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Single Nucleotide Polymorphisms in the Promoter of CYP19 Gene in Cattle Bred in Iraq

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Abstract: The present study was undertaken to characterize the genetic diversity of the aromatase cytochrome P450 (*CYP19*) gene in 34 cows (15 local, 14 Holstein, and 5 Crosses) in Iraq. The objectives of the present study are to detect SNPs (mutations) in promoter p1.1 of the *CYP19* gene in cattle bred in Iraq using sequencing techniques. We identified five single-nucleotide polymorphisms (SNP) loci of the *CYP19* gene that were detected, namely G933T, G994C, A1044G, A1062T, and C1468A. The results showed the presence of 3, 4, and 2 polymorphic sites leading to the construction of 4, 5, and 3 different haplotypes for Holstein, local, and crosses respectively. Haplotype diversity were 0.791, 0.752, and 0.700 respectively. While nucleotide diversity was 0.0017, 0.0022, and 0.0013 respectively. Besides, we carried out a phylogenetic analysis of these sequences to address the evolutionary relationship between the animal species. These fragments were assigned in the GenBank database under the accession numbers: LC490756, LC490757, LC491437, LC491438, LC491439, LC491588, and LC491589.

Keywords: CYP19 gene, Iraqi cattle, single nucleotide polymorphism, Genetic Diversity, Phylogenetic tree

Introduction

The tools of molecular genetics, which allow the detection of genes, have major effects on complex traits, such as reproductive performance. These tools can be used as selection criteria for reproductive traits for genetic improvement (Amitosh, 2018). A large number of genes affect the reproductive performance of cattle, one of them is *CYP19*. It is an important gene that is significantly associated with these important traits in cattle (El-Bayomi *et al.,* 2018). CYP19 gene belongs to the cytochromes P450 genes. P450 genes are part of a multi-gene superfamily, which contains 27 distinct genetic families, ten of which are dedicated to mammals, one of which is the *CYP19* gene (Jedrzejczak *et al.,* 2011). In mammals, reproduction is mainly regulated by estrogen, which is synthesized in ovaries trough the androgen's aromatization (Kowalewska- Luczak, 2010). The *CYP19* gene encodes the cytochrome P450 aromatase enzyme, aromatase P450 catalyzes the last step in the steroidogenesis which converts the androgens (C19) to estrogens (C18) (Damiani & Damiani, 2007), which maps to band q2.6 on

chromosomes 10 and has 11 exons in cattle (Aken *et al.,* 2016). *CYP19* utilizes different promoters in tissue-specific expression in the alternative splicing mechanism (Simpson & Davis, 2001). Different promoter regions correspond to different 5'-UTR transcripts but the coding region is identical for all tissues (Kalbe *et al.,* 2000). The placental expression of the *CYP19* gene is regulated by P1.1 promoter, and A> G mutation has been detected in this region (Keskin *et al.,* 2015). As well as two SNPs in the P1.1 region of the *CYP19* gene was identified, the first mutation was a G>A transition at position 1044 and the second one was an A>G transition at position 1179 (Mohamadnejad-Sangdehi *et al.,* 2015). Several single nucleotide polymorphisms (SNPs) studies in *CYP19* gene have been reported in different livestock species and breeds as; Slovak Simmental cattle (Trakovická *et al.,* 2015), Jersey cattle (Kowalewska-Luczak *et al.,* 2013), Rathi cattle (Amitosh *et al.,* 2017), the crossbred cows in Egypt (Saber *et al.,* 2017), Gyr dairy cows (Vega *et al.,* 2018).

This study aimed at determining single nucleotide polymorphisms in the *CYP19* gene using DNA sequencing methods and using bioinformatics tools to study this fragment in cattle bred in Iraq. As well as determining genetic diversity both within and between breed**.**

Materials & Methods

Animals and genomic DNA isolation

This study included the use of 34 cows (15 local, 14 Holstein, and 5 Crosses). Blood samples (10 ml.cow^{-1}) were collected from the jugular vein. Genomic DNA was extracted from whole blood using the gSYNC™ DNA Extraction Kit (Geneaid). A fragment (657bp) in the P.1.1 promoter region of the *CYP19* gene in cattle was amplified by using our designed primer F: 5`-GGCAAGGGCCTCATATGGTT-3` and R: 5`-TGTCAGGGAATGTGAGGTGC-3`. The PCR amplifications were conducted in a 50 µl volume containing 6 µl genomic DNA, 25 µl of Master Mix, 4 µl both primer, and 15 µl free water. The amplification conditions were as follows: initial denaturation at 94 C for 5 min followed by 35 cycles of denaturation at 94 C for 1 min, annealing at 56ºC for 40 Sec, and extension at 72ºC for 30 Sec., followed by the final extension at 72ºC for 5 min. The PCR product was detected by 2% agarose gel electrophoresis, stained with Ethedium bromide and visualized by ultraviolet light. For sequencing, the PCR product was sent to Yang ling Tianrun Aoka Biotechnology Company, China.

Data Analysis

The sequencing results of the *CYP19* gene were compared with accession no. Z69241 at the NCBI by BioEdit 7.0 software (Hall, 1999). Haplotype diversity (HD) and nucleotide diversity (π) were analyzed using DnaSP v5. 10 software (Librado & Rozas, 2009). The haplotypes network was drawn using Network 5.0.0.0 software (Bandelt *et al.,* 1999). The phylogenetic tree was drawn by using the MEGA X software (Kumar *et al.,* 2018).

Results

The *CYP19* haplotype sequences from cattle bred in Iraq have been assigned in the National Center for Biotechnology Information (NCBI), DNA Data Bank of Japan (DDBJ) and the European Nucleotide Archive (ENA) under the accession

numbers (LC490756, LC490757, LC491437, LC491438, LC491439, LC491588, and LC491589).

Genetic Diversity

The total number of sequences (N) and haplotypes (H) were 34 and 7 respectively, resulted in 5 polymorphisms number (NH) distributed to 4 local, 2 crosses and 3 Holstein (Table 1). Holstein revealed the highest value of haplotype diversity (HD) (0.791), followed by the local breed (0.752) and the cross cattle (0.700). On the contrary, local cattle recorded the highest nucleotide diversity (π) followed byHolstein and cross cattle (0.0022, 0.0017 and 0.0013 respectively).

Table (1): Genetic diversity of the *CYP19* gene among different cattle breeds.

Breeds	(N)	(H)	(NH)	(HD)	(π)
Local	15	5	4	0.752	0.0022
Crosses	5	3	2	0.700	0.0013
Holstein	14	4	3	0.791	0.0017

N: Number of Sequences; H: Haplotype; NH: Number of polymorphic; HD: Haplotype Diversity; π: Nucleotide Diversity

Haplotype Network

A total number of haplotypes of the *CYP19* gene showed by different breeds were seven (Fig. 1). Three haplotypes (H-2, H-3, and H-4) found in all breeds while the remaining four are divided into two for the local breed (H-6 and H-7) and two for Holstein (H-1 and H-5). Each pair of haplotypes (H-2, H-5 or H-3, H-4) differs from each other with a nitrogen base (592bp). The haplotypes (H-2, H-3 or H-4, H-5) differ from each other with a nitrogen base (563bp). The branches represented H-1 of Holstein cattle differed from H-3 by 28 and 89 bases. Whereas, the haplotypes H-6 and H-7 represented the local cattle differed from H-2 by 157 and 139 bases.

The results in fig. (2) observed the analysis of nucleotides in the P.1.1 promoter region of the *CYP19* gene and they recorded five SNPs; guanine to thymine (G933T), guanine to cytosine (G994C), adenine to guanine (A1044G), adenine to thymine (A1062T) and cytosine to adenine (C1468A). All SNPs are recorded first time except (A1044G).

Phylogenetic tree of *CYP19* gene

The evolutionary tree of the *CYP19* gene showed that there were three main branches (Fig. 3). The first branch included the cattle bred in Iraq. The second branch included Holstein bred in Germany. While the third branch divided into two branches, the first branch was presented by the Australian cattle and the second Indian cattle.

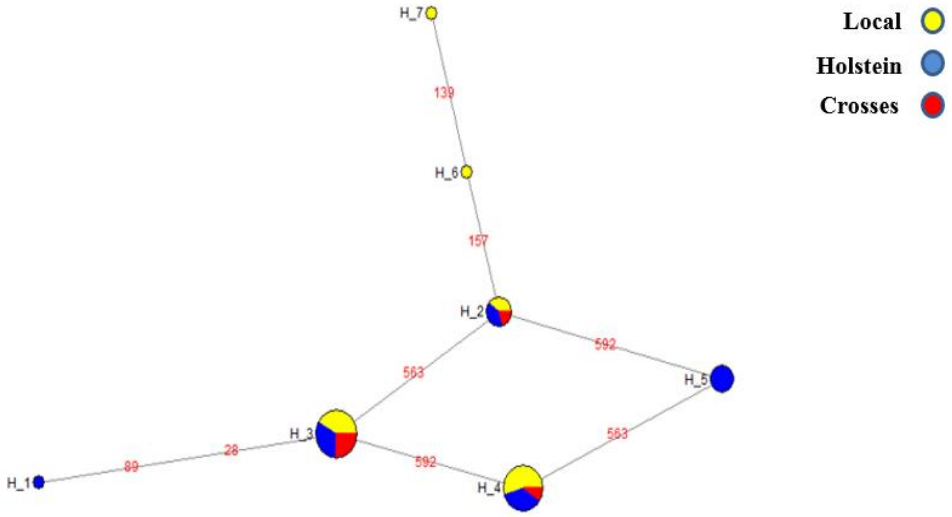

Fig. (1): Haplotype network of *CYP19* gene among studied cattle.

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Z69241   905   CTGGCTGGTAATTGTAGATATTAAATTTGTGGAGTGAATACAGTAGTCTGCATGGGCACT   964
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Lc491589   2   CTGGCTGGTAATTGTAGATATTAAATTTTTGGAGTGAATACAGTAGTCTGCATGGGCACT    61

Z69241   965   TGCTCTCGATGAGACAGGCTCCCCCATGGGAGAAACCCAGAGATCCCATCAGTCTGGATG   1024
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Lc491589  62   TGCTCTCGATGAGACAGGCTCCCCCATGGCAGAAACCCAGAGATCCCATCAGTCTGGATG    121

Z69241  1025   CCCACTGAGGCTTAGGGCAACTGTGGACAGTGTCAGTATGAAGTGGGTCCCGGACGTGTC   1084
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Lc491589 122   CCCACTGAGGCTTAGGGCAGCTGTGGACAGTGTCAGTTTGAAGTGGGTCCCGGACGTGTC    181

Z69241  1085   CCTCATTCTCCCTCTAAATATTTCTCACTGGCTCCGCTGGCTGCATAATTTACCACTGTA   1144
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Lc491589 182   CCTCATTCTCCCTCTAAATATTTCTCACTGGCTCCGCTGGCTGCATAATTTACCACTGTA    241

Z69241  1145   TCAAGCCTTCCTCATCTGAAAGATGTTGGCGCCCGGTGAAAAGTTAAATGACATCAAAGT   1204
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Lc491589 242   TCAAGCCTTCCTCATCTGAAAGATGTTGGCGCCCGGTGAAAAGTTAAATGACATCAAAGT    301

Z69241  1205   TCAAGGAGATTTCATTCACTTAACAACCTGGAAATCACACTCTACTGGTCAACAAAGGTG   1264
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Lc491589 302   TCAAGGAGATTTCATTCACTTAACAACCTGGAAATCACACTCTACTGGTCAACAAAGGTG    361

Z69241  1265   GTTCTGATCTGGAAAGAGCCTCTGGGACATTGGAAACCTGAAGTAGTAGGTGGATAAAGG   1324
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Lc491589 362   GTTCTGATCTGGAAAGAGCCTCTGGGACATTGGAAACCTGAAGTAGTAGGTGGATAAAGG    421

Z69241  1325   ATCTTAGGAGTTGTAAATCCTGCAGGGAGTCCAGAACCCAGCATTGTATTCAAAGTATAT   1384
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Lc491589 422   ATCTTAGGAGTTGTAAATCCTGCAGGGAGTCCAGAACCCAGCATTGTATTCAAAGTATAT    481

Z69241  1385   TGATTACTGAGTGTTTCTCCACAGCTTTCATTAGATTCTTAGAATGATGCGTCTGGGGCT   1444
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Lc491589 482   TGATTACTGAGTGTTTCTCCACAGCTTTCATTAGATTCTTAGAATGATGCGTCTGGGGCT    541

Z69241  1445   CTAAAGAGAATGAGAAGAGCCAGCGGAGATGGCCAAACCTGGCCACTTGCAC   1496
               ||||||||||||||||||||||||||||||||||||||||||||||||||||
Lc491589 542   CTAAAGAGAATGAGAAGAGCCAGAGGAGATGGCCAAACCTGGCCACTTGCAC    593
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Fig. (2): Sequencing of the *CYP19* gene in Iraqi Cattle (LC491589) vs. Reference Sequence (Z69241).

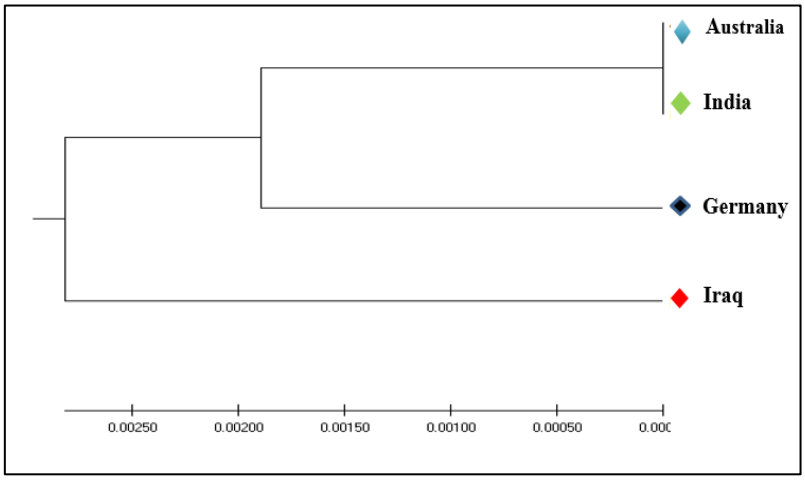

Fig. (3): The Phylogenetic tree of *the CYP19 gene* between some cattle bred in Iraq of different countries.

Analysis of molecular variance AMOVA

The results of the AMOVA of the *CYP19* gene between and within cattle breeds showed that genetic variation between breeds was 0.30 % and the variation within breeds was 99.70 % from the total variance (Table 2). This finding illustrated by the fact that genetic variation within the breed is much greater than genetic variation among breeds.

Table (2): -Molecular contrast analysis of gene *CYP19* with strains in the world.

Source of variation	df	Sum Squares	Variance Components	Variation %
Between breed	2	1.650	0.0024	0.30
Within breed	31	24.791	0.7997	99.70
Total	33	26.441	0.8021	

Discussion

Molecular markers could be powerful tools in the identification of SNPs and in revealing the current status of genetic diversity within and differentiation between livestock populations (Lenstra *et al.*, 2012). There are a few numbers of studies carried on the *CYP19* gene. The single-nucleotide polymorphisms can be used as a selection criterion for decreasing fertility problems. The present study was, therefore, aimed at determining both within and between breed genetic diversity of cattle bred in Iraq (local, Holstein, and crosses) using SNPs markers. Single-nucleotide polymorphisms (SNPs) markers are the most efficient molecular markers to evaluate genetic diversity, population differentiation, breed relationships, and

determine parentage in animal populations (Yang *et al.,* 2013). The genetic diversity of cattle has also recently been studied using SNPs markers in Ethiopia (Kukučková *et al.*, 2018) and South Africa (Makina *et al*., 2016). Single-nucleotide polymorphisms (SNPs) in position 1044 obtained from the analysis of the present study are consistent with the previous studies carried out for promoter p1.1 of the *CYP19* gene in cattle (Keskin *et al.*, 2015; Mohamadnejad-Sangdehi *et al.,* 2015; Zaborski *et al.,* 2014). However, in the present study, other SNPs were found in the position 933, 994,1062 and 1468. These SNPs are novel to the studied Iraqi cattle. The reason behind that is that Iraq considers as an origin of sheep (Ayied & Zaqeer, 2019), camel (Ayied *et al*., 2018) and cattle (Faraj *et al*., 2019; Owaid *et al*, 2019).

The partitioning of the genetic variation from an AMOVA revealed that 0.30 % of the total genetic variation was between breeds. A similar pattern of variance partitioning was observed in similar studies (Edea *et al.,* 2013; Ngono-Ema *et al.,* 2014; Sanarana *et al.,* 2016; Gororo *et al*., 2018), in which 90% or more of the variation is contained within breeds. In Ankole cattle breeds, Öner *et al.* (2019) reported within-population diversity to be 92.2 %.

Conclusion

Cattle bred in Iraq showed a high genetic diversity of the *CYP19* gene. The tree of evolution has shown the presence of cattle bred in Iraq with a separate branch from other cattle breeds. Genetic variation within breed was greater than genetic variation among breeds. *CYP19* gene of cattle bred in Iraq showed five mutations at the sites 933, 994, 1044, 1062 and 1468. Local cattle differ from Holstein cattle by two haplotypes (H1 and H5 for Holstein and H6 and H7 for local). However, both share three haplotypes (H2, H3, and H4).

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Conflicts of interest

The authors-declare-that they-have-no-conflict of interests.

Ethical approval

All applicable institutional, national and international guidelines for the care and use of animals were followed.

References

Aken, B.L.; Achuthan, P.; Akanni, W.M.; Amode, R.; Bernsdorff, F.; Bhai, J.; Billis, K.; Carvalho-Silva, D.; Cummins, C.; Clapham, P *et* (2016). The ensemble gene annotation system. Database., 1-19. https://doi.org/10.1093%2Fdatabase%2Fbaw093.

Amitosh, K. (2018). Molecular characterization of *CYP19*, *FSHR* and *LHR* genes and its association with reproductive traits in Indigenous cattle. Ph.D. Thesis. Coll. Vet. Anim. Sci., Univ. Rajasthan: 141pp. http://krishikosh.egranth.ac.in/handle/1/5810055058

Amitosh, K.; Gahlot, G.C.; Joshi, R.; Ashraf, M. & Ganguly, S. (2017). DNA polymorphism of the CYP19 (Aromatase) gene in Rathi cattle. J. Entomol. Zool. Stud.; 5(6): 1944-1946. https://www.researchgate.net/publication/321825089_DNA_polymorphism_of_Cyp19_Aromatase_gene_in_Rathi_cattle

Ayied, A.Y. & Zaqeer, B.F. (2019). Relationship between ND5 genetic

polymorphisms and milk production and the growth of lambs before weaning of Awassi sheep. IJSR, 8(1): 810-814. https://www.ijsr.net/search_index_results_paperid.php?id=ART20194226

Ayied, A.Y.; Al-Badran, A.I.; & Al-Zaalan, A.R. (2018). Assessment of genetic diversity in Iraqi camel breeds using cytochrome b. JAAVS, 6(7): 273-277. http://doi.org/10.17582/journal.aavs/2018/6.7.273.277

Bandelt, H.J.; Forster, P. & Rohl, A. (1999). Median-joining networks for inferring intraspecific phylogenies. Mol. Biol. Evol., 16(1): 37-48. https://academic.oup.com/mbe/article-abstract/16/1/37/993192

Damiani, D. & Damiani, D. (2007). Manejo farmacológico da baixa estatura: o papel dos inibidores da aromatase: Revisão. Jornal de Pediatria, 83(5): 172-177. https://doi.org/10.1590/S0021-75572007000700008

Edea, Z.; Dadi, H.; Kim, S.W.; Dessie, T.; Lee, T.; Kim, H.; Kim, J.J. & Kim, K.S. (2013). Genetic diversity, population structure, and relationships in indigenous cattle populations of Ethiopia and Korean Hanwoo breeds using SNP markers. Front. Genet. 4(35): 1-9. https://doi.org/10.3389/fgene.2013.00035

El-Bayomi, K.M.; Saleh, A.A.; Awad, A.; El-Tarabany, M.S.; El-Qaliouby, H.S.; Afifi, A.; El-Komy, S.; Essawi, W.M.; Almadaly, E.A. & El-Magd, M.A. (2018). Association of CYP19A1 gene polymorphisms with anoestrus in water buffaloes. Reprod. Fert. Develop., 30: 487- 497. https://doi.org/10.1071/RD16528

Faraj, S.H.; Ayied, A.S. & Al-Rishdy, K.A.H. (2019) FSHR gene polymorphisms and protein structure changes of cattle bred in Iraq. IJSTR, 8(11): 3325-3328. http://www.ijstr.org/research-paper-publishing.php?month=nov2019

Gororo, E.; Makuza, S.M.; Chatiza, F.P.; Chidzwondo, F. & Sanyika, T.W. (2018). Genetic diversity in Zimbabwean Sanga cattle breeds using microsatellite markers. S. Afr. J. Anim. Sci., 48(1): 128-141. https://doi.org/10.4314/sajas.v48i1.15

Hall, T.A. (1999). BioEdit: a user-friendly biological sequence alignment editor and analysis program for Windows 95/98/ NT. Nucl. Acids Symp., 41: 95-98. https://bioedit.software.informer.com/

Jedrzejczak, M.; Grzesiak, W.; Szatkowska, I.; Dybus, A.; Muszyńska, M. & Zaborski, D. (2011). Association between polymorphisms of CYP19, CYP21, and ER1 genes and milk production traits in Black and White cattle. Turk. J. Vet. Anim. Sci., 35(1): 41-49. https://www.researchgate.net/publication/228496295_Association_between_polymorphisms_of_CYP19_CYP21_and_ER1_genes_and_milk_production_traits_in_Black-and-White_cattle

Kalbe, C.; Furbass, R.; Schwerin, M.& Vanselow, J. (2000). Cis-acting elements regulating the placenta-specific promoter of the bovine Cyp19 gene. J. Mol. Endocrinal., 25: 265-273. https://doi.org/10.1677/jme.0.0250265

Keskin, A.; Öner, Y.; Yilmazbaş-mecitoğlu, G.; Güner, B.; Karakaya, E.; Elmaci, C. & Gümen, A. (2015). Distributions of *CYP19*, *ERα* and *PGR* allele frequencies between fertile and subfertile holstein-friesian heifers. Kafkas. Univ. Vet. Fak. Derg., 21(6): 893-898. https://doi.org/10.9775/kvfd.2013.8900

Kowalewska-Uczak, I. (2010). Polymorphism of the *CYP19* gene and milk production traits of dairy cattle. Turk. J. Vet. Anim. Sci., 34(6): 493-496 . https://doi.org/10.3906/vet-0707-30

Kowalewska-Luczak, I.; Michniewicz, E. & Kulig, H. (2013). Effect of CYP19 SNPs on milk production traits of jersey cows. Acta Sci. Pol., Zootechnica, 12(1), 33-40. https://asp.zut.edu.pl/2013/12_1/asp-2013-12-1-170.pdf

Kukučková, V.; Moravčíková, N.; Curik, I.; Simčič, M.; Mészáros, G. & Kasarda, R. (2018). Genetic diversity of local cattle. Acta Bioch. Pol., 65(3): 421-424. https://doi.org/10.18388/abp.2017_2347

Kumar, S.; Stecher, G.; Li, M.; Knyaz, C. & Tamura, K. (2018). MEGA X: Molecular Evolutionary Genetics Analysis, across computing platforms. Mol. Biol. Evol., 35: 1547-1549. https://doi.org/10.1093/molbev/msy096

Lenstra, J.; Groeneveld, L.; Eding, H.; Kantanen, J.; Williams, J.; Taberlet, P.; Nicolazzi, E.; Sölkner, J.; Simianer, H. & Ciani, E. (2012). Molecular tools and analytical approaches for the characterization of farm animal genetic diversity. Anim. Genet., 43: 483-502. https://doi.org/10.1111/j.1365-2052.2011.02309.x

Librado, P. & Rozas, J. (2009). DnaSP v5: a software for comprehensive analysis of DNA polymorphism data. Bioinformatics, 25(11): 1451-1452. https://doi.org/10.1093/bioinformatics/btp187

Makina, S.O.; Whitacre, L.K.; Decker, J.E., Taylor, J.F.; MacNeil, M.D.; Scholtz, M.M.; Marle-Köster, E.; Muchadeyi, F.C.; Makgahlela, M.L. & Maiwashe, A. (2016). Insight into the genetic composition of South African Sanga cattle using SNP data from cattle breeds worldwide. Genet. Sel. Evol. (Paris), 48 (1): 88-94. https://doi.org/10.1186/s12711-016-0266-1

Mohamadnejad-Sangdehi, F.; Rahimi-Mianji, G.; Safdari-Shahroudi, M.; Razavi-Sheshdeh, S.A. & Gholami, M. (2015). Distribution of allele frequencies at 5′-flanking region of CYP19 and ERα genes between Iranian simmental and three indigenous cattle breeds. Iranian J. Appl. Anim. Sci., 5(2): 301-307. http://ijas.iaurasht.ac.ir/article_513309.html

Ngono-Ema, P.; Manjeli, Y.; Meutchieyié, F.; Keambou, C.; Wanjala, B.; Desta, A.; Ommeh, S.; Skilton, R. & Djikeng, A. (2014). Genetic diversity of four Cameroonian indigenous cattle breeds using microsatellite markers. J. Livest. Sci., 5: 9-17.

Öner, Y.; Yılmaz, O.; Eriş, C.; Ata, N.; Ünal, C. & Koncagül, S. (2019). Genetic diversity and population structure of Turkish native cattle breeds. S. Afr. J. Anim. Sci., 49(4): 628-635. http://doi.org/10.4314/sajas.v49i4.4

Owaid, J.M.; Ayied, A.Y. & Ahmed, F.A. (2019). Genetic variation analysis of ATPase gene and its association with milk component in cattle. IJANS, 8(3): 55-60. https://www.iaset.us/journals/international-journals/international-journal-of-applied-and-natural-sciences

Saber, Y.H.; Seida, A.A.; Ragab, R.S.A.; Balabel, E.A.; Hanafi, E.M. & Wahid M.A. (2017). Oxidant/antioxidant status and CYP19 gene polymorphism in crossbred cows in relation to ovarian inactivity. Global Vet., 18(1): 14-19. https://www.idosi.org/gv/gv18(1)17.htm

Sanarana, Y.; Visser, C.; Bosman, L.; Nephawe, K.; Maiwashe, A. & Van Marle-Köster, E. (2016). Genetic diversity in South African Nguni cattle ecotypes based on microsatellite markers. Trop. Anim. Health Prod., 48, 379-385. https://doi.org/10.1007/s11250-015-0962-9

Simpson, E.R. & Davis, S.R. (2001). Minireview: Aromatase and the regulation of estrogen biosynthesis-some new perspectives. Endocrinology., 142: 4589-4594. https://doi.org/10.1210/endo.142.11.8547

Trakovická, A.; Moravčíková, N.; Miluchová, M. & Gábor, M. (2015). Analysis of CYP19 gene polymorphism as a factor affecting milk production of cattle. J. Microbiol. Biotechnol. Food Sci., 4(2): 111-113. https://doi.org/10.5513/JCEA01/19.4.2363

Vega, W.H.O.; Quirino, C.R.; Bartholazzi-Junior, A.; Rua, M.A.S.; Serapiao, R.V. & Oliveira, C.S. (2018). Variants in the CYP19A1 gene can affect *in vitro* embryo production traits in cattle. J. Assisted Reprod. Genet., 35(12): 2233-2241. https://doi.org/10.1007/s10815-018-1320-4

Yang, W.; Kang, X.; Yang, Q.; Lin, Y. & Fang, M. (2013). Review on the development of genotyping methods for assessing farm animal diversity. J. Anim. Sci. Biotechnol., 4(2): 1-6. https://doi.org/10.1186%2F2049-1891-4-2

Zaborski, D.; Grzesiak, W. & Pilarczyk, R. (2014). Detection of difficult calving's in the Polish holstein-friesian black and white heifers. J. Appl. Anim. Res., 44(1): 42-53. https://doi.org/10.1080/09712119.2014.987293

تعدد أشكال النيوكليوتيدات الفردية (SNPs) في منظم جين CYP19 في الأبقار المرباة في العراق

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المستخلص أجريت الدراسة الحالية لوصف التنوع الجيني لجين اروماتيز السيتوكروم P450 (CYP19) في 34 بقرة (15 محلية و 14 هولشتاين و 5 صلبان) في العراق. أهداف هذه الدراسة هي الكشف عن SNPs (الطفرات) في المنظم p1.1 لجين CYP19 في الأبقار المرباة في العراق باستخدام تقنيات التسلسل. اكتشفت خمسة تشكلات متعددة للتشكلات أحادية النوكليوتيد (SNP) في جين CYP19 ، وهي G933T و G994C و A1044G و A1062T وC1468A . أوضحت النتائج وجود 3 و 4 و 2 مناطق متعددة الأشكال مما أدى إلى بناء 4 و 5 و 3 أنماط احادية مختلفة لابقارالهولشتاين والمحلية والمضربة على التوالي. كان تنوع النمط الاحادي يساوي 0.791 و 0.752 و 0.700 للسلالات المدروسة على التوالي. بينما كان تنوع النوكليوتيدات 0.0017 و 0.0022 و 0.0013 على التوالي. إلى جانب ذلك ، اجري تحليل جيني للسلالات باستخدام هذه التسلسلات لحساب العلاقة التطورية بين الأنواع الحيوانية. تم تسجيل التسلسلات والطفرات التي تم الكشف عنها في قاعدة بيانات GenBank تحت أرقام الانضمام LC490756 و LC490757 و LC491437 و LC491438 و LC491439 و LC491588 و LC491589.

الكلمات المفتاحية: جين CYP19 ، الابقار العراقية، التشكل الوراثي للنيوكليتيدات المفردة، التنوع الوراثي، شجرة التطور.