Iraqi Journal of Agricultural Sciences –2026:57(7):2027-2037
P-ISSN: 0075- 0530 /E-ISSN: 2410-0862
DOI: https://doi.org/10.36103/8ztt5t05

Association of Fabp T3499a Genotype with Body Measurements, Temperature, and Milk Production Parameters in Iraqi Buffaloes

S. K. Kazem [1], N. N. Al-Anbari [2] S.N. Alwaeli[3]

*[1, 2] Department of Animal Production, College of Agricultural Engineering Sciences, University of Baghdad

[3]Office of Agricultural Research.

ABSTRACT

The study aimed to detect the genotype of the FABP gene T>A: 3499 in a sample of 41 buffaloes to investigate the relation between this genotype and several productive traits. The study was conducted from October 1st, 2024, to January 30th, 2025, at the Ruminant Research Station in Abu Ghraib. By detecting the genotype of the FABP gene at the T>A: 3499 site, two genotypes, TT and TA, were identified. Their distribution ratios were 80.49% and 19.51%, respectively (P≤0.01). The allelic frequencies for the T and A alleles were 0.90 and 0.10, respectively. Significant differences (P≤0.01) were found in body length, Heart girth, and body temperature during the 2nd month of the study. Regarding milk production and composition, the first month was represented by milk density, the 2nd month by the daily milk yield (DMY), and the 3rd by DMY and density. The TA genotype showed superiority over the TT genotype for heart girth, milk density in the first month, DMY in the 3rd month. In conclusion, the study of genetic structures in the FABP gene: T>A: 3499, the resulting changes can be used in the process of genetic improvement of Iraqi buffaloes performance.

Keywords: Allelic frequencies, Bubalus bubalis, Genotype, Productive traits .

Received: 11/4/2025, Accepted: 13/7/2025, Published: 31/7/2026

INTRODUCTION

Buffaloes have been domesticated in Iraq for a long period. Domesticated animals are the result of selection, improvement, and domestication processes (Al-Saedy, 2014). They have been subject to the influence of genetic erosion and mutation and constitute a part of biological diversity. Therefore, the preservation of these breeds is important. Appropriate management and conservation within development programs in biological and local research represent some strategies to preserve these indigenous breeds, aiming to protect their genetic characteristics as part of the breeding system (Al-Sarai & Al-Anabri, 2019). Animal species, and buffaloes in particular within Iraq, have received limited attention regarding genetic improvement. This is compounded by difficulties in the processes of genetic improvement and selection, as well as in distinguishing genetic structures due to the underutilization of record-keeping (Jaayid & Dragh, 2013). FABP is an abbreviation for Fatty Acid Binding Protein. FABPs are a group of intracellular carriers of bioactive lipids that influence fatty acid transport (Abbasi et al.,2020; Shinoda et al.,2020). The FABP family comprises numerous small proteins with a molecular weight of approximately 15 kilodaltons. In humans, rats, and mice, this gene consists of four exons, and its expression is prominent in adipose tissue and the mammary gland (Ye et al., 2022). The protein encoded by the FABP gene acts as a substrate in the synthesis of thyroid hormones. In cattle and buffaloes, this gene is located on chromosome 14 and represents one of the Quantitative Trait Loci (QTLs) associated with

Iraqi Journal of Agricultural Sciences –2026:57(7):2027-2037
P-ISSN: 0075- 0530 /E-ISSN: 2410-0862
DOI: https://doi.org/10.36103/8ztt5t05

milk yield, fat percentage, mastitis resistance, subcutaneous fat thickness, and carcass weight. It also plays a role in fatty acid metabolism (Hoashi et al., 2008). The role of FABPs in intracellular fatty acid transport has been substantiated by a series of experiments (Storch & Thumser, 2000), leading to their definition as transport proteins (Chmurzynska, 2006). Subtypes of the FABP gene are involved in active lipid metabolism (Damcott et al., 2004; Michal et al., 2006). These subtypes include: liver (L-FABP/FABP1), intestine (I-FABP/FABP2) (Gajda et al.,2022; Xiang et al.,2025), heart (H-FABP/FABP3), adipocytes (A-FABP/FABP4/ap2) (Chen et al.,2021; Chiyonobu et al.,2018), skin (E-FABP/FABP5-mall), epidermis (Il-FABP/FABP6), brain (B-FABP/FABP7), myelin (M-FABP/FABP8), and testis (T-FABP/FABP9) (Ibrahim et al., 2014). The second and third exons are highly conserved across almost all protein-encoding FABP genes with four exons and three introns. While the positions of introns and exons are similar, their lengths are variable, particularly the intron length, due to differences in genome size between species. In contrast, the length of the exons shows relatively minor variation across most FABPs (Zhang et al.,2024; Zhang et al., 2020). FABP3 is distributed in smaller quantities in the brain, kidneys, adrenal gland, lungs, testes, and lymphocytes (Yardibi et al., 2013; Zhang et al.,2013). It is found in tissues with high fatty acid demand, such as the lactating mammary gland, cardiac muscle, and skeletal muscle (Tsukahara et al., 2014). Previous studies have revealed that FABP4 polymorphism may influence growth (Fan et al., 2022; Prentice et al., 2021), carcass composition in sheep, meat tenderness, the degree of intramuscular fat deposition, muscle fat content in sheep and pigs, carcass traits, meat quality, fat deposition in cattle, milk production and quality in cattle, milk fat composition in buffaloes, and resistance to wool rot in sheep (Hoashi et al., 2008;, Xiang et al., 2025). [Author(s)] studied the significant association between FABP4 variables and fatty acid (FA) compositions/classes in the Longissimus Thoracis muscle of lambs. The levels of C16:1 and C18:1n9c were significantly higher ($P < 0.05$) in individuals with the TT genotype compared to those with the CT genotype at the g.57765038C locus. The current study aims to detect genetic identification in the FABP gene on Iraqi buffaloes (distribution ratios of genetic structures and allelic frequencies) and the relation of the T>A: 3499 variation with several productive traits.

MATERIALS AND METHODS

This study was conducted at the Ruminant Research Station, Abu Ghraib, affiliated with the Livestock Research Department, Agricultural Research Directorate, Ministry of Agriculture. The study period spanned from October 1, 2024, to January 12, 2025, encompassing the 2024-2025 production season. The aim was to investigate the relation between genotypes of the *FABP* gene, specifically the T>A: 3499 variation, and the productive performance of Iraqi buffaloes. A sample of 44 buffaloes was utilized for the field component of the study. Genetic and molecular analyses (laboratory component) were performed at the Agricultural Molecular Biology Laboratory, Department of Animal Production, College of Agricultural Engineering Sciences, University of Baghdad. These analyses aimed to detect the genetic structures of the *FABP* gene and their distribution ratios.

Blood samples :"Forty-four blood samples, each with a volume of 3 ml, were collected from each buffalo via jugular venipuncture using a 10 ml syringe. The collected blood was immediately transferred into sterile tubes containing EDTA (ethylenediaminetetraacetic acid) as an anticoagulant and transported to the laboratory in a refrigerated container. Upon arrival, the samples were promptly stored at the appropriate temperature until DNA extraction was performed.

DNA Extraction : For the purpose of conducting molecular analysis of the FABP gene, frozen blood samples previously collected from buffaloes were thawed. These samples were then subjected to laboratory analyses to determine the genetic structures of the gene. The required analyses were performed following the manufacturer's instructions provided with the Geneaid DNA

Iraqi Journal of Agricultural Sciences –2026:57(7):2027-2037
P-ISSN: 0075- 0530 /E-ISSN: 2410-0862
DOI: https://doi.org/10.36103/8ztt5t05

extraction kit (Korean company). DNA was extracted from the blood samples in the Agricultural Molecular Biology Laboratory, Department of Animal Production, Faculty of Agricultural Engineering Sciences. To purify the extracted DNA, the sample was centrifuged for 30 seconds. Subsequently, the GD column was removed from the microcentrifuge tube (Eppendorf), and the purified DNA samples were stored in a deep freezer for subsequent use in Polymerase Chain Reaction (PCR) technology.

Electrical relay of genetic material (DNA) : To verify the efficiency of the DNA extraction process and to prepare samples for downstream applications, the extracted DNA was visualized on an agarose gel. The following materials were used: agarose powder, 10X Tris-Borate-EDTA (TBE) buffer, ethidium bromide, and a 100 base pair (bp) DNA ladder marker.

Molecular characterization of the FABP gene: Primers were selected for the FABP gene which includes the following sequences (Helalia et al., 2022):

Forward: 5-ATACGGTTCACATTGAGAGGGA-3

Reverse: 5-ACCCCTATGATGCTATTCCACA-3

To conduct molecular detection and determine the genotype of the *FABP* gene in Iraqi buffaloes, specific primers were obtained from Macrogen (Korea) in a lyophilized form. These primers were designed to anneal to their complementary sequences within the buffalo DNA. The optimal annealing temperature for these primers was determined to be 60.4 °C, resulting in an amplicon size of 290 base pairs (bp). The lyophilized primers were reconstituted to create a stock solution and a working solution, following the manufacturer's instructions. The stock solution was prepared by adding nuclease-free water to achieve a final concentration of 100 picomoles per microliter (pmol/µl). The working solution was then prepared by diluting 20 microliters of the 100 pmol/µl stock solution with 180 microliters of deionized water, resulting in a final working concentration of 10 picomoles per microliter (pmol/µl) for each primer. The tubes containing the working solution were briefly vortexed for 2nd to ensure a homogeneous mixture, as shown in table (1).

Table 1. Reaction conditions for the studied cutting of the FABP gene using PCR technology by temperature and number of cycle

Stage	Temperature conditions	Time	Number of cycle
Initial denaturation	94	4 min	1
Denaturation	94	1 min	
Annealing	60.6	1 min	
Extension	72	1 min	32
Final extension	72	5 min	1
The final stage of codding	4	-	-

Measure the studied qualities

A manual milking system was employed twice daily (morning and evening) for all animals. Milk yield was recorded using a graduated cylinder for each buffalo on a daily basis throughout the experimental period. Milk composition, including fat, protein, lactose, solids-not-fat (SNF), and milk density, was determined using a Milk Analyzer in the laboratories of the Ruminant. Research Station, Agricultural Research Directorate, Ministry of Agriculture, Abu Ghraib. Milk density = device reading /1000+ 1. These components were estimated monthly, with three readings taken throughout the experiment. Body measurements of the experimental animals were also recorded during the study period using a measuring tape. These Measurements included height at the withers, body length, and heart girth. For the first three months of the milk season after parturition, daily milk production was calculated once every two weeks from each buffalo in graduated cylinders (manual milking system twice a day, morning and evening).

Temperature measurement

The temperature was determined by:

1- The mercury thermometer temperature was calibrated by using our hand to shake it.

Iraqi Journal of Agricultural Sciences –2026:57(7):2027-2037
P-ISSN: 0075- 0530 /E-ISSN: 2410-0862
DOI: https://doi.org/10.36103/8ztt5t05

2- The thermometer was placed in the rectal opening of the animal for one minute and taken out, and we read the result. And after reading, the mercury thermometer was moved by hand to whistle it and repeat the process for all animals

Statistical analysis: The data were statistically analyzed using the Statistical Analysis System (SAS, 2018) software to investigate the effect of the genetic structures of the FABP gene (T>A: 3499 polymorphism) on milk yield, milk composition, growth traits, body temperature, and serum levels of cholesterol and triglycerides. Significant differences between means were compared using Duncan's multiple range test (Duncan, 1955) following the Least Squares Means (LSMEANS) procedure.The following statistical model was employed to study the relationship between the genetic structures of the *FABP* gene (T>A: 3499 polymorphism) and the studied traits:

$$Yijk=\mu+Gi+Aj+eijk$$

Where: Yijk: The kth observation for the ith genotype and the jth age of the buffalo. μ: The overall mean for the trait. Gi: The effect of the ith genotype of the *FABP* gene (T>A: 3499 polymorphism). Aj: The effect of the jth age of the buffalo. eijk: The random error, assumed to be normally distributed with a mean of zero and variance σe2 Furthermore, the Chi-square ($\chi 2$) test was utilized to compare the percentage distribution of genotypes within the studied buffalo sample. Allelic frequencies were calculated according to the Hardy-Weinberg equilibrium principle, as described (Falconer & Mackay, 2004).

RESULTS AND DISCUSSION

Genomic DNA was extracted. A specific fragment of the Fatty Acid Binding Protein (*FABP*) gene was then amplified using Polymerase Chain Reaction (PCR) technology, following the manufacturer's instructions provided with the Bioneer kit (Korean company) as detailed in Chapter Three (Research Methodology). Subsequently, the amplified DNA samples were subjected to gel electrophoresis, and the resulting separation patterns were visualized. The results of sequencing showed a change in the nitrogenous base from Thiamine to Adenine in the studied segment of the FABP gene at sequencing 3499 base pairs of complete. gene sequences, which resulted in two genetic structures, TT and TA, with the absence of the AA mutant model as shown in Figure (1).

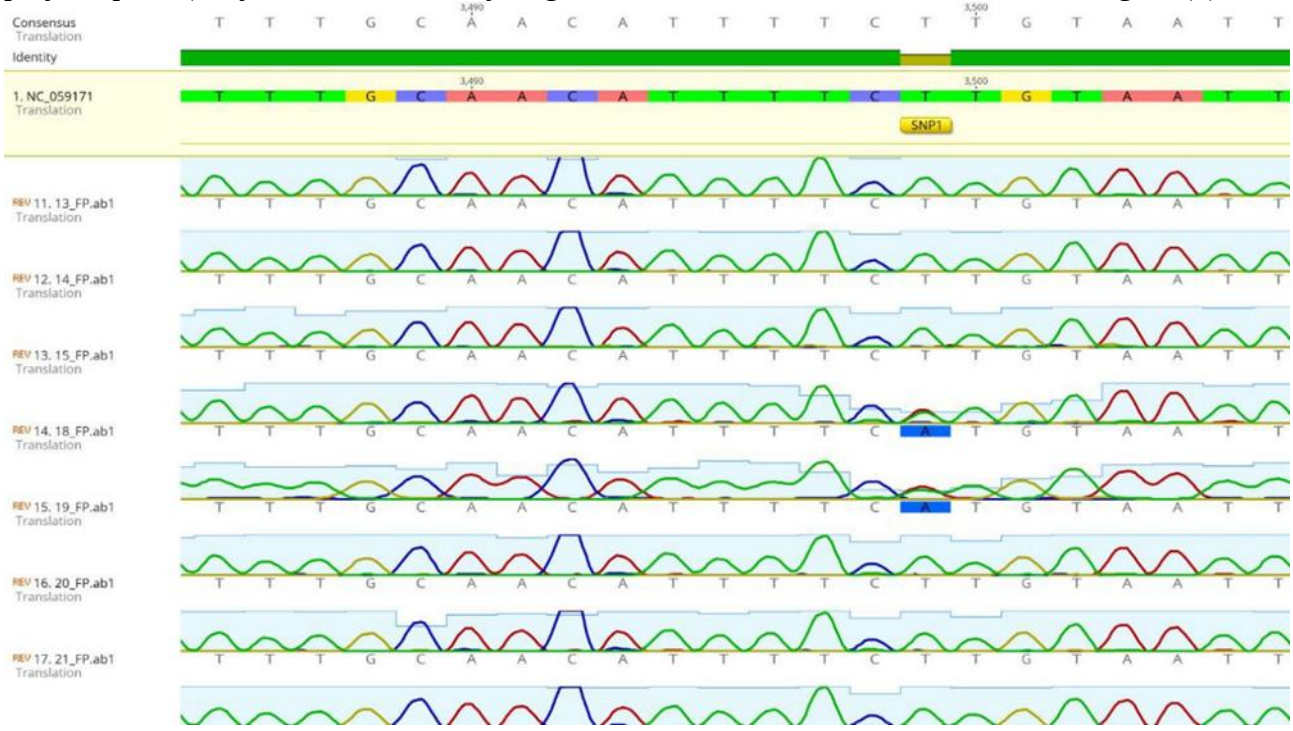

Figure 1. Sequencing technology output for second heterogeneity (SNP:T 3499 A) within the studied segment of the FABP gene

Iraqi Journal of Agricultural Sciences –2026:57(7):2027-2037
P-ISSN: 0075- 0530 /E-ISSN: 2410-0862
DOI: https://doi.org/10.36103/8ztt5t05

Table (2) presents the number and percentages of the FABP gene polymorphism in the studied buffalo sample, revealing significant differences (P≤0.01) between the proportions of the different genotypes. These proportions were 80.49%, 19.51%, and 0.00% for the TT, TA, and AA genotypes, respectively. This indicates that the percentage of individuals with the heterozygous TA genotype was lower than the proportion of individuals with the homozygous wild-type TT genotype, while individuals with the homozygous mutant AA genotype were not observed in the studied buffalo sample. The allelic frequency of the T allele for the FABP gene was 0.90, while the frequency of the A allele was 0.10. This result reflects the prevalence of the T allele for this gene in the studied sample. The observed differences in genotype distribution and allelic frequencies for the studied FABP gene fragment in Iraqi buffaloes may be attributed to variations in sample size, the specific gene region analyzed, geographical location, breed, and the influence of random genetic drift.

Table 2. Number and percentage of FABP / T>A gene genetic makeups: 3499/ in domestic buffaloes

Genotype	Number	Percentage (%)
TT	33	80.49
TA	8	19.51
AA	0	0.00
Total	41	100%
Chi-square value (χ^2)	----	35.740 **
Allele:		Frequency:
T		0.90
A		0.10

**(P≤0.01)

Relationship of FABP / T>A gene polymorphism : 3499 in body dimensions of domestic buffaloes : Table (3) demonstrates that the genetic makeup of the *FABP* gene exerts a highly significant effect (P≤0.01) on heart girth in the studied buffalo samples. The average heart girth reached 183.00 ± 13.71 cm in the TA genotype, which was significantly greater than that of the TT genotype, averaging 167.64 ± 6.88 cm. A significant effect (P≤0.05) was also observed for body length, with the TT genotype exhibiting a higher average of 108.51 ± 4.22 cm compared to the TA genotype, which averaged 96.37 ± 11.79 cm. However, height at the withers was not significantly affected. The genotype of the *FABP* gene, particularly its polymorphism, plays a crucial role in influencing body dimensions, including heart girth in buffaloes, as well as other livestock species. The *FABP* family, including *FABP4*, is essential for the binding and transport of fatty acids, which in turn affects lipid metabolism and deposition. These processes are directly related to growth characteristics and body measurements (Sun et al.,2021; Wirth et al.,2022; Ye et al.,2022.

Table 3. Relationship of FABP/T>A Gene: 3499 in Body Dimensions of Local Buffalo

Genotype	**Number**	**Average ± standard error (cm)**		
		Body length	**Height at front**	**Heart girth**
TT	33	108.51± 4.22	130.63± 3.49	167.64± 6.88
TA	8	96.37± 11.79	137.12± 11.71	183.00± 13.71
Significant	---	*	N. S.	**

N. S. : Non Significant*(P≤0.05) ،**(P≤0.01)

Relationship of FABP / T>A gene polymorphism : 3499 in milk production and composition/ first month: Table (4) indicates that the daily milk yield and the percentages of milk components during ist month of lactation in the studied Iraqi buffaloes, represented by daily milk yield (kg), fat percentage, lactose percentage, protein

Iraqi Journal of Agricultural Sciences –2026:57(7):2027-2037
P-ISSN: 0075- 0530 /E-ISSN: 2410-0862
DOI: https://doi.org/10.36103/8ztt5t05

percentage, solids-not-fat (SNF) percentage, and milk density, did not exhibit significant differences, with the exception of milk density, which was significantly affected (P≤0.05). Milk density values were 1.029 ± 0.32 and 1.031 ± 0.40 for buffalo milk with the TT and TA genotypes, respectively, demonstrating that the milk density percentage in the TA genotype was higher than that in the TT genotype. The increase in milk density in domestic buffaloes is closely related to the Fatty Acid Binding Protein (FABP) gene family, particularly FABP3 and FABP4, which play a significant role in milk fat synthesis and quality. Research suggests that single nucleotide polymorphisms (SNPs) identified within these genes can influence milk traits, including fat percentage and total yield. For instance, the SNP g.307 C>T in the FABP3 gene has shown varying allelic frequencies across different buffaloes populations, although it has not been significantly associated with milk fat traits in river buffaloes (Dubey et al., 2016). Furthermore, the expression of FABP genes in mammary epithelial cells is modulated by fatty acids, suggesting a regulatory mechanism that can promote milk synthesis (Ye et al., 2022).

Table 4. Relationship of FABP/T>A: 3499 in milk Production and Composition / First Month of Local Buffaloes

Genotype	Number	Average ± standard error					
		Daily milk Production rate (kg)	Fat percentage	Lactose percentage	Proteein percentage	Percentage of non fat solids	Milk density
TT	25	10.42±0.98	5.93± 0.27	5.21±0.08	3.50±0.06	9.50±0.15	1.029±0.32
TA	5	10.22±1.05	5.85±0.23	5.20±0.05	3.49±0.03	9.45±0.11	1.031±0.40
Significant	---	N.S.	N.S.	N.S.	N.S.	N.S.	*

N. S. : Non Significant *(P≤0.05)

Association of FABP / T>A gene : 3499 in milk production and composition/ second month of local buffalo: We note through Table (5) that the proportions and production of milk ingredients for 2nd month of the local buffalo studied, represented by the daily milk production rate (kg), the percentage of fat, lactose, protein, non-fat solids and milk density, all did not show significant differences, except for the daily milk production rate (kg), which was significantly affected (P≤0.05), as the milk production rate was 9.92 ±0.79 and 8.64 ±0.62 in buffalo milk with a genetic structure TT and TA. Respectively, the rate of milk production in the TT genotype is higher than the rate of milk production in the genotype.TA The increase in milk production in local buffaloes is significantly influenced by genetic factors, especially the genes of the family of fatty acid binding proteins (FABP) and other related genes, highlighting their role in milk fat synthesis and overall performance, and are essential for the transport and metabolism of long-chain fatty acids, which directly affects the synthesis of milk fat (Ye et al., 2022).

Table 5. Relationship of FABP / T>A: 3499 / in milk production and composition / for the second month of local buffaloes

Genotype	Number	Average ± standard error					
		Daily milk production rate (kg)	Fat percentage	Lactose percentage	Proteein percentage	Percentage of non fat solids	Milk density
TT	25	9.92±0.79	5.76± 0.21	5.06±0.05	3.42±0.04	9.27±0.13	1.030±0.35
TA	5	8.64±0.62	6.07±0.23	5.02±0.05	3.34±0.05	9.10±0.11	1.030±0.33
Significant	---	*	N.S.	N.S.	N.S.	N.S.	N.S.

N. S. : Non Significant, *(P≤0.05)

Relationship of FABP / T>A gene : 3499 in milk production and composition/ third month : We note through Table (6) that the production and proportions of milk components for 3rd month of the studied local buffaloes, represented by the daily milk production rate (kg), the length of the milk season, the percentage of fat, lactose, protein, non-fat solids and milk density showed a significant effect (P≤0.05) on both the daily

Iraqi Journal of Agricultural Sciences –2026:57(7):2027-2037
P-ISSN: 0075- 0530 /E-ISSN: 2410-0862
DOI: https://doi.org/10.36103/8ztt5t05

milk production rate (kg) and milk density significantly according to the different genotype of the FABP gene, as the average daily milk yield was the highest in the TA genotype at 10.86 ±0.89, while the rate was lower in the TT genotype at 9.18 ±0.68, while the milk density in the TT genotype was 1.029 ±0.91 higher than the TA genotype by 1.028 ±0.59, while no significant effect was observed on the length of the milk season and the percentage of fat and lactose, protein and non-fat solids in the studied piece. The reason for this is as mentioned in the explanation of the increase in daily milk yield and milk density in the genotype relationship of the FABP/T>A gene: 3499 SNP2 in milk production and composition / for 1st,2nd months of local buffaloes.

Table 6. Relationship of FABP/T>A Gene: 3499 in Milk Production and Composition / Third Month of Local Buffaloes

Genotype	Number	Average ± standard error						
		Length of milk season (days)	Lactation period	Fat percentage	Lactose percentage	Proteein percentage	Percentage of non fat solids	Milk density
TT	25	9.18±0.68	188.64±19.31	6.12±0.41	4.58±0.27	3.32±0.04	8.87± 0.07	1.029± 0.91
TA	5	10.86±0.89	197.02±25.78	5.78±0.56	4.47±0.39	3.28±0.04	8.89± 0.11	1.028± 0.59
Significant	---	*	N.S.	N.S.	N.S.	N.S.	N.S.	*

N. S. : Non Significant *(P≤0.05)

Relationship of genotype of the FABP / T>A gene : 3499 at body temperature : Table (7), examining the relationship between the *FABP* gene genotype and body temperature in the studied buffalo samples, indicates a significant effect (P≤0.05) in the TT genotype, with an average of 38.41 ± 0.08 °C, which was higher than the average of 37.58 ± 0.13 °C observed in the TA genotype for the average body temperature during 2nd month. No significant differences were found in the average body temperature during the first month. Elevated body temperature is generally associated with reduced milk production and its major components (protein, fat, solids, and lactose) (Key et al., 2014). Our current investigation into the relationship between the *FABP* gene polymorphisms T>A: 3798/SNP1 and T>A: 3499/SNP2 and body temperature in domestic buffaloes aligns with the findings of, which demonstrated an inverse relationship between high temperature and milk production.

Table 7. Relationship of FABP / T>A gene: 3499 / and body temperature of domestic buffaloes

Genotype	Number	Average ± standard error	
		Average body temperature (C) first month	Body temperature rate (C) Second month
TT	33	37.93±0.11	38.41±0.08
TA	8	37.88±0.18	37.58±0.13
Significant level	----	N.S.	*

*(P≤0.05), Non Signifigant

This study's findings demonstrated that polymorphisms in the FABP gene, specifically the T>A substitution at position 3499, significantly affected several productive traits, including heart girth, daily milk yield across different lactation stages, and milk density in Iraqi buffaloes. These results are consistent with recent studies indicating that variations within the FABP3 and FABP4 genes contribute to the regulation of lipid metabolism, which, in turn, affects milk composition and growth traits in ruminants. For instance, (Bhatti et al., 2020) reported significant associations between FABP4 gene polymorphisms and milk yield and fat percentage in Holstein cows, while (Huang et al., 2022) demonstrated that genetic variations within FABP genes are strongly linked to fat metabolism and meat quality traits in buffalo. Similarly, (Gao et al., 2021) identified novel single-nucleotide polymorphisms (SNPs) in the FABP3 gene that contributed to differences

in milk production traits in dairy cattle. Furthermore, the observed relationship between genotype and body temperature during lactation could be partly explained by the role of FABP genes in regulating metabolic processes and responses to heat stress (Alvarez-Rodriguez & San, 2023, Kadegowda & Loor, 2019).

CONCLUSION

These findings highlight the importance of utilizing FABP gene markers in selection programs aimed at improving productive performance and enhancing resilience to environmental conditions in local buffalo populations.

CONFLICT OF INTEREST

The authors declare that they have no conflicts of interest

AUTHOR/S DECLARATION

The authors declare that they have not received a fund.

REFERENCES

Abbasi, N., Long, T., Li, Y., Yee, B. A., Cho, B.S., et al. (2020). DDX5 promotes oncogene C3 and FABP1 expressions and drives intestinal inflammation and tumorigenesis. Life Sci. Alliance 3(10):e202000772. https://doi.org/10.26508/lsa.202000772.

Al-Saedy, J. Kh. (2014). Mesopotamian Buffaloes: The Origin. Journal of Buffalo Science. 3: 30-33. https://doi.org/10.6000/1927-520X.2014.03.01.6.

Al-Sarai, T., & Al-Anabri, N., (2019). Polymorphism of mtrn1a gene and Its association with some productive traits in Iraqi buffaloes (Bubalus Bubalis). Plant Archives 19(2), 3546-3550. https://doi.org/10.31018/jans.v19i2.2050

Alvarez-Rodriguez, J. & San, A., (2023). Genetic markers and heat stress resilience in dairy ruminants: A review. Journal of Dairy Research, 90(2), pp.123–135. https://doi.org/10.1017/S0022029923000079.

Bhatti, M.A., Zhou, X., Xu, L. & Zhao, S., (2020). Association of FABP4 gene polymorphisms with milk yield and milk fat percentage in Chinese Holstein cows. Animal Biotechnology, 31(5);477–484. https://doi.org/10.1080/10495398.2019.1691989.

Chen, Y., Dai, Y., Song, K.., Huang , Y., Zhang, L., et al. (2021). Pre-emptive pharmacological inhibition of fatty acid-binding protein 4 attenuates kidney fibrosis by reprogramming tubular lipid metabolism. Cell Death Dis. 12(6):572. https://doi.org/10.1038/s41419-021-03850-1

Chiyonobu, N., Shimada, S., Akiyama, Y., Mogushi, K., Itoh, M., et al. (2018). Fatty acid binding protein 4 (FABP4) overexpression in intratumoral hepatic stellate cells within hepatocellular carcinoma with metabolic risk factors. Am. J. Pathol. 188(5):1213–24. https://doi.org/10.1016/j.ajpath.2018.01.012.

Chmurzynska, A. (2006). The multigene family of fatty acid-binding proteins (FABPs): Function, structure and polymorphism. J. App. Genet., 47(1), 39–48. https://doi.org/10.1007/BF03195782.

Damcott, C.M., Moffett, S.P., Feingold, E., Barmada, M.M., Marshall, J.A., Hamman, R.F., & Ferrell, R.E., (2004). Genetic variation in fatty acid-binding protein-4 and peroxisome proliferator-activated receptor gamma interactively influence insulin sensitivity and body composition in males. Metabolism: Clinical and Exp., 53: 303-309. https://doi.org/10.1016/j.metabol.2003.08.008.

Dubey, P. K., Goyal, S., Mishra, S. K., Arora, R., Mukesh, M., Niranjan, S. K.,. & Kataria, R. S., (2016). Identification of polymorphism in fatty acid binding protein (FABP3) gene and its association with milk fat traits in river buffalo (Bubalus bubalis). Tropical Animal Health and Production, 48(5), 849-853. https://doi.org/10.1007/s11250-016-1017-6.

Duncan, D. B. (1955). Multiple Range and Multiple F Tests. Biometrics, 11, 1.https://doi.org/10.2307/3001478.

Falconer, D. S. & Mackay, T. F. C., (2004). Introduction to quantitative genetics (4th ed.). Longman, Harlow, UK. https://doi.org/10.1093/genetics/167.4.1529

Fan, X., Xu, M., Ren, Q., Fan, Y., Liu, B., et al. (2022). Downregulation of fatty acid binding protein 4 alleviates lipid peroxidation and oxidative stress in diabetic retinopathy by regulating peroxisome proliferator-activated receptor γ-mediated ferroptosis. Bioengineered 13(4):10540–51.

Iraqi Journal of Agricultural Sciences –2026:57(7):2027-2037
P-ISSN: 0075- 0530 /E-ISSN: 2410-0862
DOI: https://doi.org/10.36103/8ztt5t05

https://doi.org/10.1080/21655979.2022.2062533.

Gajda, A. M., Tawfeeq, H. R., Lackey, A. I., Zhou, Y. X., Kanaan, H., et al. (2022). The proximal intestinal fatty acid-binding proteins liver FABP (LFABP) and intestinal FABP (IFABP) differentially modulate whole body energy homeostasis but are not centrally involved in net dietary lipid absorption: Studies of the LFABP/IFABP double knockout mouse. Biochim. Biophys. Acta Mol. Cell Biol. Lipids 1868(1):159238. https://doi.org/10.1016/j.bbalip.2022.159238.

Gao, H., Wang, S., Wu, H., & Yang , J., (2021). Identification of novel SNPs in FABP3 gene and their associations with milk production traits in dairy cattle. Animals, 11(2), p.435. https://doi.org/10.3390/ani11020435.

Helalia, S., El Makawy, A., Abo-Bakr, N., Hassan, N., & Hassanana. M., (2022). Recognition of genetic polymorphism in FABP4 and TG lipid metabolism-related genes in Egyptian buffalo. International Journal of Innovative Science, Engineering and Technology (IJISET), 9(11- 18). https://ijiset.com/vol9/v9s11/IJISET_V9_I11_18.pdf

Hoashi, S., Hinenoya, T., Tanaka, A., Ohsaki, H., Sasazaki, S., Taniguchi, M., Oyama, K., Mukai, F., & Mannen, H., (2008). Association between fatty acid compositions and genotypes of FABP4 and LXR-alpha in Japanese Black cattle. BMC Genet. 9:84. https://doi.org/ 10.1186/1471-2156-9-84

Huang, J., Yu, H., Li, R., & Li, C., (2022). Polymorphisms in fatty acid-binding protein genes associated with fat metabolism and meat quality traits in buffalo. BMC Genomics, 23(1), p.67. https://doi.org/10.1186/s12864-022-08317-6

Ibrahim, A.H.M., Shehata, M.F., Ismail, I.M., & Gad, S.M.A. (2014). Association of fatty acid binding protein 4 (FABP4) polymorphisms with growth and carcass traits of Barki sheep. J. Ame. Sci., 10, 10-15. https://www.jofamericanscience.org/journals/am-sci/am1005s/002_26980bam1005s14_10_15.pdf

.Kadegowda, A.K.G. & Loor, J. J., (2019). Role of fatty acid-binding proteins in mediating metabolic regulation in dairy cows. Journal of Dairy Science, 102(11), pp.99609971. https://doi.org/10.3168/jds.2019-16605

Key, N., Sneeringer, S., & Marquardt, D., (2014). Climate change, heat stress and U.S. dairy production. A Report Summary from the Economic Research Service, United States Department of Agriculture,1-175. http://www.ers.usda.gov/publications/pub-details?pubid=45282

Michal, j.J., Zhang, Z.W., Gaskins, C.T., & Jiang, Z., (2006). The bovine fatty acid binding protein 4 gene is significantly associated with marbling and subcutaneous fat depth in Wagyu x Limousin F2 crosses. Anim. Genet., 37, 400-402. https://doi.org/10.1111/j.1365-2052.2006.01485.x

Prentice, K. J., Saksi, J., Robertson, L. T., Lee, G. Y., Inouye, K. E., et al., (2021). A hormone complex of FABP4 and nucleoside kinases regulates islet function. Nature600(7890):720726.https://doi.org/10.1038/s41586-021-04137-3.

SAS. (2018). Statistical Analysis System, User's Guide. Version 9.6th ed. SAS Institute Inc., Cary, NC, USA.

Shinoda, Y., Wang, Y., Yamamoto, T., Miyachi, H., & Fukunaga, K.., (2020). Analysis of binding affinity and docking of novel fatty acid-binding protein (FABP) ligands. J. Pharmacol. Sci. 143(4):264–271.https://doi.org/10.1016/j.jphs.2020.04.005

Storch, J., & Thumser, A.E., (2000). The fatty acid transport function of fatty acid-binding proteins. Biochim Biophys Acta, 1486, 28–44. https://doi.org/ 10.1016/S1388-1981(00)00109-6

Sun, F., Chen, G., Yang, Y., & Lei, M., (2021). Fatty acid-binding protein 4 silencing protects against lipopolysaccharide-induced cardiomyocyte hypertrophy and apoptosis by inhibiting the Toll-like receptor 4–nuclear factor-κB pathway. J. Int. Med. Res.49(3):300060521998233. https://doi.org/10.1177/0300060521998233

Tsukahara, R., Haniu, H., Matsuda, Y., & Tsukahara, T., (2014). Heart-type fatty-acid-

Iraqi Journal of Agricultural Sciences –2026:57(7):2027-2037
P-ISSN: 0075- 0530 /E-ISSN: 2410-0862
DOI: https://doi.org/10.36103/8ztt5t05

binding protein (FABP3) is a lysophosphatidic acid-binding protein in human coronary artery endothelial cells. FEBS Open Bio., 4, 947–951. https://doi.org/10.1016/j.fob.2014.10.014.

Wirth, K., Shinoda, S., Sato-Dahlman, M., Dickey, D. M., Bernlohr, D. A., et al., (2022). Fatty acid binding protein 4 regulates pancreatic cancer cell proliferation via activation of nuclear factor E2-related factor 2. Surg. Obes. Relat. Dis. 18(4):485–493. https://doi.org/10.1016/j.soard.2021.12.002PubMed Central

Wu, G., Tawfeeq, H. R., Lackey, A. I., Zhou, Y., Sifnakis, Z., et al., (2022). Gut microbiota and phenotypic changes induced by ablation of liver- and intestinal-type fatty acid-binding proteins. Nutrients 14(9):1762. https://doi.org/10.3390/nu14091762.

Xiang, J., Li, H., Guo, Z., Li, T., Yamada, T ., Li, X., Bao, S., Da, L., Borjigin, G., Cang, M., et al,. (2025). Effect of FABP4 Gene Polymorphisms on Fatty Acid Composition, Chemical Composition, and Carcass Traits in Sonid Sheep. Animals, 15, 226. https://doi.org/ 10.3390/ani15020226.

Yardibi, H., Gürsel, F.E., Ates, A., Akis, I., Hostruk, G.T., & Oztabak, K., (2013). BTN1A1, FABP3 and TG genes polymorphism in East Anatolian red cattle breed and South Anatolian red cattle breed. Afr. J. Biotechnol., 12(20); 2802-2807. https://doi.org/10.5897/AJB2013.12297

Ye, T., Shaukat, A., Yang, L.V., Chen, C., Zhou, Y., & Yang, L., (2022). Evolutionary and association analysis of Buffalo FABP Family genes reveal their potential role in milk performance. genes, 13, 600. https://doi.org/10.3390/genes13040600.

Zhang, J., Wang, Q., Cao, Y., Hou, M., Zhao, R., Chen, Y., & Li, J. (2024). Genome-wide association analysis identifies genetic variants associated with muscle fatty acids and amino acids in grass carp (Ctenopharyngodon idella). Agriculture Communications, 2, 100043. https://doi.org/10.1016/j.agrcom.2024.100043

Zhang, Y., Kent, J. r. J. W., Lee, A., Cerjak, D., Ali, O., Diasio, R., Olivier, M., Blangero, K.., Carless, M. A., & Kissebah, A. H., (2013). Fatty acid binding protein 3 (fabp3) is associated with insulin, lipids and cardiovascular phenotypes of the metabolic syndrome through epigenetic modifications in a northern european family population. BMC Med. Genomics, 6(9), 1–14.. https://doi.org/10.1111/j.1365-2052.2007.01648.x

Zhang, Y., Colli, L., & Barker, J., (2020). Asian water buffalo: domestication, history and genetics. Animal Genetics. Zhang, Y., Sun, D. & Yu, Y., (2007).Genetic diversity and differentiation of Chinese domestic buffalo based on 30 microsatellite markers. Animal Genetics.38:6-17. https://doi.org/10.1111/age.12911

Iraqi Journal of Agricultural Sciences –2026:57(7):2027-2037
P-ISSN: 0075- 0530 /E-ISSN: 2410-0862
DOI: https://doi.org/10.36103/8ztt5t05

علاقة الأنماط الجينية لجين FABP عند الموقع T3499A بقياسات الجسم ودرجة الحرارة وبعض صفات الحليب في الجاموس العراقي

صفا كامل كاظم[1] ، نصر نوري الانباري[2]، سيف نبيل الوائل[3]
قسم الإنتاج الحيواني- كلية علوم الهندسة الزراعية- جامعة بغداد- العراق

المستخلص

هدفت الدراسة الى الكشف عن الانماط الوراثية لجين FABP التغاير T>A: 3499 لعينه مكونة من 41 جاموسة وعلاقتها بعدد من الصفات الإنتاجية للمدة من 2024/10/1 الى2025/1/30 في محطة بحوث المجترات في ابي غريب. من خلال الكشف عن الأنماط الوراثية لجين FABP ظهر لدينا التغاير T>A: 3499 وبتركيبين وراثيين وهي TT و TA وبلغت نسب توزيعها 80.49 و19.51% على التوالي (P≤0.01) وبتكرار اليلي 0.90 و0.10 لكل من الاليلين T و A على التوالي. وفروق معنوية (P≤0.01) في طول الجسم ومحيط الصدر ودرجة حرارة الجسم للشهر الثاني، أما معدل أنتاج وتركيب الحليب في الشهر الأول متمثلة بكثافة الحليب والشهر الثاني متمثلة بمعدل أنتاج الحليب اليومي والشهر الثالث متمثلة بمعدل أنتاج وكثافة الحليب، أذ تفوق TA على TT لكل من محيط الصدر وكثافة الحليب للشهر الأول ومعدل أنتاج الحليب للشهر الثالث. يمكن ان نستنتج من خلال دراسة التراكيب الوراثية في جين FABP/ 3499: T>A، للاستفادة منها في التحسين الوراثي لاداء الجاموس العراقي

الكلمات المفتاحية: تكرارات الأليلات، *Bubalus bubalis* ، الطرز الوراثية، الصفات الإنتاجية.