Genetic variants in the serum amyloid A2 (SAA2) gene as a potential marker for milk production traits in Chinese Holstein cows

Sayed Haidar Abbas Raza1,2 | Chengcheng Liang1,2 | Ahmed Mohajja Alshammari3 | Bandar H. Aloufi3 | Linsheng Gui4 | Rajwali Khan5 | Linsen Zan1,2

1State Key Laboratory of Animal Genetics Breeding & Reproduction, College of Animal Science and Technology, Northwest A&F University, Yangling, P. R. China
2National Beef Cattle Improvement Center, Northwest A&F University, Yangling, P. R. China
3Faculty of Science, Biology Department, University of Hail, Hail, Saudi Arabia
4State Key Laboratory of Plateau Ecology and Agriculture, Qinghai University, Xining, P. R. China
5Department of Livestock Management, Breeding and Genetics, The University of Agriculture, Peshawar, Pakistan

Correspondence
Linsen Zan, State Key Laboratory of Animal Genetics Breeding & Reproduction, College of Animal Science and Technology, Northwest A&F University, No. 22 Xinong Road, Yangling, Shaanxi 712100, P. R. China. Email: zanlinsen@163.com

Sayed Haidar Abbas Raza and Chengcheng Liang contributed equally to this work.

Funding information
National Natural Science Foundation of China, Grant/Award Number: 31972994; Key Research and Development Program of Ningxia Province, Grant/Award Number: 2019BEF02004; National Beef and Yak Industrial Technology System, Grant/Award Number: CARS-37

Abstract
Background: This study was conducted to detect potential polymorphisms of the serum amyloid A2 (SAA2) gene and explore their relationships with milk production traits in Chinese Holstein cows.
Objectives: This study used: sequencing technology conducted in 532 Chinese Holstein cows.
Methods: Three single nucleotide polymorphisms (SNPs) were identified within intron 1, named g.14061A>G, g.14072G>C and g.14819C>T. Eight estimated haplotypes were identified, of which three major haplotypes had a frequency of Hap3 (-ACC-), Hap5 (-GCC-) and Hap2 (-AGT-), with 17.9%, 12.30% and 8.10%, respectively.
Results: The association analysis of single markers (g.14061A>G and g.14819C>T) and combined genotypes (Hap1/5) revealed prominent effects on milk production traits in Chinese Holstein cows (p < 0.05).
Conclusions: Our results suggest that the SAA2 gene is associated with economic traits in Chinese Holstein cows and may be used as candidate gene for marker-assisted selection and management in breeding programs.

KEYWORDS
genetic variability, milk production traits, SAA2 gene, single nucleotide polymorphism

This is an open access article under the terms of the Creative Commons Attribution License, which permits use, distribution and reproduction in any medium, provided the original work is properly cited.
© 2022 The Authors. Veterinary Medicine and Science published by John Wiley & Sons Ltd.

Vet Med Sci. 2022:8:1835–1840.
1 | INTRODUCTION

In mammals, serum amyloid A (SAA) is comprised of five isoforms with high conservation and various biological functions, designated as SAA1, SAA2, SAA3, M-SAA3.2 and SAA4, respectively (Kovačević-Filipović et al., 2012). SAA is synthesized primarily by hepatocytes, macrophages, vascular endothelial cells and adipocytes (Ahmed et al., 2012; Artl et al., 2000). Clinical studies confirmed that SAA is considered a biomarker of inflammation and angiocardiopathy, with dramatic increases in SAA plasma levels in response to inflammatory and atherosclerotic cardiovascular diseases (Smole et al., 2020). The SAA2 gene encodes the amphipathic alpha-helical apolipoprotein (Chait et al., 2005) that plays a pivotal role in mobilization of cholesterol during tissue repair and regeneration and was described as a ‘gatekeeper’ for its function in normal tissues (Urieli-Shoval et al., 2000). When released, the SAA2 gene readily bound to high-density lipoprotein (HDL), and then rerouted HDL transport (Benditt & Eriksen, 1977). Via modulating the ability of HDL, the SAA2 gene contributed to reverse transport of cholesterol and removed excess cholesterol from the body (De Beer et al., 2014). Compared to cows with lower milk protein and fat percentage, expression of the SAA2 gene was remarkably reduced in the mammary gland with extremely high milk protein and fat percentage (Cui et al., 2014). Therefore, these findings lend credence to the hypothesis that the SAA2 gene is an excellent candidate marker for milk composition traits in dairy cattle.

The purpose of the present research was to analyze the influence of SAA2 gene polymorphisms on the comparison of milk traits in Chinese Holstein cows and to determine the changes in milk traits during lactation depending on polymorphisms of the analyzed genes.

2 | MATERIALS AND METHODS

2.1 | Animals and phenotypic data

A total of 532 Chinese Holstein dairy cows belonging to 24 sire families were collected from Xi’an Caotan Animal Husbandry Co. LTD (Shaanxi Province, China). All of the cows were fed with the same regular total mixed ration composed of concentrated feed and coarse fodder and were routinely milked three times a day (07:00, 15:00, 23:00). The milk yields were recorded with a computerized herd management system. The dairy herd improvement (DHI) in milk samples were provided from Xi’an Caotan Animal Husbandry Co. LTD.

2.2 | DNA isolation

Genomic DNA from blood samples were collected by TIANamp Blood DNA kit (Tiangen, Beijing, China). The quality of DNA was measured using a NanoDrop ND-2000c Spectrophotometer (Thermo Scientific).

2.3 | PCR amplification and single nucleotide polymorphism detection

According to the sequence of the bovine SAA2 gene (GenBank accession no. AC_000186.1), four pairs of PCR primers were designed with Primer Premier Software (Version 4.0). Detailed information of primers is depicted in Table 1. PCR was performed in a 30 μl reaction mixture containing Mix (TaKaRa, Dalian, China) 15.0 μl, upstream primer 0.6 μl, downstream primer 0.6 μl, ddH₂O 11.8 μl, DNA 2.0 μl. PCR conditions were as follows: initial denaturation at 95°C for 5 min, followed by 35 cycles at 94°C for 30 s; annealing temperature for 30s; 72°C for 40 s; and a final extension at 72°C for 10 min, and then sequenced using an ABI 3730 sequencer (ABI, Foster City, CA, USA).

Gene frequencies and Hardy–Weinberg equilibrium (HWE) were computed using POPGENE software (Version 3.0). The extent of linkage disequilibrium (LD) between the identified single nucleotide polymorphisms (SNPs) was estimated using Haploview 3.32 software (Broad Institute of MIT and Harvard, Cambridge, MA, USA) (Raza, Shi-jun, et al., 2020; Raza, Khan, et al., 2020; Raza, Liu, 2020; Wei et al., 2018).

2.4 | Statistical analysis

The associations of the SNPs and milk production traits were analyzed by analysis of variance (ANOVA) the SPSS 16.0 software (IBM Company, NY, USA). The equation was as follows: $Y_{ijklm} = \mu + Y_i + G_j + L_k + S_l + E_{ijklm}$, where $Y_{ijklm}$ is the trait observation, $\mu$ is the overall mean, $Y_i$ is the fixed effect of the $i$th year ($i = 1, 2, 3$ and $4$), $G_j$ is the fixed effect of the $j$th genotype ($j = 1, 2$ and $3$), $L_k$ is the fixed effect of the $k$th calving...
The additive, dominance, and allele substitution effects of single SNPs were evaluated by SPSS 16.0 software (IBM Company, NY, USA). The equation is as follows:

\[
\text{Additive} = \frac{\text{homozygous genotypes 1} - \text{homozygous genotypes 2}}{2};
\]

\[
\text{Dominance} = \text{heterozygous genotype} - \frac{\text{homozygous genotypes 1} + \text{homozygous genotypes 2}}{2};
\]

\[
\text{Allele substitution} = \text{additive} + \text{dominance (allele frequencies of homozygous genotypes 1 – allele frequencies of homozygous genotypes 2)}.
\]

3 | RESULTS AND DISCUSSION

3.1 Polymorphisms and genetic diversity

The bovine SAA2 gene is located on chromosome 29 of the bovine genome. The total length of SAA2 is 3447 bp, comprising the genomic coordinates starting from 26458422 to 26461868 (NC_037356.1, Reference genome bos taurus published in GenBank in the NCBI database). This gene comprises 04 exons, the ORF that started from the start codon to the stop codon is 393 bp, and the putative protein contains 131 amino acids (Figure 1).

In the current study, three SNPs, including g.14061A>G, g.14072G>C and g.14819C>T, were identified by DNA direct sequencing. All three loci mapped on intron 1 of the SAA2 gene. The genotype TT of g.14819C>T was not observed in the sampled population, probable explanations may be that (1) this genotype at g.14819C>T locus may never exist in the population and (2) the experimental population size was insufficient to capture full genetic variation (Gui et al., 2015).

3.2 Genetic diversity analysis

Table 2 lists the genotype frequencies, maximum allele frequency, PCI and HWE of SAA2 gene in Chinese Holstein dairy cows. AA of g.14061A>G was the most prevalent genotype (64.29%). GG of g.14072G>C was more frequent (54.70%) compared to the others genotype. CC was the most prevalent genotype (73.87%) at g.14819C>T locus. The \( \chi^2 \) test indicated that the g.14061A>G and g.14072G>C were in HWE (\( p < 0.05 \)), while the g.14819C>T was severely out of HWE (\( P > 0.05 \)). It was speculated that the g.14819C>T loci carried out significance selection pressure (Lee et al., 2008), resulting in the loss of certain alleles, except those for the favoured traits (Huang et al., 2011).

3.3 Haplotypes analysis

As presented in Table 3, eight estimated haplotypes were detected in the Chinese Holstein dairy cows. The frequency of Hap1 haplotype (−AGC−) was 51.00%, followed by Hap3 haplotype (−ACC−), Hap5 haplotype (−GCC−) and Hap2 haplotype (−AGT−), with 17.9%, 12.30% and 8.10%, respectively. High-frequency haplotypes probably presented at the sampled population long ago, which may be directly or indirectly regulated by different rearing environments (Sawyer et al., 2006). Due to the absence of statistical significance, the Hap4 (−ACT−), Hap6 (−GGT−) and Hap8 (−GCT−) were ignored (frequency < 5.00%).

3.4 Association analysis

So far, litter polymorphism on the SAA2 gene is reported regarding herbivore breeding and reproduction. Previously, two mutations (c.17G>C and c.114G>A) within the 5′-regulatory region of the SAA2 gene were found to be statistically significance for milk yield, fat yield and protein yield in Chinese Holstein cows as a result of alteration in SAA2 gene transcriptional activity (Yang et al., 2015). In addition, both c.-84
**TABLE 2** Population genetic analysis of single nucleotide polymorphisms (SNPs) in serum amyloid A2 (SAA2) gene

| Loci (gene) | Genotypic frequency (%) | Maximum allele frequency (%) | HWE |
|-------------|--------------------------|-----------------------------|-----|
| g.14061A>G  | AA 64.29, AG 29.70, GG 6.02 | 79.14 (A) | p > 0.05 |
|             |                           | 54.70, GC 37.59, CC 7.71    | 73.50 (G) | p > 0.05 |
| g.14819C>T  | CC 73.87, CT 26.13, TT - | 86.94 (C) | p < 0.05 |

Abbreviation: HWE, Hardy–Weinberg equilibrium.

**TABLE 3** Frequencies analysis of serum amyloid A2 (SAA2) gene haplotypes

| Haplotype | g.14061A>G | g.14072G>C | g.14819C>T | Frequency (%) |
|-----------|------------|------------|------------|---------------|
| Hap1      | A          | G          | C          | 51.00         |
| Hap2      | A          | G          | T          | 8.10          |
| Hap3      | A          | C          | T          | 17.90         |
| Hap4      | A          | C          | T          | 2.10          |
| Hap5      | G          | G          | C          | 12.30         |
| Hap6      | G          | G          | T          | 2.00          |
| Hap7      | G          | C          | T          | 5.60          |
| Hap8      | G          | C          | T          | 1.00          |

**TABLE 4** Association of genotypes of single nucleotide polymorphisms (SNPs) in serum amyloid A2 (SAA2) gene with comparison of milk traits in Chinese Holstein cows

| Loci       | Genotypes (N) | Milk fat percentage (%) | Milk protein percentage (%) | Lactose percentage (%) |
|------------|----------------|-------------------------|----------------------------|------------------------|
| g.14061A>G | AA (342)       | 4.17 ± 0.03b            | 3.26 ± 0.02b               | 5.13 ± 0.01            |
|            | AG (158)       | 4.35 ± 0.04b            | 3.30 ± 0.02b               | 5.12 ± 0.01            |
|            | GG (32)        | 5.19 ± 0.07a            | 3.77 ± 0.05a               | 5.04 ± 0.03            |
| g.14072G>C | GG (291)       | 4.27 ± 0.04             | 3.29 ± 0.02                | 5.13 ± 0.01            |
|            | GC (200)       | 4.33 ± 0.04             | 3.32 ± 0.03                | 5.11 ± 0.01            |
|            | CC (41)        | 4.21 ± 0.08             | 3.32 ± 0.05                | 5.13 ± 0.02            |
| g.14819C>T | CC (393)       | 4.24 ± 0.03             | 3.29 ± 0.02                | 5.08 ± 0.01b           |
|            | CT (139)       | 4.42 ± 0.05             | 3.32 ± 0.05                | 5.24 ± 0.02a           |

Note: Values with different superscripts letters are significantly different (p < 0.05).

G>C and c.114G>A were detected in the SAA2 gene of Polish Holstein-Friesian cattle. Individuals with the CC genotype of c.-84 G>C were characterized by the highest content of protein and the lowest content of fat in milk (Kowalewska-Luczak et al., 2021). In the current study, association analysis between SNPs of the SAA2 gene and milk production traits (Table 4), as well as the significant additive effects, dominant effects and allele substitution effects were observed (Table 5). Furthermore, individuals carrying GG genotype at g.14061A>G locus had significantly higher milk fat percentage and milk protein percentage than individuals with AA genotype (p < 0.05). Compared to animals with genotype TT, the role of CT genotype at g.3208C>T locus caused the highest average for lactose percentage (p < 0.05). Different from previous studies, the location of mutations was found on the introns in the current study. The mutation differences may be explained by the diversity of the sample population. 

Haplotypes composed of SNPs provided greater power than single-marker analysis for associations of inheritable characters because of the ancestral structure captured in the distribution of haplotypes.
**TABLE 5** Genetic effects of the three single nucleotide polymorphisms (SNPs) in serum amyloid A2 (SAA2) gene on the milk production traits

| Loci            | Genotype       | Milk fat (%) | Milk protein (%) | Lactose (%) |
|-----------------|----------------|--------------|------------------|-------------|
| g.14061A>G      | Additive       | −0.510 ± 0.255 | −0.035           | 0.094       |
|                 | Dominant       | −0.330 ± 0.215 | −0.020           | 0.088       |
|                 | Allele substitution | −0.760 ± 0.438 | −0.013           | 0.088       |
| g.14072G>C      | Additive       | 0.030 ± 0.015  | 0.000            | 0.000       |
|                 | Dominant       | 0.090 ± 0.015  | −0.020           | −0.020      |
|                 | Allele substitution | 0.088 ± 0.009  | −0.013           | −0.013      |
| g.14819C>T      | Additive       | 2.120 ± 1.645  | 2.540 ± 2.000    | 2.700       |
|                 | Dominant       | 2.300 ± 1.167  | 2.700            | 2.700       |
|                 | Allele substitution | 3.160 ± 2.168  | 4.705 ± 4.000    | 4.705       |

*significant difference (p < 0.05).

**TABLE 6** Association of dipotypes of serum amyloid A2 (SAA2) gene with comparison of milk traits in Chinese Holstein cows

| Dipotypes (N) | Milk fat percentage (%) | Milk protein percentage (%) | Lactose percentage (%) |
|---------------|-------------------------|-----------------------------|------------------------|
| Hap1/1 (146)  | 4.09 ± 0.05b            | 3.21 ± 0.02                 | 5.12 ± 0.01            |
| Hap1/2 (51)   | 4.27 ± 0.08ab            | 3.34 ± 0.04                 | 5.19 ± 0.02            |
| Hap1/3 (84)   | 4.18 ± 0.06ab            | 3.23 ± 0.03                 | 5.10 ± 0.02            |
| Hap1/5 (54)   | 4.38 ± 0.07a             | 3.22 ± 0.04                 | 5.10 ± 0.02            |
| Hap1/7 (56)   | 4.27 ± 0.07ab            | 3.30 ± 0.04                 | 5.09 ± 0.02            |

Note: Values with different superscripts letters are significantly different (p < 0.05).

In summary, three SNPs (g.14061A>G, g.14072G>C and g.14819C>T) and eight haplotypes were discovered within the SAA2 gene of Chinese Holstein cows. The association analysis of single markers (g.14061A>G and g.14819C>T) and combined genotypes (Hap1,5) revealed prominent effects on comparison of milk traits in Chinese Holstein cows. Further research should be conducted in a large population before they could be applied as genetic markers for selection purposes.

**CONCLUSION**

**ACKNOWLEDGEMENTS**

This research was funded by the National Natural Science Foundation of China (31972994), Key Research and Development Program of Ningxia Province (2019BEF02004) and National Beef and Yak Industrial Technology System (CARS-37).

**CONFLICT OF INTEREST**

The authors declare no conflict of interest.

**AUTHOR CONTRIBUTION**

Conceptualization, data curation, formal analysis, investigation, software validation, visualization, writing—original draft and writing—review and editing: Sayed Haidar Abbas Raza. Conceptualization, data curation, formal analysis, investigation: Chengcheng Liang. Formal analysis, validation and writing—review and editing: Ahmed Mohajja Alshammari. Conceptualization, formal analysis, methodology and writing—review and editing: Bandar H. Aloufi. Formal analysis and Writing—review and editing: Linsheng Gui. Software, validation and writing —review and editing: Rajwali Khan. Funding acquisition, investigation, methodology, project administration, resources, supervision and writing—review and editing: Linshen Zan.

**ETHICS STATEMENT**

The experimental animals were dealt as per standard operating procedures (SOPs) formatted by Chinese Council of Animals Care, and further approved by ‘Experimental Animal Management Committee Approval Number is (EAMC 2020-1298)’ of the Northwest Agricultural and Forestry University. The sampling was performed after human killing of the experimental animals at College of Animal Science, Shaanxi, Yangling, China.
DATA AVAILABILITY STATEMENT
The data that support the findings of this study are available from the corresponding author upon reasonable request.

PEER REVIEW
The peer review history for this article is available at https://publons.com/publon/10.1002/vms3.796.

ORCID
Sayeed Haidar Abbas Raza https://orcid.org/0000-0002-0961-1911
Rajwali Khan https://orcid.org/0000-0001-5191-3457
Linsen Zan https://orcid.org/0000-0002-2645-0179

REFERENCES
Ahmed, M. S., Jadhav, A. B., Hassan, A., & Meng, Q. H. (2012). Acute phase reactants as novel predictors of cardiovascular disease. ISRN Inflammation, 2012, 953461.
Akey, J., Jin, L., & Xiong, M. (2001). Haplotypes vs single marker linkage disequilibrium tests: What do we gain? European Journal of Human Genetics, 9, 291–300.
Artl, A., Marsche, G., Lestavel, S., Sattler, W., & Malle, E. (2000). Role of serum amyloid A during metabolism of acute-phase HDL by macrophages. Arteriosclerosis, Thrombosis, and Vascular Biology, 20, 763–772.
Benditt, E. P., & Eriksen, N. (1977). Amyloid protein SAA is associated with high density lipoprotein from human serum. PNAS, 74, 4025–4028.
Chai, Y., Sun, Y., Guo, L., Li, D., & Ding, Y. (2015). Investigating the role of introns in the regulation of regenerating gene 1 expression. Oncology Letters, 9, 875–880.
Chait, A., Han, C. Y., Oram, J. F., & Heinecke, J. W. (2005). Thematic review series: The immune system and atherogenesis. Lipoprotein-associated inflammatory proteins: Markers or mediators of cardiovascular disease? Journal of Lipid Research, 46, 389–403.
Cui, X., Hou, Y., Yang, S., Xie, Y., Zhang, S., Zhang, Y., Zhang, Q., Lu, X., Liu, G. E., & Sun, D. (2014). Transcriptional profiling of mammary gland in Holstein cows with extremely different milk protein and fat percentage using RNA sequencing. BMC Genomics, 15, 226.
De Beer, M. C., Wroblewski, J. M., Noffsinger, V. P., Rateri, D. L., Howatt, D. A., Balakrishnan, A. J., Ji, A., Shridas, P., Thompson, J. C., & van der Westhuysen, D. R. (2014). Deficiency of endogenous acute-phase serum amyloid A does not affect atherosclerotic lesions in apolipoprotein e-deficient mice. Arteriosclerosis, Thrombosis, and Vascular Biology, 34, 255–261.
Gui, L. S., Zhang, Y.-R., Liu, G.-Y., & Zan, L.-S. (2015). Expression of the SIRT2 gene and its relationship with body size traits in Qinchuan cattle (Bos taurus). International Journal of Molecular Sciences, 16, 2458–2471.
Gui, L. S., Huang, Y.-M., Hong, J. Y., & Zan, L. S. (2016). Polymorphisms in the LPL gene and their association with growth traits in Jiaxian cattle. Genetcs and Molecular Research, 15, gmr.15027590.
Hao, D., Thomesen, B., Bai, J., Peng, S., Lan, X., Huang, Y., Wang, X., & Chen, H. (2020). Expression profiles of the MXD3 gene and association of sequence variants with growth traits in Xianan and Qinchuan cattle. Veterinary Medicine and Science, 6, 399–409.
Huang, Y.-Z., He, H., Sun, J.-J., Wang, J., Li, Z.-J., Lan, X.-Y., Lei, C.-Z., Zhang, C.-L., Zhang, E.-P., & Wang, J.-Q. (2011). Haplotypc combination of SREBP-1c gene sequence variants is associated with growth traits in cattle. Genome, 54, 507–516.
Kovačević-Filipović, M., Ilić, V., Vujčić, Ž., Dojinov, B., Stevanov-Pavlović, M., Mijačević, Z., & Božić, T. (2012). Serum amyloid A isoforms in serum and milk from cows with Staphylococcus aureus subclinical mastitis. Veterinary Immunology and Immunopathology, 145, 120–128.
Kowalewska-Łuczak, I., Ewa, C.-P., & Alicja, K. (2021). Relationship between polymorphism in the CRH gene and the traits of body conformation of Salers cows. Animal Biotechnology, 32, 1:38–42.
Lee, S., Kasif, S., Weng, Z., & Cantor, C. R. (2008). Quantitative analysis of single nucleotide polymorphisms within copy number variation. PLoS One, 3, e3906.
Li, X., Buitenhuys, A. J., Lund, M. S., Li, C., Sun, D., Zhang, Q., Poulsen, N. A., & Su, G. (2015). Joint genome-wide association study for milk fatty acid traits in Chinese and Danish Holstein populations. Journal of Dairy Science, 98, 8152–8163.
Palombo, V., Milanesi, M., Sgorlon, S., Capomaccio, S., Mele, M., Nicolazzi, E., Ajmone-Marsan, P., Pilla, F., Stefanon, B., & D’Andrea, M. (2018). Genome-wide association study of milk fatty acid composition in Italian Simmental and Italian Holstein cows using single nucleotide polymorphism arrays. Journal of Dairy Science, 101, 11004–11019.
Raza, S. H. A., Khan, R., Schreurs, N. M., Guo, H., Gui, L., Mei, C., & Zan, L. (2020). Expression of the bovine KLF6 gene polymorphisms and their association with carcass and body measures in Qinchuan cattle (Bos taurus). Genomics, 112, 423–431.
Raza, S. H. A., Liu, G. Y., Zhou, L., Gui, L. S., Khan, R., Jimmeng, Y., Chugang, M., Schreurs, N. M., Ji, R., & Zan, L. (2020). Detection of polymorphisms in the bovine leptin receptor gene affects fat deposition in two Chinese beef cattle breeds. Gene, 758, 144957. https://doi.org/10.1016/j.gene.2020.144957
Raza, S. H. A., Shijun, L., Khan, R., Schreurs, N. M., Manzari, Z., Abd El-Aziz, A. H., Ullah, I., Kaster, N., Shah, M. A., & Zan, L. (2020). Polymorphism of the PLIN1 gene and its association with body measures and ultrasound carcass traits in Qinchuan beef cattle. Genome, 63, 483–492. https://doi.org/10.1139/gen-2019-0184
Sawyer, L. A., Sandrelli, F., Pasetto, C., Peixoto, A. A., Rosato, E., Costa, R., & Kyriacou, C. P. (2006). The period gene Thr-Gly polymorphism in Australian and African Drosophila melanogaster populations: Implications for selection. Genetics, 174, 465–480.
Smole, U., Gour, N., Phelan, J., Hofer, G., Köhler, C., Kratzer, B., Tauber, P. A., Xiao, Y., Yao, N., & Dvorak, J. (2020). Serum amyloid A is a soluble pattern recognition receptor that drives type 2 immunity. Nature Immunology, 21, 756–765.
Uriei-Showal, S., Linke, R. P., & Matzner, Y. (2000). Expression and function of serum amyloid A, a major acute-phase protein, in normal and disease states. Current Opinion in Hematology, 7, 64–69.
Wei, D., Raza, S. H. A., Zhang, J., Gui, L., Rahman, S. U., Khan, R., Hosseini, S. M., Kaleri, H. A., & Zan, L. (2018). Polymorphism in promoter of S14X gene shows association with its transcription and body measurement traits in Qinchuan cattle. Gene, 656, 9–16.
Wu, J., Li, A., Cai, H., Zhang, C., Lei, C., Lan, X., & Chen, H. (2019). Intron retenion as an alternative splice variant of the cattle ANGPTL6 gene. Gene, 709, 17–24.
Yang, S., Li, C., Xie, Y., Cui, X., Li, X., Wei, J., Zhang, Y., Yu, Y., Wang, Y., & Zhang, S. (2015). Detection of functional polymorphisms influencing the promoter activity of the SAA2 gene and their association with milk protein production traits in Chinese Holstein cows. Animal Genetics, 46, 591–598.

How to cite this article: Raza, S. H. A., Liang, C., Alshammarri, A. M., Aloufi, B. H., Gui, L., Khan, R., & Zan, L. (2022). Genetic variants in the serum amyloid A2 (SAA2) gene as a potential marker for milk production traits in Chinese Holstein cows. Veterinary Medicine and Science, 8, 1835–1840. https://doi.org/10.1002/vms3.796