frequency was higher, and the DEL allele frequency was lower in the Lori Bakhtiari- and Zel breeds. Furthermore, the TT genotype frequency between the breeds was higher than the DEL / DEL genotype frequency. Our results showed that the weaning weight trait was significant ($P < 0.05$), and the Del/Del genotype had the highest weaning weight. Additionally, these data indicate that, the Del/Del genotype had the most elevated fat tail in the Lori-Bakhtiari breed. In addition, our results showed that the fat and triglyceride related traits of carcass between the T/T and Del/Del genotypes were significant than those of the other carcass traits. Overall, these data indicate that, the Del/Del genotype had the highest fat and triglycerides traits.

It is presumed that, similar to the previous reports, this genomic region on chromosome 5 is associated with fat traits in the fat tail in the Lori-Bakhtiari breed. As suggested by Moradi et al. [8], there are many QTLs associated to growth- and fat storage traits in sheep. Some studies have been reported fat-related QTL in the proposed genomic regions of sheep chromosome 5 and its cow homologous region 7. McClure et al. [28] reported that in commercial Angus cattle on chromosome 7, the two QTLs are associated with the Back Fat Thickness Trait (ATTH) [29]. Furthermore, Karamichou et al. [17], showed that, there are some QTLs associated with intramuscular fatty acid composition on chromosome 5 in Scottish Blackface sheep by a partial genome scan. The breed is one of the most critical factors influencing fat deposition in sheep carcasses [7]. So, our results showed that the T/T genotype is the highest fat carcass trait in the Zel breed and the Del /Del genotype is the highest cholesterol trait in the Lori Bakhtiari breed. Genetically, the carcass fat percentage can be reduced using genetic selection aimed to reducing the backfat thickness [30].

The ability to increase weight, accompanied by fat loss carcass, requires genotypes that can produce more meat and less fat in the fat tail. Our results showed that the Del genotypes had the highest rate of carcass traits and carcass fat percentage in Lori-Bakhtiari and Zel breeds. Investigation of gene function in the genomic regions of the targeting signatures in the orthologous areas of sheep and cattle showed that the *PPP2CA* gene causes increased lipogenesis in type II diabetes and insulin resistance diseases and also increases the replication of the hepatitis C virus [31, 32, 33, 34]. Overall, our current results suggest that the *PPP2CA* gene, depending on the metabolic pathway, leads to

inactive hormone-sensitive lipase and increases fat storage, as well as being a candidate gene for fat storage and carcass quality [8].

CONCLUSION

The efficiency of fat deposition in the fat tails is significantly higher than that of the other components of the carcass. Therefore, a decrease in fat tail size is often advantageous; gene identification and genomic selection will aid to produce higher live weight breeds with less fat. Finally, these findings will provide a greater understanding of the genes involved in fat storage in the fat tails. This study highlights the *PPP2CA* gene as a candidate gene is related to fat storage in the fat tail. These results are hopeful because they show that other effective genes in fat storage in the fat tail and carcass quality can be identified by more studies.

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Conflict of Interest. The authors declared that there is no conflict of interest.

Authorship Contributions. Concept: M.Z., A.S., M.S., Design: M.Z., M.M.S., A.S., M.S., Data Collection or Processing: M.Z., M.M.S., A.S., M.S., Analysis or Interpretation: M.Z., M.M.S., A.S., M.M., M.S., Literature Search: M.Z., A.S., M.M., M.N., M.S., Writing: M.Z., A.S., M.M., M.N., M.S.

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