

Associations Between Microsatellites Markers and Growth Traits in Goat

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Abstract

The rapid progress in the field of biotechnology gives us a great chance to improve the productivity of our native animals in short time, relatively. The situation in Saudi Arabia not differ in compare with other country in our region which have a big challenge to increase the meat production for food security purposes. The situation in goat is very far from the point which other farm animals like cattle reached today, where a complete QTLs maps for most important traits is available. But by the same way, long time ago we have a complete comparative map between goat and both sheep and cattle. According to that in the previous investigation in both sheep and cattle we collected a total of 19 loci distributed in goat different chromosomes along with a total of 1050 records from 525 individual of a crossbred of Aradi and Damascus Goat were used to perform the linkage analysis. The studied traits were body weight at birth, 4, 8, 12, 16, 20, and 24 weeks of age. The association between microsatellite markers and body weights traits were estimated by stepwise partial regression. Twelve markers (BMS2325, BMS332, BM17132, BMS1316, BM1827, BM1225, BMS2142, BM1558, BMS2809, BMS1348, BMC4216 and BM1329) successfully linked to studied traits. These markers are. In general, our work design and plan successfully worked and could explained some of genetic vitiation by using microsatellites markers. Further work to build a complete QTLs map for meat production traits is necessary to make a complete view about this important species.

Keywords: Arabian goat, EBV, QTLs, MAS

1. Introduction

The rapid and advanced progress in the field of biotechnology gives us a great chance to improve the productivity of our native animals in short time, relatively. The situation in our kingdom of Saudi Arabia not differ in compare with other country in our region which have a big challenge to increase the meat production for food security purposes.

The molecular tools are very expensive, but the benefits are very interested. Also, among these tools some are cheaper and effective like individual marker assisted selection, when no need to make a complete genome mapping. The situation in goat is very far from the point which other farm animals like cattle reached today, where a complete QTLs maps for most important traits is available. But by the same way, long time ago we have a complete comparative map between goat and both sheep and cattle.

Day after day, the advanced and rapid progress in the field of biotechnology gives us a huge opportunity in improving the productive traits in animals. Saudi Arabia like other country in our region have a big challenge to increase the meat production for food security purposes.

Growth rate and body weight are some of the most important trait indicators of goat meat production. some studies in Saudi Arabia performed to improve both milk and meat production of meat (Kebede et al., 2012; Rashidi et al., 2011; Al-Atiyat et al., 2010; Tabbaa & Al-Atiyat, 2009), among them one of the most important study hold in Qassim University by Animal Breeding and Genetic Group (Al-Saef, 2013; Khalil et al., 2010) to improve production traits of Aradi by crossing with Damascus breed.

Molecular genetic approaches are promising because they enable the analysis of genetic variability at the DNA level by detecting causative genes for reproductive traits (Ahlawat et al., 2015). These techniques have developed rapidly in recent years and have been successfully applied to animal selection methods. They are used to identify loci that cause genetic variation in quantitative traits (Pecetti et al., 2021). In addition of that, many other applications have been developed with the purpose to speed up the genetic improving programs in goat, such as genomic selection (Mucha et al., 2015). Several previous studies have been performed to identify relevant genomic regions Goat weight and body shape characteristics (Tao et al., 2020; Shi et al., 2020; Xu et al., 2020; Gu et al., 2022).

Wenne, (2023), used microsatellites as molecular markers with applications in exploitation and conservation of aquatic animal populations. This review covers the use of microsatellites in genetic diversity studies, including the identification of quantitative trait loci (QTL) in animal populations, which is relevant for growth traits in goats.

Many investigators report an association between microsatellites markers and body weight traits. Generally, eight markers found to be linked to body weight located in chromosomes 2 (BM6444, BM2113), 3 (AGLA293), 6 (BM9058, MCM204), 23 (AGLA269, ADCY1AP) and 26 (CSR163). Five markers found to be linked to birth weight located in chromosomes 5 (MCM527, BMS1247), 8 (URB024, BMS1967) and 11(ETH3). Four markers found to be linked to body weight at 8 weeks of age located in chromosomes 1 (CSSM046, BMS4000) and 14(ILSTS02, LS30). Three markers located in chromosome 1 (MCM58, ILSTS04) and 4 (CSR100) found to be linked with body weight at 20 weeks of age. Six markers located in chromosome 1 (BM4129), 3 (CP34), 6 (HH55), 11 (BM17132) 21 (CSSM13) and 24 (DIK2568) found to be linked with body weight at 43 weeks of age.

Five markers located in chromosome 3 (CP34), 6 (HH55), 11 (BM17132) and 21 (CSSM13) found to be linked with body weight at 56 weeks of age. Four markers located in chromosome 6 (HH55), 21 (CSSM13), 24 (DIK2568) and 26 (JMP23) found to be linked with body weight at 83 weeks of age. Two markers located in chromosome 11 (HEL10) and 23 (URB031) found to be linked with body weight at 98 weeks of age. One marker (BM4129 loci) located in chromosome 1 found to be linked with average daily gain trait. Two markers located in chromosomes 6 (BM1329) and 16 (BM1225) found to be linked with slaughter weight.

2. Materials and Methods

2.1 Sample Preparation

Blood samples from Aradi×Damascus cross animals were taken and kept in ICE tank until reaching our laboratory and that time the DNA extraction began. DNA from whole blood sample was isolated. After that, DNA samples were taking to determine the quantity and quality using NanoDrop. Then, we made DNA dilutions depending on DNA concentration in each sample; the original tubes were kept frozen at -80 °C and new liquates Kept in -20 °C until used to DNA extraction. DNA of these animals were taken from whole fresh blood samples using EDTA as anticoagulant.

According to that in the previous investigation in both sheep and cattle we collected a total of 19 loci distributed in chromosome markers from chromosomes BTA 3, 4, 5, 6, 9, 11, 12, 15, 16, 19, 20, 22, 23, 25 and 26. Which are the homologues chromosomes of CHI 3, 4, 5, 6, 9, 11, 12, 15, 16, 19, 20, 22, 23, 25 and 26 in goat, respectively.

The selected markers were HUI246, BMS2904, BMS2809, CSSM34, BM1329, BMS2151, BMS2325, RM150, BM1827, BMS1316, BMS2533, BMS1348, BMS2142, BM1225, BM1558, BM1258, BMC4216, BMS332, and BM17132. Table 1 indicates primer sequence both forward and reverse for markers used in the present study.

Before the beginning of the experiment, 3 samples were tested for each marker to be sure that the marker will be amplified in our population, and then we will cull the non-amplifying markers or homozygote markers in the population. Then, markers showing good amplification and multi alleles were amplified for all samples to be used in genotyping all animals.

2.2 Morphological Data Collected

Data for body weight traits were collected from production records of Goat Improvement Unit (Agriculture experimental station, Animal and Poultry Production, College of Agriculture and Food, Qassim University, Kingdom of Saudi Arabia) for the period from January 2011 to January 2022 (11 Years).

2.3 Estimated Breeding Values (EBV)

In the present study, we used a total of 3675 records from 525 individual from a crossbred of Aradi and Damascus Goat to perform the linkage analysis. The studied traits were body weight at birth, 4 weeks, 8 weeks, 12 weeks, 16 weeks, 20 weeks, and 24 weeks of age.

Table 1. Primer sequence both forward and reverse for markers used in the present study

Chr.	Marker	Primer	
		Forward	Reverse
BTA3	HUJ246	actccagttttcttctctggg	tgccatgtagtagctgtgtgc
BTA 3	BMS2904	tggcagtgagagaggggac	tccactgagagcgtgtctg
BTA 4	BMS2809	atttgcctcctgtgttg	tcaaaagtcctgctagaatcc
BTA 5	CSSM34	ccataactctgggactttctca	atgttcagccaatctctctgtcc
BTA 6	BM1329	ttgttaggcaagtccaagtc	aacaccgcagcttcatcc
BTA 9	BMS2151	ccattaagaggaaattgtgtca	atggagtcactgaaaggtactga
BTA 11	BMS2325	tccatcttgacagaagtgtgc	agggccaggaatgctagtg
BTA 11	RM150	gaacagtggttacctgtctgc	ctgcctaaccttctggcgctc
BTA 12	BM1827	aagcaaggaaattccggg	aaagatttgacacaactgagc
BTA 12	BMS1316	ccttcatggaagaaatttctg	ggagttacagtcctatgggttc
BTA 15	BMS2533	tgaagtaagtaagcacacaagca	ttgatcatcttagtccatcc
BTA 16	BMS1348	aaataaatgtcacctatggggc	agggtgcgactgagacatgc
BTA 19	BMS2142	aagcaggttgatgatcttacc	gtcggcactgaaaatgattatg
BTA 19	BM17132	atctgccagtatcacatcaaca	gttactttccaggcatgaagc
BTA 20	BM1225	tttctcaacagaggtgtccac	accctatcaccatgctctg
BTA 22	BM1558	tgaggaaagccttggcag	actgggcctagctccttctc
BTA 23	BM1258	gtatgtattttcccaccctgc	gagtcagacatgactgagcctg
BTA 25	BMC4216	tgagggaaaaggagatgg	gagtggttcacaaaatgtgc
BTA 26	BMS332	aattgcatggaagtctcagc	gacaaaaccttttagcacagg

Note. All primer sequences were taken for the NAGRP (2024) and GoSatdb (2024).

The collected data were used to estimate the EBV for each Animal by the use of MTDREMEL program of Boldman et al. (1995) using the following model which included year-season effect (2 seasons per each year (11 years), 1 for hot months and 2 for moderate months). Effect of litter size at birth for each does ranged from 1 up to 3.

$$EBV_{ijk} = Y_{ij} - (\mu + YS_i + LSB_j + E_{ijk}) \quad (1)$$

where,

EBV_{ij} = Estimating breeding value of the animal on ij^{th} trait; Y_{ij} = Observed values of the ij^{th} animal; μ = Overall mean; YS_i = Effect of i^{th} year season (1, 2, ... 12); LSB_j = Effect of j^{th} litter size (1, ... 3); E_{ijk} = Random error.

2.4 Linkage Analysis

After identifying the genotypes for all individuals using the whole set of markers, the linkage analysis was performed and phenotypic values was processed for statistical analysis for detection of linkage between studied markers and traits.

For data of single-marker analysis, a total of 525 animals a crossbred of Aradi and Damascus Goat were used in regression analysis to detect the association between markers and traits using program of SAS (1999).

The association between microsatellite markers and milk production traits were estimated by stepwise partial regression analysis in which milk production traits were treated as the dependent variable and the microsatellite markers were treated as independent variables.

Partial regression analysis was employed to detect the effects of markers linked to the total estimated breeding value (EBV) variation for milk production traits. The percentage of the total genetic variation explained by the association between each single marker of the total markers used and each trait has R^2 (coefficient of determination) value. The model of statistical analysis was as follow using stepwise partial regression.

$$Y_{\alpha_{ijk}} = a_{\alpha} + \sum \beta_i M_j + e_{ijk} \quad (2)$$

where,

Y_{ijk} = Accession means for study trait to; a_{α} = Intercept function for the set of independent variables within β within M ; β_i = The partial regression coefficients that specified the empirical relationship between Y and M_j ; M_j = Microsatellite markers ($j = 1, 2, \dots, 17$); E_{ijk} = Random error.

3. Results and Discussion

Tables 2 and 3 show summary of stepwise regression procedure on body weights at different studied age to, coefficient of determination R^2 and probability ($p \leq$) of significant of dependency of different markers on body weight at birth (BWB) trait. In all solutions used as mentioned before in tables above, only two markers BM17132 and BM1827 showed highly significant effect ($p \leq 0.0062$ and 0.0146 , respectively) in both backward and forward solutions.

At four weeks of age (BW4) trait in all solutions used as mentioned before in tables above, five markers BMS332, BM17132, BM1827, BMS2325 and BMS2142 showed a significant effect ($p \leq$ ranged from 0.0046 for BM17132 and 0.049 for BMS2142) in both backward and forward solutions.

In all solutions used for 8 weeks body weight, three markers BMS332, BMS2325 and BM1558 showed a significant effect ($p \leq$ were 0.0192 , 0.006 and 0.0314 , respectively) in both backward and forward solutions.

For body weight at 12 weeks of age in all solutions used, four markers BMS2325, BM1225, BMS1316 and BMS2809 showed a significant effect ($p \leq$ were 0.0172 , 0.0455 , 0.0345 and 0.0436 , respectively) in both backward and forward solutions. The maximum R^2 value was 0.0259 in 11th forward step and 0.0271 in the 1st backward step.

For body weight at 16 weeks of age in all solutions used, three markers BMS2325, BMC4216 and BMS1348 showed a significant effect ($p \leq$ were 0.0308 , 0.0087 and 0.047 , respectively) in both backward and forward solutions. The maximum R^2 value was 0.0248 in 9th forward step and 0.0261 in the 2nd backward step.

For body weight at 20 weeks of age in all solutions used, two markers BMS2325, and BM1225 showed a significant effect in both forward and backward solutions. The maximum R^2 value was 0.0158 in 12th forward step and 0.0167 in the 2nd backward step.

For body weight at 24 weeks of age in all solutions used, four markers BMS1316, BM1329, BM17132 and BMS332 showed a significant effect ($p \leq$ were 0.01 , 0.002 , 0.0477 and 0.02 , respectively) in both backward and forward solutions.

These results agree with that found by Raadsma et al. (2009) in Sheep for BW43 and BW56 traits. Also, in cattle McClure et al. (2010) for mature body weight trait. Locus BM1827 found to be linked with weight at 4 and 8 weeks of age. These results agree with that found by McClure et al. (2010), for both body weight at birth, and mature weight traits.

Locus BMS2325 found to be linked with weight at 4, 8, 12, 16 and 20 weeks of age, these results agree with that found by McClure et al. (2010) (for both birth and yearly weights).

Locus BMS332 found to be linked with weight at 4, 8, and 24 weeks of age, these results agree with that found by Hanotte et al. (2003) for mature body weight

Locus BM1558, found to be linked with weight at 8 weeks of age, these results agree with that found by McClure et al. (2010) in cattle for body weight at birth and yearly Weight trait.

Locus BMS2325 found to be linked with weight at 4, 8, 12, 16 and 20 weeks of age, these results agree with that found by McClure et al. (2010) (for both birth and yearly weights).

Locus BMS1316 found to be linked with weight at 12 and 24 weeks of age these results agree with that found by Alexander et al., 2007 for body weight at birth trait in cattle. McClure et al. (2010) for both mature and yearly body weight traits.

Table 2. Summary of stepwise selection of weight at birth, 4 and 8 weeks of age

Step	Weight at birth		Weight at 4 weeks		Weight at 8 weeks	
	Marker	Partial R ²	Marker	Partial R ²	Marker	Partial R ²
1	BM17132*	0.006	BMS332*	0.005	BMS332*	0.005
2	BM1827*	0.007	BM17132*	0.008	BMS2325*	0.007
3	BMS332	0.004	BM1827*	0.005	BM1558*	0.004
4	BMS2325	0.003	BMS2325*	0.006	BMS2142*	0.003
5	BMS2142	0.003	BMS2142*	0.004		

Table 3. Summary of stepwise selection of weight at 12, 16 and 20 weeks of age

Step	Weight at 12 weeks		Weight at 16 weeks		Weight at 20 weeks	
	Marker	Partial R ²	Marker	Partial R ²	Marker	Partial R ²
1	BMS2325*	0.005	BMS2325	0.004*	BM1225	0.003
2	BM1225*	0.004	BMC4216	0.007*	BMS2325*	0.004
3	BMS1316*	0.004	BMS1348	0.004*	BM1329	0.002
4	BMS2809*	0.004	CSSM34	0.002	BMS1316	0.002
5	BM1329	0.002				

Locus BM1225 found to be linked with weight at 12 and 20 weeks of age. These results agree with that found by Cavanagh et al. (2010) in Sheep for slaughter weight traits. Also, that found by McClure et al. (2010), for body weight at birth in cattle. Locus BMS2809, found to be linked with weight at 12 weeks of age, these results agree with that found by McClure et al. (2010) in cattle for body weight at birth and yearly Weight trait.

Locus BMS332 found to be linked with weight at 4, 8, and 24 weeks of age, these results agree with that found by Hanotte et al. (2003) for mature body weight. Locus BM17132 found to be linked with weight at 0, 4 and 24 weeks of age these results agree with that found by Raadsma et al. (2009) in Sheep for BW43 and BW56 traits. Also, in cattle McClure et al. (2010) for mature body weight trait. Locus BMS1316 found to be linked with weight at 12 and 24 weeks of age these results agree with that found by Alexander et al. (2007) for body weight at birth trait in cattle. McClure et al. (2010) for both mature and yearly body weight traits. Locus BM1329, found to be linked with weight at 24 weeks of age, these results agree with that found by Cavanagh et al. (2010) in Sheep for slaughter weight trait. Also, Kneeland et al. (2004) and Gutierrez-Gil et al. (2009) for body weight at birth trait.

4. Conclusion

Twelve out of nineteen markers of microsatellite type used in the present study successfully linked to studied traits. Locus BMS2325 found to be linked with weight at 4, 8, 12, 16 and 20 weeks of age. Locus BMS332 found to be linked with weight at 4, 8, and 24 weeks of age. Locus BM17132 found to be linked with weight at 0, 4 and 24 weeks of age. Locus BMS1316 found to be linked with weight at 12 and 24 weeks of age. Locus BM1827 found to be linked with weight at 4 and 8 weeks of age. Locus BM1225 found to be linked with weight at 12 and 20 weeks of age.

References

- Ahluwat, S., Sharma, R., Roy, M., Mandakmale, S., Tantia, M. S., & Prakash, V. (2015). Association analysis of novel SNPs in BMPR1B, BMP15 and GDF9 genes with reproductive traits in Black Bengal goats. *Small Rumin. Res.*, *132*, 92-98. <https://doi.org/10.1016/j.smallrumres.2015.10.010>
- Al-Atiyat, R. M., Rewe, T., Herold, P., & Zárata, A. (2010). A Simulation study to compare different breeding scenarios for Black Bedouin Goat in Jordan. *Eg. J. Sheep Goats Sci.*, *5*(1), 83-92. <https://doi.org/10.21608/ejsgs.2010.27080>
- Alexander, L. J., Geary, T. W., Snelling, W. M., & Macneil, M. D. (2007). Quantitative trait loci with additive effects on growth and carcass traits in a Wagyu-Limousin F2 population. *Animal Genetics*, *38*(4), 413-6. <https://doi.org/10.1111/j.1365-2052.2007.01616.x>
- Al-Saef, A. M. (2013). Genetic and phenotypic parameters of body weights in Saudi Aradi goat and their crosses with Syrian Damascus goat. *Small Ruminant Res.*, *112*(1-3), 35-38. <https://doi.org/10.1016/j.smallrumres.2012.12.021>

- Boldman, K., Kriese, L. A., Van Vleck, L. D., Van Tassell, C. P., & Kachman, S. D. (1995). *A manual for use of MTDFREML*. A set of programs to obtain estimates of variance and covariances (Draft). USDA, ARS, Lincoln, NE.
- Cavanagh, C. R., Jonas, E., Hobbs, M., Thomson, P. C., Tammen, I., & Raadsma, H. W. (2010). Mapping Quantitative Trait Loci (QTL) in sheep. III. QTL for carcass composition traits derived from CT scans and aligned with a meta-assembly for sheep and cattle carcass QTL. *Genet. Sel. Evol.*, *42*, 36. <https://doi.org/10.1186/1297-9686-42-36>
- GoSatdb. (2024). Retrieved March 26, 2024, from <http://webapp.cabgrid.res.in/goat/database1.html>
- Gu, B., Sun, R., Fang, X., Zhang, J., Zhao, Z., Huang, D., ... Zhao, Y. (2022). Genome-Wide Association Study of Body Conformation Traits by Whole Genome Sequencing in Dazu Black Goats. *Animals*, *12*, 548. <https://doi.org/10.3390/ani12050548>
- Gutierrez-Gil, B., Williams, J. L., Homer, D., Burton, D., Haley, C. S., & Wiener, P. (2009). Search for quantitative trait loci affecting growth and carcass traits in a cross population of beef and dairy cattle. *J. Anim. Sci.*, *87*(1), 24-36. <https://doi.org/10.2527/jas.2008-0922>
- Hanotte, O., Ronin, Y., Agaba, M., Nilsson, P., Gelhaus, A., Horstmann, R., ... Teale, A. (2003). Mapping of quantitative trait loci controlling trypanotolerance in a cross of tolerant West African N'Dama and susceptible East African Boran cattle. *Proc Natl Acad Sci, USA*, *100*(13), 7443-8. <https://doi.org/10.1073/pnas.1232392100>
- Kebede, T., Haile, A., Dadi, H., & Alemu, T. (2012). Genetic and phenotypic parameter estimates for reproduction traits in indigenous Arsi-Bale goats. *Trop. Anim. Health Prod.*, *11*, 34-38. <https://doi.org/10.1007/s11250-011-0034-8>
- Khalil, M. H., Mohamed, K. M., Al-Saef, A. M., Zeitouna, M. M., & El-Zarei, M. F. (2010). Crossbreeding components for growth, carcass and meat composition traits in crossing Saudi Aradi with Damascus goats. *Small Ruminant Research*, *94*, 10-16. <https://doi.org/10.1016/j.smallrumres.2010.05.020>
- Kneeland, J., Li, C., Basarab, J., Snelling, W. M., Benkel, B., Murdoch, B., ... Moore, S. S. (2004). Identification and fine mapping of quantitative trait loci for growth traits on bovine chromosomes 2, 6, 14, 19, 21, 23 within one commercial line of Bos Taurus. *J Anim Sci*, *82*, 3405-3414. <https://doi.org/10.2527/2004.82123405x>
- McClure, M. C., Morsci, N. S., Schnabel, R. D., Kim, J. W., Yao, P., Rolf, M. M., ... Taylor, J. F. (2010). A genome scan for quantitative trait loci influencing carcass, post-natal growth and reproductive traits in commercial Angus cattle. *Animal Genetics*, *41*(6), 597-607. <https://doi.org/10.1111/j.1365-2052.2010.02063.x>
- Mucha, S., Mrode, R., MacLaren-Lee, I., Coffey, M., & Conington, J. (2015). Estimation of genomic breeding values for milk yield in UK dairy goats. *J. Dairy Sci.*, *98*, 8201-8208. <https://doi.org/10.3168/jds.2015-9682>
- NAGRP. (2024). *Cattle Genome Coordination Program*. Retrieved March 26, 2024, from <https://www.animalgenome.org/cattle/maps/COMRAD>
- Pecetti, L., Barre, P., Delaunay, S., Lambroni, P., Annicchiarico, P., & Julier, B. (2021). QTL analysis for grazing tolerance, autumn dormancy and growth habit offers prospects for marker-assisted selection in lucerne. *Euphytica*, *217*(8), 171. <https://doi.org/10.1007/s10681-021-02897-7>
- Raadsma, H. W., Thomson, P. C., Zenger, K. R., Cavanagh, C., Lam, M. K., Jonas, E., ... Nicholas, F. W. (2009). Mapping quantitative trait loci (QTL) in sheep. I. A new male framework linkage map and QTL for growth rate and body weight. *Genetics, Selection, Evolution*, *41*, 34. <https://doi.org/10.1186/1297-9686-41-34>
- Rashidi, A., Bishop, S. C., & Matika, O. (2011). Genetic parameter estimates for pre-weaning performance and reproduction traits in Markhoz goats. *Small Ruminant Res.*, *1*, 100-106. <https://doi.org/10.1016/j.smallrumres.2011.05.013>
- SAS (Statistical Analysis System). (1999). *Statistical Methods*. SAS Institute Inc., Cary, NC.
- Shi, S. Y., Li, L. J., Zhang, Z. J., Wang, E. Y., Wang, J., Xu, J. W., ... Huang, Y. Z. (2020). Copy number variation of MYLK4 gene and its growth traits of *Capra hircus* (goat). *Anim Biotechnol.*, *31*(6), 532-537. <https://doi.org/10.1080/10495398.2019.1635137>
- Tabbaa, M., & Al-Atiyat, R. (2009). Breeding objectives, selection criteria and factors influencing them for goat breeding in Jordan. *Small Ruminant Res.*, *84*, 8-15. <https://doi.org/10.1016/j.smallrumres.2009.03.007>

- Tao, L., He, X. Y., Jiang, Y. T., Lan, R., Li, M., Li, Z. M., ... Chu, M. X. (2020). Combined approaches to reveal genes associated with litter size in Yunshang black goats. *Anim. Genet.*, *51*, 924-934. <https://doi.org/10.1111/age.12999>
- Wenne, R. (2023). Microsatellites as Molecular Markers with Applications in Exploitation and Conservation of Aquatic Animal Populations. *Genes*, *14*(4), 808. <https://doi.org/10.3390/genes14040808>
- Xu, Z., Wang, X., Zhang, Z., An, Q., Wen, Y., Wang, D., ... Huang, Y. (2020). Copy number variation of CADM2 gene revealed its association with growth traits across Chinese *Capra hircus* (goat) populations. *Gene*, *741*, 144519. <https://doi.org/10.1016/j.gene.2020.144519>

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Authors Contributions

Dr. Elzarei was responsible for study design, genotyping, linkage analysis, and manuscript writing. Mr. Alhasyani, Mr. Al-Sharari, and Mr. Alodhiby were responsible for microsatellite genotyping. Dr. Mousa was responsible for EBV calculation. All authors read and approved the final manuscript.

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Data Sharing Statement

No additional data are available.

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