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## The Effects of Somatotropic Axis Gene Polymorphisms on Milk Yields in Simmental Cattle

Z. Sönmez<sup>1</sup>, S. Kopuzlu<sup>2</sup>, M. Özdemir<sup>2</sup>

*1Department of Agricultural Biotechnology, Faculty of Agriculture, Ataturk University, Erzurum, Turkey*

*2Department of Animal Science, Faculty of Agriculture, Ataturk University, Erzurum, Turkey*

**ABSTRACT:** Due to the increasing world population, scientists aim to obtain high-yield products using new techniques and methods to meet needs in the fields of food, agriculture, and livestock. It is very important to select the candidate genes and markers correctly, especially in the QTL and MAS techniques in livestock. Somatotropic axis genes affect yield traits, growth, reproduction, and milk production in cattle. In the study, we determined GH/AluI and IGFI/SnaBI gene polymorphisms using the PCR-RFLP technique in DNA samples obtained from 70 Simmental cattle. The allele frequencies of the genes were in the same proportion as 0.62 and 0.38, L and V for the GH gene and T and C for the IGFI gene. There was no significant relationship between the polymorphic genotypes of the genes we examined and lactation milk yields, 305-day milk yields, daily milk yields, and lactation periods of Simmental cattle. The probability of using bGH/AluI and IGFI/SnaBI genetic variations as markers in association studies with milk yield in cattle is extremely low.

**Keywords:** Axis genes; RFLP; MAS; Simmental; milk yield

*Corresponding Author:*

Z.Sonmez, Atatürk University, Department of Agricultural Biotechnology, Erzurum, Turkey  
E-mail address: zeynepsonmez@atauni.edu.tr

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## INTRODUCTION

Nowadays, genome sequencing of organisms and the development of comprehensive single-nucleotide polymorphism (SNP) data, along with advancements in genotype identification technologies, have made genetic association maps in the entire genome possible. Somatotrophic axis genes, consisting mainly of growth hormone (GH), insulin-like growth factors (IGF I and II), carrier proteins and receptors associated with them (GHR, IGFR, IGFBP), take part in metabolism and physiological processes. They also play a role in many physiological processes, including the regulation of ionic and osmotic balance, the regulation of lipid, carbohydrate and protein metabolisms, growth, reproduction, immune function and behaviour (Renaville et al., 2002; Gabillard et al., 2003; Besseau et al., 2013; Hax et al., 2017).

The IGF I hormone consisting of 70-amino-acid with a weight of 7649 kilodaltons connected by disulfide bridges in the form of A and B chains. The cleavage sites of the SnaBI restriction enzyme, recognized by Ge et al. (2001), the C>T cleavage site at base 512 in the regulatory region of the IGFI gene, have been studied extensively. The IGF-I hormone is functionally separated since it is released by two different tissues. First, it is released by the liver and acts as an extension of the GH axis through the tonic pituitary stimulation of hepatic synthesis (Oster et al., 1995). Second, the GH hormone determines the level

of IGF-I in circulation along with nutritional factors (Laron, 2001; Delafontaine et al., 2004).

The bovine growth hormone (bGH) represents a single-chain polypeptide hormone weighing 22 kDa produced in the pre-pituitary gland and comprising 191 amino acids. Studies on bGH polymorphism-shave intensely determined L (leucine at codon 127) and V (valine at codon 127) allelic polymorphisms located on the 5th exon and coinciding with the recognition region of the AluI (GH-AluI) restriction enzyme (Zhang et al., 1993). The hormone bGH is known to play an essential role in biological processes, including breast development, lactation, ageing, growth and regulation of metabolism, ovulation in female individuals, and control of sexual behaviours (Ge et al., 2003). Polymorphisms in the GH gene are known to correlate with different production yields, such as milk yield and quality, growth (Pal et al., 2005; Kovacs et al., 2006; Zhou et al., 2006), carcass composition and quality (Grochowska et al., 2001). Furthermore, this gene also plays an important role in postpartum growth and overall metabolism, as well as lactation in cattle (Fedota et al., 2016).

Studies on various cattle breeds have generally reported the L allele in the GH/Alu gene polymorphism and the B (T) allele in the IGFI/SnaBI gene polymorphism at higher frequencies. Tables 1 and 2 present some studies on the GH/AluI and IGFI/SnaBI genes.

**Table 1.** Summary of the results obtained from the literature and the current study on the frequency of IGFI/SnaBI

Breeds	N	Allele frequencies		References
		A	B	
<b>IGF-I/SnaBI</b>				
South Anatolian Red (SAR)	50	0.23*	0.77*	Akis et al., 2010
East Anatolian Red (EAR)	50	0.38*	0.62*	Akis et al., 2010
Charolais (Coahuila)	68	0.26	0.74	Reyna et al., 2010
Charolais (Nuevo León)	68	0.46*	0.54*	Reyna et al., 2010
Beefmaster (Tamaulipas)	<b>25</b>	<b>0.03</b>	<b>0.97</b>	Reyna et al., 2010
Angus	275	0.40	0.60	Rogberg-Muñoz et al., 2013
Charolais	238	0.47	0.53	Jeanmasset et al., 2014
Black Hereford	36	0.48	0.52	Daşet al., 2019
Limousin	34	0.42	0.58	Daşet al., 2019
Brahman	24	0.34	0.66	Daş et al., 2019
Holstein	250	0.46*	0.54 *	Bonakdar et al., 2010
<b>IGF-1/SnaBI (Eco105I)</b>				
Montbeliarde	163	0.67*	0.33*	Szewczuk, 2016
Necdi	84	0.10	0.90	Yazdanpanah et al., 2013
Pesisir cattle	183	0.02	0.98	Putra et al., 2017
Jersey	227	0.52*	0.48 *	Piątkowska et al., 2021
Polish Holstein	147	0.56*	0.44 *	Piątkowska et al., 2021a
Polish Holstein	181	0.52*	0.48 *	Piątkowska et al., 2021b

Holstein–Friesian bulls	296	0.44 *	0.56 *	Ardicli et al., 2018
Kazakhstan Holstein	100	0.58*	0.42*	Beishova et al., 2019
Holstein	95	0.59*	0.41 *	Silveira et al., 2019
Native Sudanese Baggaracattle (Nyalawi)	64	0.93	0.07	Omer et al., 2018
Native Sudanese Baggaracattle (Mesairi)	63	0.92	0.08	Omer et al., 2018
Holstein-Friesian	70	0.59*	0.41 *	Nicolini et al., 2013
Iranian Holstein	60	0.40*	0.60*	Araroutı et al., 2013
Polish Holstein	191	0.54*	0.46 *	Szewczuk et al., 2013
Holstein	381	0.4(-/-)	0.6(+/+)	Hax et al., 2017
Kazakhstan black and white tawny	99	0.55*	0.45*	Ulyanov et al., 2021

**Table 2.** Summary of the results obtained from the literature and the current study on the frequency of GH/AluI

Breeds	N	Allele frequencies		References
		L	V	
<i>bGH</i>				
Native Antioquia (Colombia)	178	0.87	0.13	Echeverri et al., 2015
Italian Holstein	695	0.86	0.14	Fontanesi et al., 2015
Grey steppe	76	0.79	0.21	Özdemir, 2011
Holstein	177	0.90	0.10	Özdemir, 2011
Brown Swiss	177	0.90	0.10	Özdemir, 2011
East Anatolian Red	51	0.95	0.05	Özdemir, 2011
East Anatolian Red	76	0.84	0.16	Özkan et al., 2009
South Eastern Red	180	0.44*	0.56*	Yardibiet al., 2009
East Anatolian Red	76	0.84	0.16	Özkan et al., 2009
East Anatolian Red	50	0.43*	0.57*	Yardibiet al., 2009
Holstein	410	0.87	0.13	Amiri et al., 2018
Holstein Friesian	578	0.87	0.13	Pal et al., 2020
Kazakhstan Holstein	100	0.82	0.18	Beishova et al., 2019
Pesisir cattle	175	0.79	0.21	Afriani, 2018
Holstein	158	0.90	0.10	Gilmanov et al., 2021
Holstein's calves	59	0.96	0.04	Çınar et al., 2018
Slovak spotted ows	110	0.68*	0.32*	Hazuchova et al., 2013
Egyptian water buffaloes	200	0.80	0.20	El-Komy et al., 2021
Slovak spotted black-and-white cows	58	0.64*	0.36*	Moravcikova et al., 2012
Limousin	114	0.71,	0.29	Sedykh et al., 2020
Hereford	115	0.69*	0.31*	Sedykh et al., 2020
Kazakhstan black and white tawny	99	0.7	0.3	Ulyanov et al., 2021
Holstein	186	0.82	0.18	Özdemir et al., 2015
Holstein	115	0.65*	0.35*	Sönmez et al., 2018

Our study aimed to identify the genotypes of somatotrophic axis genes in 70 heads of Simmental cattle by the RFLP method and correlate the genotype polymorphisms of the relevant gene regions with milk yield traits

## MATERIALS AND METHODS

### Animal care, Animal DNA isolation and Primer Sets

In the present study, we collected blood samples from 70 heads of Simmental cattle with low degrees of relatedness for analysis. Animals were raised on a private Simmental cattle farm in Erzurum province.

DNA was isolated from whole blood using the Puregene DNA kit following the manufacturer's instruction (Gentra Systems Minnesota USA). In the PCR step, for growth hormone (bGH)-AluI, the 245-bp DNA region, the primers F: 5'-GTA GGG GAG GGT GGAAA TG -3 and R: 5' TGA CCCTCA GGT ACG TCT CC -3 (Özdemir, 2011), and for the 249-bp IGF1/SnaBI gene, F: 5'-ATT-ACA-AAG-CTG-CCT-GCC-CC-3' and R: 5'-ACC-TTA-CCC-GTA-TGA-AAG-GAA-TAT-ACG Primers -T-3' (Ge et al., 2001) were used.

### PCR conditions

Ten pmol/μL of each primer and 2.5 μL of dNTP-

mix (D7595: Sigma, St. Louis, MO, USA, 0.25mM), 0.5 units of Taq DNA polymerase (D1806: Sigma), 100 ng of template DNA, 5 µL of 10x PCR Buffer (100 mM Tris-HCl, pH 8.3, 500 mM KCl, 15 mM MgCl<sub>2</sub> and 0.01% gelatin), 1.5 µL of 0.25 mM MgCl<sub>2</sub>, and dH<sub>2</sub>O making the total volume of 30 µL were used for PCR amplification.

PCR amplification conditions for GH were as follows: 5 min at 94°C, 50 s at 94°C, and 50 s at 58°C; PCR amplification conditions for the IGFI gene were as follows: 5 min at 94°C, 30 s at 94°C, and 50 s at 61°C, and 30 cycles for both genes, with the final elongation temperature set at 72°C for 5 min and 1 cycle.

For the amplified IGFI and bGH genes, 2-5 U of the AluI and SnaBI restriction enzymes were added to each 7 µL PCR product and incubated at 37°C for 12 hours. After incubation, the samples were run on 3.0% agarose gel at 45 Volts for 2.5 hours, and bands were observed under UV light. The bGH and IGFI allele gene frequencies of each Simmental breed were calculated by counting. POPGENE software v1.32 (Yeh et al., 1999) was utilized to reveal whether the genotype frequencies were in Hardy-Weinberg equilibrium. SPSS 21.0 software program was used to analyze the association of genotypes with the population's milk data.

To research the impacts of IGFI and GH gene polymorphisms on lactation and some other milk yield traits in Simmental cattle raised on a private enterprise in Erzurum, a correlation analysis was conducted between the relevant polymorphic regions and the milk yield records of animals in different lactations, whose yield records were systematically kept between 2017 and 2020.

The statistical association analysis used milk yield traits, including real milk yield, 305-day milk yield, lactation period, and daily milk yield of the Simmental cattle breed. Data were analyzed by the SPSS 25.0 statistics package program (IBM SPSS 25.0 Corp. Inc.) based on the general linear model (Harvey, 1994). The analysis evaluated the effects of environmental factors, e.g., genotype, lactation order, and calving seasons, thought to affect the relevant yield trait.

According to the yield traits in the research, the following statistical model was employed.

$$Y_{ijk} = \mu + a_i + b_j + c_k + e_{ijk}$$

Where

$Y_{ijk}$  is any of the milk yield traits (real milk yield, 305-day milk yield, lactation period, and daily milk yield),

$\mu$  is the population average,

$a_i$  is the  $i^{\text{th}}$  genotype effect,

$b_j$  is the effect of the  $j^{\text{th}}$  lactation order ( $j$ : 3; 1<sup>st</sup> Lactation: 1, 2<sup>nd</sup> Lactation: 2, 3<sup>rd</sup> Lactation: 3, 4<sup>rd</sup> Lactation: 4, 5<sup>th</sup> Lactation: 5, 6<sup>th</sup> Lactation: 6, 7<sup>th</sup> Lactation: 7),

$c_k$  is the effect of the  $k^{\text{th}}$  calving season ( $k$ : 2; 1: winter-spring, 2: summer-autumn),

$e_{ijk}$  is the margin of error.

## RESULTS

The figures show the PCR amplification results and base sizes of PCR products (Figure 1).

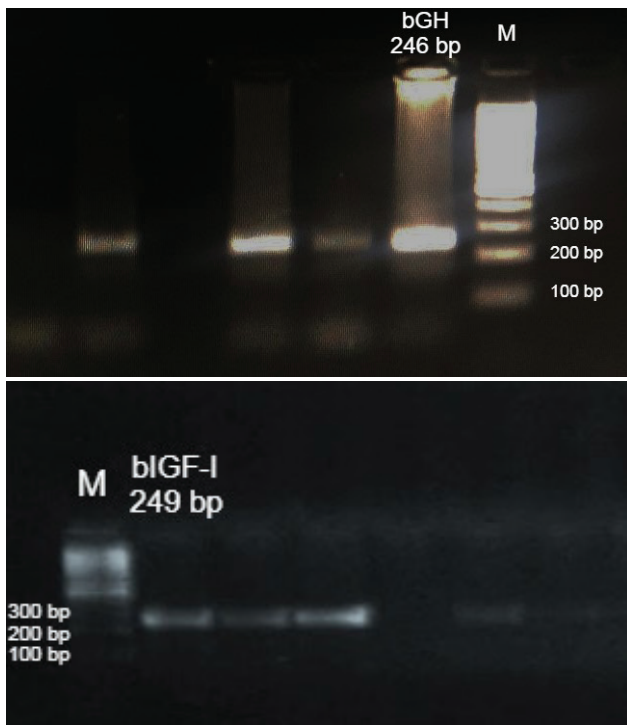
The 249 bp PCR products were digested by SnaBI for the IGFI gene, and the result of digestion was one band (249 bp) for the CC genotype, three bands (249, 223, and 26 bp) for the TC genotype, and two bands (223 and 26 bp) for the TT genotype (Figure 2).

The 246 bp products were acquired after the PCR process, and PCR products were digested by the AluI restriction enzyme for the GH gene. At the end of digestion, one band (246 bp) for the VV genotype, three bands (246, 171, and 52 bp) for the LV genotype, and two bands (171 and 52 bp) for the LL genotype were expected. The band of 52 bp could not be observed on agarose gel electrophoresis (Figure 3).

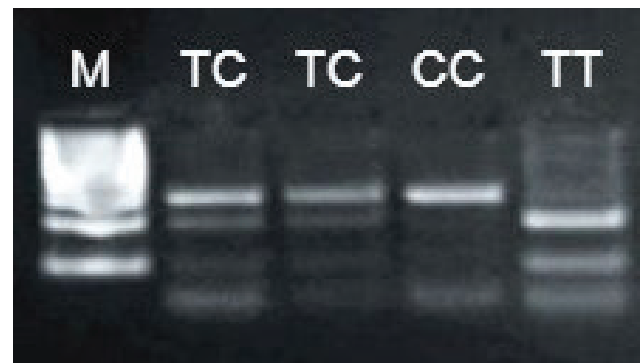
As a result of determining allele and genotype frequencies in Simmental cattle, it was found that the LL, LV, and VV genotype frequencies for the GH gene were 0.33, 0.57, and 0.10, respectively, while the TT, CT, and CC genotype frequencies for the IGFI gene were 0.35, 0.55, and 0.10, respectively. The LL and VV allele frequencies for the GH gene and the TT and CC allele frequencies for the IGFI gene were measured similarly as 0.62 and 0.38 (Table 3).

Hardy-Weinberg genetic equilibrium test showed that the distributions of these genotype frequencies were not in equilibrium in the analysed breed ( $P > 0.05$ ).

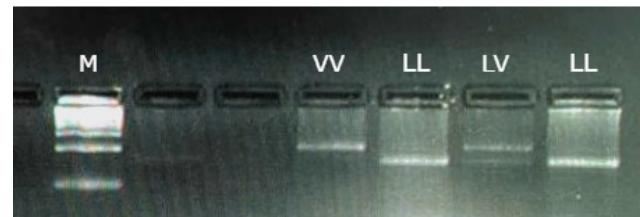
The overall averages for milk yield, 305-day milk yield, daily milk yield, real milk yield, and lactation



**Figure 1.** PCR results of the bGH and IGFI gene regions (1<sup>st</sup> primer pair 246, 2<sup>nd</sup> primer pair 249, with Standard GENESTA 100 bp DNA marker images, respectively)



**Figure 2.** IGFI-SnaBI RFLP results (CC, CT, and TT genotypes with Standard GENESTA100 bp DNA marker images, respectively)



**Figure 3.** GH-AluI RFLP results (VV, LV, and LL genotypes with Standard GENESTA 100 bp DNA marker images)

**Table 3.** The genotype and allele frequencies and H-W equilibrium IGFI-SnaBI and GH-AluI genes

IGFI allele and genotype frequencies					GH allele and genotype frequencies						
Genotype	N	T	C	% Frequency	H-W <sup>a</sup>	Genotype	N	L	V	% Frequency	H-W <sup>a</sup>
TT	23	46	0	34.85	0.20	LL	23	46	0	33.33	0.11
CT	36	36	36	54.55		LV	39	39	39	56.52	
CC	7	0	14	10.61		VV	7	0	14	10.14	
Total	66	82	50	100.00		Total	69	85	53	100.00	
P	132	0.62	0.38			P	138	0.62	0.38		

a. P-value for the test for Hardy-Weinberg equilibrium, in which P>0.05 indicates that the sampled population is not in Hardy-Weinberg equilibrium.

**Table 4.** Effects of IGFI/SnaBI genotypes on milk yields in Simmental cattle

Variation Sources	N	Daily milk yield		Lactation milk yield		305-day milk yield		Lactation period	
		$\bar{X} \pm S_x$	$\bar{X} \pm S_x$	$\bar{X} \pm S_x$	$\bar{X} \pm S_x$	$\bar{X} \pm S_x$	$\bar{X} \pm S_x$		
IGFI/SnaBI	CC	36	18,279±0,702	5468,285±283,960	5571,231±218,310	301,822±13,997			
	CT	39	18,265±0,690	5085,252±279,220	5515,907±214,666	282,320±13,763			
	TT	8	17,044±1,483	4916,054±600,087	5286,936±461,350	304,416±29,579			
	<b>P</b>		<b>0,732</b>	<b>0,536</b>	<b>0,857</b>	<b>0,545</b>			
Calving season	1	48	17,742±0,786	4783,274±318,281	5228,148±244,696	278,548±15,688			
	2	35	17,984±0,809	5529,786±327,522	5687,901±251,801	313,824±16,144			
	<b>P</b>		<b>0,817</b>	<b>0,081</b>	<b>0,160</b>	<b>0,094</b>			
	Lactation order	2	10	17,026±1,439	4994,060±582,260	5272,492±447,645	297,624±28,700		
3		17	18,423±1,067	5300,083±432,062	5677,206±332,172	290,881±21,297			
4		18	17,422±1,085	5577,652±438,982	5493,044±337,492	332,631±21,638			
5		18	18,687±0,983	5294,563±397,867	5674,684±305,882	280,223±19,611			
6		14	17,440±1,165	5044,346±471,381	5327,560±362,400	298,212±23,235			
7		6	18,177±1,745	4728,477±706,436	5303,162±543,112	277,545±34,821			
<b>P</b>			<b>0,876</b>	<b>0,893</b>	<b>0,924</b>	<b>0,502</b>			
Total	83	17,863±0,605	5156,530±244,727	5458,025±188,148	296,186±12,063				

$\bar{X}$ : General Means,  $S_x$ : Standard deviation

period were 5458,025kg, 17,863 kg, 5156,530 kg, and 296,186days, respectively. Among the polymorphic regions, the highest average for all milk yield values was obtained with the CC genotype and the lowest value was obtained with the TT genotype for the IGFI/SnaBI polymorphic region, while the difference between the highest and lowest average milk yield values was not insignificant.

The differences between the genotype according to the GH/AluI fragment differences and the milk

yield averages of 91 Simmental cattle in 6 lactations and the genotype, calving season, and lactation order factors were statistically insignificant ( $p>0.05$ ). The overall averages for milk yield, 305-day milk yield, daily milk yield, real milk yield, and lactation period were 5443,264 kg, 18,355 kg, 5619,733 kg, and 301,545days, respectively. Among the yield records, the highest genotype average was observed in the LL genotype, while the lowest yield average was observed in the LV genotype.

**Table 5.** Effects of GH/AluI genotypes on milk yields in Simmental cattle

Variation Sources		N	Daily milk yield $\bar{X} \pm S_{\bar{x}}$	Lactation milk yield $\bar{X} \pm S_{\bar{x}}$	305-day milk yield $\bar{X} \pm S_{\bar{x}}$	Lactation period $\bar{X} \pm S_{\bar{x}}$
GH/AluI	LL	33	18,349±0,728	5541,241±292,225	5624,453±228,070	304,904±14,130
	LV	47	18,167±0,623	5059,354±250,305	5499,343±195,353	282,277±12,103
	VV	11	18,549±1,215	5729,198±487,804	5735,402±380,712	317,454±23,587
	<b>P</b>		<b>0,954</b>	<b>0,290</b>	<b>0,824</b>	<b>0,273</b>
Calving period	1	54	18,447±0,672	5262,943±269,631	5508,863±210,436	289,717±13,037
	2	37	18,262±0,742	5623,586±297,773	5730,602±232,400	313,374±14,398
	<b>P</b>		<b>0,847</b>	<b>0,350</b>	<b>0,461</b>	<b>0,206</b>
Lactation order	2	10	17,306±1,332	5093,744±534,652	5297,029±417,275	295,945±25,852
	3	17	18,875±1,040	5584,882±417,492	5817,002±325,836	297,047±20,187
	4	20	18,008±0,970	5689,066±389,565	5602,114±304,040	326,819±18,836
	5	21	18,983±0,965	5408,306±387,470	5738,397±302,405	283,487±18,735
	6	16	17,388±1,046	5304,829±419,796	5345,561±327,634	312,241±20,298
	7	7	19,570±1,552	5578,758±623,270	5918,292±486,438	293,732±30,137
	<b>P</b>		<b>0,681</b>	<b>0,940</b>	<b>0,794</b>	<b>0,600</b>
Total		91	18,355±0,522	5443,264±209,579	5619,733±163,568	301,545±10,134

$\bar{X}$ : General Means,  $S_{\bar{x}}$ : Standard deviation

## DISCUSSION

The study carried out in the Simmental breed because of LL and CC genotypes are seen at the same rate distributions so allele frequencies are similar for GH/AluI and IGFI/SnaBI genes. Tables 1 and 2 present the allele and genotype frequencies obtained in previous polymorphic studies on the GH and IGFI genes in cattle. Among these studies, those that show similarities and differences with our studies are marked. The distributions of allele and genotype frequencies for both genes are generally similar to previous studies, and it is seen that the L allele is dominant for the GH hormone, while the T allele is dominant for the IGFI gene. According to the Hardy-Weinberg equilibrium test, the distributions of genotype frequencies in the herd were estimated to be in not balanced because the herd was raised in a closed barn environment, external migration was absent, and there was high mortality due to uncontrolled breeding.

In two different studies in which we correlated the

yields of GH/AluI gene polymorphisms in 118 and 186 numbers of Holstein cattle breeds from different farms, no significant relationship was found between genotypes and milk yields. A similar relationship could not be found between GH-AluI and IGFI-SnaBI gene polymorphisms and milk yield in Simmental cattle (Sönmez et al., 2018; Özdemir et al., 2018). Therefore, considering our three association studies, we examined previous studies to determine the potential for these gene regions to be used as markers.

In our study of associating the IGFI/SnaBI gene polymorphism with milk yield in 70 cattle breeds, we thought that the relevant polymorphic gene marker was not associated with milk yields may be due to a small number of samples. However, similar results were obtained in previous milk yield association studies on different breeds and with a large number of samples. Studies on milk yield generally report that the IGFI/SnaBI gene polymorphism does not have a significant effect. Similar to our study, in the study

that examined the impact of the IGFI gene polymorphism on milk yield in three breeds (227 Jersey, 147 Polish Holstein-Friesian black-and-white (HO) and 181 Polish Holstein-Friesian red-and-white (RW)) in different lactations, the average milk yield was high in individuals with the CC genotype, but there was no significant difference between this average and other genotype averages (Piałkowska et al., 2021). The study in which the serum IGF-I concentration and reproductive performance of Holstein dairy cows were associated with IGF-I gene polymorphisms reported no significant relationship between milk production and body condition score and IGF-I genotypes (Silveira et al., 2019). In different studies conducted on a number of which is over 100 Holstein cattle showed that the IGFI/SnaBI polymorphism did not significantly affect milk yield, but the fat and protein ratios in milk were high, especially in individuals with the AB (CT) genotype (Bonakdar et al., 2010; Zhang et al., 2018; Beishova et al., 2017; Beishova et al., 2018; Beishova et al., 2019). For the IGFI gene, Ge et al. (2001) reported that the c. 512 C>T polymorphic marker defined by studies on milk yield in cattle breeds was generally not associated with milk yield. However, it was reported that different SNPs identified for the IGFI gene were associated with milk yield (Mullen et al., 2011; Lynch et al., 2010; Gui et al., 2018). The IGFI-SnaBI polymorphism studies conducted in different cattle breeds reported that the CC genotype was positively associated with the meat and fat weight of the carcass (Ge et al., 2001; Reyna et al., 2010; Siadkowska et al., 2006). Especially among studies on meat yield, studies are showing that the IGFI gene affects meat quality parameters and meat colour change, positively associated with live body weight at slaughter, cold carcass weight, meat and fat weight in valuable cuts, body weight, subcutaneous back fat, and waist circumference musculature (Curi et al., 2005; Siadkowska et al., 2006; Ardicli, 2018; Szwczuk et al., 2013). In the study determining the effects of the IGFI gene polymorphism on the reproductive data of different cattle breeds, it was revealed that the genotypes defined with IGF-SnaBI were effective on reproductive data but did not affect milk yield. Studies on reproductive data associated the SNP identified in the IGF-1 gene with the resumption of the postpartum lying phase and affected reproductive parameters in Holstein cows (Nicolini et al., 2013; Ararouti et al., 2013). In another study, the SNP within the GH/IGF-1 pathways was associated with the reproductive performance of Holstein cows under

heat stress conditions and associated with services per conception (SPC) (Leyva-Corona et al., 2018). While most studies have reported that the IGFI gene affects reproductive data, some studies have reported no significant relationship between IGF-I SnaBI genotypes in Holstein cattle kept under different breeding conditions and the fertility of Holstein cows raised in semi-intensive or intensive regimens (Hax et al., 2017).

Studies have demonstrated that the GH/AluI gene polymorphism, like the IGFI/SnaBI gene polymorphism is more effective on growth data and body weight than milk yield, especially in cattle. Similar to our study among the association studies on the GH hormone, a study conducted on black and white calico heifers reported that the amount of milk and the protein and fat ratios in milk were high in LL genotype heifers (Gilmanov et al., 2021) but the difference between the highest and lowest average milk yield values was not significant. In the studies GH-AluI gene polymorphism was determined in different breeds and the relationships between the obtained genotype data and body weight gain and body measurements were investigated genotype data showed that the GH-AluI polymorphism was related to the weaning body weights and the length of the chest circumference (Çınar et al., 2018; Afriani and Putra, 2018). In the association analyses conducted milk production length according to GH-AluI genotypes was not found significant, however, other SNPs identified in the GH gene were found to be associated with milk yields. (Zhou et al., 2006; Maylinda, 2011; Moravcikova et al., 2012; Hazuchova et al., 2013). Studies conducted on different cattle types and buffaloes have reported that GH-AluI gene polymorphisms affect meat yield, pre-slaughter body weight, carcass meat weight, slaughter weight and growth data (Pereira et al., 2005; Curi et al., 2006; Sedykh et al., 2020; El-Komy et al., 2021)

Parallel to our research, polymorphic association studies analyzing somatotrophic axis genes together have generally associated these genes with growth and reproduction data but not with milk yield, especially GH/AluI and IGFI/SnaBI (Balogh et al., 2008; Ulyanov et al., 2021). The two different META analysis studies show that the common L allele was dominant and no significant difference was found in the results of the meta-analysis and subgroup analysis for the milk yields in the LL, LV, and VV genotypes Akcay et al., 2020; Bangar et al., 2021). The results of the



meta-analysis on bGH/AluI and IGFI/SnaBI genetic variations in cattle confirm the results of our study.

In association analysis studies published to determine the potential of the gene polymorphisms to be used as markers in cattle breeding, the above-mentioned genes appear to have significant implications for body weight, meat yield, and reproductive performance in general. Studies to be conducted in the field of animal breeding estimate the effects of the determined bGH/AluI and IGFI/SnaBI genetic variations on different breeds with different performance traits and their potential to be used as markers in breeding

programs. However, previous studies and our work have shown that bGH/AluI and IGFI/SnaBI genetic variations in cattle are less likely to be used as markers in milk data analyses.

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## CONFLICTS OF INTEREST

The Authors have no conflict of interest to declare

## REFERENCES

- Afriani, T., & Putra, D. E. (2018). Association of GH, IGF1R, and PIT1 genes polymorphism with average daily gain and body measurement in Pesisir cattle. *Nusantara Bioscience*, 10 (4), 221-225.
- Akçay, A., Daldaban, F., Celik, E., Arslan, K., & AKYÜZ, B. (2020). Meta-analysis of allele and genotype frequency of growth hormone (bGH) gene AluI polymorphism, which is effective on milk yield in Holstein cattle. *Kafkas Üniversitesi Veteriner Fakültesi Dergisi*, 26 (5).
- Akis, I., Oztabak, K., Gonulalp, I., Mengi, A., & Un, C. E. M. A. L. (2010). IGF-1 and IGF-1R gene polymorphisms in East Anatolian Red and South Anatolian Red cattle breeds. *Russian journal of genetics*, 46 (4), 439-442.
- Amiri, S., Jemmali, B., Ferchichi, M. A., Jeljeli, H., Boulbaba, R., & Ben Gara, A. (2018). Assessment of growth hormone gene polymorphism effects on reproductive traits in Holstein dairy cattle in Tunisia. *Archives Animal Breeding*, 61 (4), 481-489.
- Ararouti, T., Mirzaei, A., & Sharifiyazdi, H. (2013). Assessment of single nucleotide polymorphism in the 5' and 3'-flanking region of Insulin-like growth factor-I (IGF-I) gene as a potential genetic marker for fertility in Holstein dairy cows. *Istanbul Üniversitesi Veteriner Fakültesi Dergisi*, 39 (2), 175-182.
- Ardicli, S. E. N. A., Samli, H., Dincel, D. E. N. I. Z., Ekiz, B., Yalcintan, H., Vatanserver, B., & Balci, F. (2018). Relationship of the bovine IGF1, TG, DGAT1 and MYF5 genes to meat colour, tenderness and cooking loss. *Journal of the Hellenic Veterinary Medical Society*, 69 (3), 1077-1087.
- Balogh, O., Szepes, O., Kovacs, K., Kulcsar, M., Reiczigel, J., Alcazar, J. A., & Huszenicza, G. (2008). Interrelationships of growth hormone AluI polymorphism, insulin resistance, milk production and reproductive performance in Holstein-Friesian cows. *Veterinari Medicina*, 53 (11), 604-616.
- Bangar, Y. C., & Magotra, A. (2021). Meta-analysis of SNP in growth hormone gene associated with milk traits in dairy cows. *Tropical animal health and production*, 53 (2), 1-7.
- Beishova I, Nametov AM, Chuzhebaeva GD, Tegza, IM and Belaya AV (2018). Assessment of pairwise combinations' association of polymorphic variants of the genes of bPIT-1, bGH, bGHR/bIGF somatotrophic cascade with meat productivity of the cattle bred in Kazakhstan. *J. Pharm. Sci. Res.* 10 (8): 1906-1911.
- Beishova IS and Poddudinskaya TV (2017). Analiz geneticheskoi struktury po genam somatotropinovogo kaskada (bPit- 1, bGH, bGHR) porod krupnogo rogatogo skota otechestvennoi selektsii [Analysis of the genetic structure of somatotropin cascade genes (bPit-1, bGH, bGHR) of domestic cattle breeds]. 3i: intellect, idea, innovation 2 (1): 261-265.
- Beishova, I. S., Ulyanov, V., Shaikamal, G., Papusha, N., & Belaya, E. V. (2019). Features of Holstein cattle bred in Kazakhstan by the polymorphic genes of the somatotropin cascade. *Adv. Anim. Vet. Sci*, 7 (1), 60-65.
- Besseau, L., Fuentès, M., Sauzet, S., Beauchaud, M., Chatain, B., Covès, D., & Falcón, J. (2013). Somatotrophic axis genes are expressed before pituitary onset during zebrafish and sea bass development. *General and Comparative Endocrinology*, 194, 133-141.
- Bonakdar, E., Rahmani, H. R., Edriss, M. A., & Tabatabaei, B. S. (2010). IGF-I gene polymorphism, but not its blood concentration, is associated with milk fat and protein in Holstein dairy cows. *Genetics and Molecular Research*, 9 (3), 1726-1734.
- Çınar, M., Akyüz, B., Metin Kılıcı, J., Arslan, K., Kaliber, M., & Aksel, E. (2018). Effects of GH-AluI and MYF5-TaqI polymorphisms on weaning weight and body measurements in Holstein young bulls. *Kafkas Üniversitesi Veteriner Fakültesi Dergisi*, 24 (6).
- Curi, R. A., De Oliveira, H. N., Silveira, A. C., & Lopes, C. R. (2005). Association between IGF-I, IGF-IR and GHRH gene polymorphisms and growth and carcass traits in beef cattle. *Livestock Production Science*, 94 (3), 159-167.
- Curi, R. A., Palmieri, D. A., Sugisawa, L., Oliveira, H. N. D., Silveira, A. C., & Lopes, C. R. (2006). Growth and carcass traits associated with GH1/Alu I and POU1F1/Hinf I gene polymorphisms in Zebu and crossbred beef cattle. *Genetics and Molecular Biology*, 29 (1), 56-61.
- Piątkowska, C. E., Szatkowska, I., Zaborski, D., Grzesiak, W., Tabor-Osińska, S., Wasielewska, M., & Pawlina, E. (2021). Single Nucleotide Polymorphism in the Promoter Region of the IGF-1 Gene is Associated with Milk Production in Holstein and Jersey Cattle-Is the Aspect of Present Research Still Relevant in the Era of Genomic Selection? *Pakistan Journal of Zoology*, 53 (6).
- Daş, A., Şahin, T., Akbulut, Ö., Bengü, A. Ş., & Bozkaya, F. (2019). Determination of genetic polymorphisms of leptin, ghrelin and insulin-like growth factor-1 (IGF-1) genes in beef cattle raised in Turkey. *Harran Üniversitesi Veteriner Fakültesi Dergisi*, 8 (1), 108-115.
- Delafontaine, P., Song, Y. H., & Li, Y. (2004). Expression, regulation, and function of IGF-1, IGF-1R, and IGF-1 binding proteins in blood vessels. *Arteriosclerosis, thrombosis, and vascular biology*, 24 (3), 435-444.
- Echeverri J, Saldamando C I, Herrera A L, 2015. Genetic structure analysis of a Holstein cow population in Colombia. *Rev Colomb Cienc Pec*; 28:54-63.
- El-Komy, S. M., Saleh, A. A., Abd El-Aziz, R. M., & El-Magd, M. A. (2021). Association of GH polymorphisms with growth traits in buffaloes. *Domestic Animal Endocrinology*, 74, 106541.
- Fedota O M, Ruban S, Yu Lysenko N G, Kolisnyk A I, Goraichuk I V, Tyzhnenko T V, 2016. SNP L127V of Growth Hormone Gene In

- Breeding Herd of Aberdeen Angus In Kharkiv Region, Eastern Ukraine. *Journal for Veterinary Medicine, Biotechnology and Biosafety* 2 (3), uDC 575. 113. 1:636. 223. 1 (477. 54)
- Fontanesi L, Scotti E, Samore AB, Bagnato A, Russo V. 2015. Association of 20 candidate gene markers with milk production and composition traits in sires of Reggiana breed, a local dairy cattle population. *Live-stock Science* 176: 14-21.
- Gabillard, J. C., Duval, H., Cauty, C., Rescan, P. Y., Weil, C., & Bail, P. Y. L. (2003). Differential expression of the two GH genes during embryonic development of rainbow trout *Oncorhynchus mykiss* in relation with the IGFs system. *Molecular Reproduction and Development: Incorporating Gamete Research*, 64 (1), 32-40.
- Ge W, Davis ME, Hines HC, Irvin KM, Simmen RCM. 2001. Association of a genetic marker with blood serum insulin-like growth factor-1 concentration and growth traits in Angus cattle. *J Anim Sci*. 79:1757-1762.
- Ge, W., Davis, M. E., Hines, H. C., Irvin, K. M., & Simmen, R. C. M. (2003). Association of single nucleotide polymorphisms in the growth hormone and growth hormone receptor genes with blood serum insulin-like growth factor I concentration and growth traits in Angus cattle. *Journal of Animal Science*, 81 (3), 641-648.
- Gilmanov, K. K., Vafin, R. R., & Tyulkin, S. V. (2021, March). Influence of complex genotypes of GH and PRL genes on milk productivity and milk quality of cows. In *IOP Conference Series: Earth and Environmental Science* (Vol. 699, No. 1, p. 012036). IOP Publishing.
- Grochowska, R., Lunden, A., Zwierzchowski, L., Snochowski, M., Oprzadek, J., 2001. Association between gene polymorphism of growth hormone and carcass traits in dairy bulls. *Anim. Sci.* 72: 441-447.
- Gui, L. S., Wang, Z. Y., Jia, J. L., Zhang, C. T., Chen, Y. Z., & Hou, S. Z. (2018). IGF-1 gene polymorphisms influence bovine growth traits in Chinese Qinchuan Cattle. *KAFKAS ÜNİVERSİTESİ VETERİNER FAKÜLTESİ DERGİSİ*, 24 (3).
- Harvey, A., Ruiz, E., & Shephard, N. (1994). Multivariate stochastic variance models. *The Review of Economic Studies*, 61 (2), 247-264.
- Hax, L. T., Schneider, A., Jacometo, C. B., Mattei, P., da Silva, T. C., Farina, G., & Corrêa, M. N. (2017). Association between polymorphisms in somatotrophic axis genes and fertility of Holstein dairy cows. *Theriogenology*, 88, 67-72.
- Hazuchova, E., Moravčíková, N., Kadlečík, O., Trakovická, A., Kasarda, R., and Pavlík, I., 2013. Effect of polymorphisms in the bovine growth hormone gene and impact of inbreeding depression on milk performance traits in Slovak Spotted Cattle. *Journal of Microbiology, Biotechnology and Food Sciences*, 2 1, 1324-1334
- Jeanmas, A., Sopannarath, P., Tumwasorn, S., & Loongyai, W. (2014). Association of SNP marker in the IGF1 gene with carcass traits in crossbred cattle among Thai Native, Brahman and Charolais. *Agriculture and Natural Resources*, 48 (4), 605-610.
- Kovacs K, Volgyi-Csik J, Zsolnai A, Gyorkos I, Fesus L, 2006. Associations between the AluI polymorphism of growth hormone gene and production and reproduction traits in a Hungarian Holstein-Friesian bull dam population. *Archiv für Tierzucht*, 49, 236-249.
- Laron, Z. (2001). Insulin-like growth factor 1 (IGF-1): a growth hormone. *Molecular Pathology*, 54 (5), 311.
- Leyva-Corona, J. C., Reyna-Granados, J. R., Zamorano-Algandar, R., Sanchez-Castro, M. A., Thomas, M. G., Enns, R. M., & Luna-Nevarez, P. (2018). Polymorphisms within the prolactin and growth hormone/insulin-like growth factor-1 functional pathways associated with fertility traits in Holstein cows raised in a hot-humid climate. *Tropical animal health and production*, 50 (8), 1913-1920.
- Lynch, C. O., Mullen, M. P., Waters, S. M., Howard, D. J., O'Boyle, P., Berry, D. P., & Diskin, M. G. (2010). Single nucleotide polymorphisms in the growth hormone and insulin-like growth factor 1 gene are associated with production and fertility traits in dairy cows. *Advances in Animal Biosciences*, 1 (1), 314-314.
- Maj, A., Snochowski, M., Siadkowska, E., Rowinska, B., Lisowski, P., Robakowska-Hyzorek, D., & Zwierzchowski, L. (2008). Polymorphism in genes of growth hormone receptor (GHR) and insulin-like growth factor-1 (IGF1) and its association with both the IGF1 expression in liver and its level in blood in Polish Holstein-Friesian cattle. *Neuroendocrinology Letters*, 29 (6), 981.
- Maylinda, S. (2011). Genetic polymorphism of growth hormone locus and its association with bodyweight in Grati dairy cows. *International Journal of Biotechnology and Molecular Biology Research*, 2 (7), 117- 120.
- Moravčíková, N., Trakovická, A., & Hazuchová, E. (2012). The association of bovine growth hormone gene polymorphism with milk performance traits in Slovak Spotted cows. *Anim Sci Biotechnol*, 45 (1), 206-210.
- Mullen, M. P., Lynch, C. O., Waters, S. M., Howard, D. J., O'boyle, P., Kenny, D. A., Buckley, F., Horan, B. and Diskin, M. G., 2011. Single nucleotide polymorphisms in the growth hormone and insulin-like growth factor-1 genes are associated with milk production, body condition score and fertility traits in dairy cows. *Genet. mol. Res.*, 10: 1819-1830. [https:// doi. org/10. 4238/vol10-3gmr1173](https://doi.org/10.4238/vol10-3gmr1173).
- Nicolini, P., Carriquiry, M., & Meikle, A. (2013). A polymorphism in the insulin-like growth factor 1 gene is associated with postpartum resumption of ovarian cyclicity in Holstein-Friesian cows under grazing conditions. *Acta Veterinaria Scandinavica*, 55 (1), 1-8.
- Omer, R. M. A., Masri, M. A. R. M., Jawasreh, K. I., Nour, I. A., Biraima, A. D. A., Musa, L. M. A., & AhMED, M. K. A. (2018). Molecular Detection of Selected Genetic Polymorphisms in Growth Hormone and Insulin-Like Growth Factor 1 Genes in Indigenous Sudanese Baggara Cattle. *Kafkas Üniversitesi Veteriner Fakültesi Dergisi*, 24 (2).
- Oster, S. M. (1995). *Strategic management for nonprofit organizations: Theory and cases*. Oxford University Press.
- Özdemir M, 2011. Determination of allele frequencies of growth hormone AluI polymorphism in Brown Swiss, Holstein, native East Anatolian Red and Turkish Grey breeds. *International Journal of Dairy Technology*. 64 (3):350-352.
- Özdemir M, Sönmez Z, Topal M, 2015. Organik yetiştirilen Holstein Irkında GH/Alu I ve CSN3/Hinf I Gen Polimorfizmlerinin Belirlenmesi. 9. Ulusal Zootečni Bilim Kongresi, P838-847, 3-5 Eylül 2015, Konya.
- Ozdemir, M., Topal, M., & Aksakal, V. (2018). The relationships between performance traits and the bGH/Alu and Pit-1/Hinf I polymorphisms in Holstein cows. *Indian Journal of Animal Research*, 52 (2), 186-191.
- Özkan, E., Soysal, M. İ., Dinç, H., Sönmez, G., Okyar, M., Togan İ., 2009. Türkiye sığır ırklarında büyüme hormonu AluI ve MspI polimorfizminin PZR-RFLP yönteminin kullanılarak belirlenmesi. 6. Ulusal Zootečni Kongresi, 24-26 Haziran, Erzurum, 93-102
- Pal A, Chakravarty A K, Bhattacharya T K, Sharma A, 2005. Polymorphism of growth hormone gene and its association with expected milk production traits in dairy bulls. *J. Appl. Anim. Res.* 27 (1): 29-33.
- Pal, A., & Chakravarty, A. K. (2020). Mutations in growth hormone genes affect the stability of protein structure leading to reduced growth, reproduction, and milk production in crossbred cattle—an insight. *Domestic Animal Endocrinology*, 71, 106405.
- Pereira, A. P., Alencar, M. M. D., Oliveira, H. N. D., & Regitano, L. C. D. A. (2005). Association of GH and IGF-1 polymorphisms with growth traits in a synthetic beef cattle breed. *Genetics and Molecular Biology*, 28 (2), 230-236.
- Putra, D. E. (2017). Polymorphism of Insulin-like Growth Factor 1 Gene (IGF1/TasI, IGF1/SnaBI, IGF1/RsaI) and the Association with Daily Gain of Pesisir Cattle Local Breed from West Sumatera, Indonesia. *Pakistan Journal of Biological Sciences: PJBS*, 20 (4), 210-216.
- Renaville, R., Hammadi, M., & Portetelle, D. (2002). Role of the somatotrophic axis in the mammalian metabolism. *Domestic animal endocrinology*, 23 (1-2), 351-360.
- Reyna XFDLR, Montoya HM, Castellon VV, Rincon AMS, Bracamonte MP, Vera WA (2010). Polymorphisms in the IGF1 gene and their effect on growth traits in Mexican beef cattle. *Genet. Mol. Res.*, 9 (2):875-883.
- Rogberg-Muñoz, A., Cantet, R. J., Fernández, M. E., Lirón, J. P., Prando, A., Birchmeier, A. N., & Giovambattista, G. (2013). Longitudinal analysis of the effects of IGF1-SnaBI genotypes on the growth curve of Angus bull calves. *Livestock Science*, 154 (1-3), 55-59.
- Sedykh, T. A., Gizatullin, R. S., Dolmatova, I. Y., Gusev, I. V., & Kalashnikova, L. A. (2020). Growth Hormone Gene Polymorphism in relation to Beef Cattle Carcass Quality. *Russian Agricultural Sciences*, 46 (3), 289-294.
- Siadkowska, E., Zwierzchowski, L., Oprzadek, J., Strzalkowska, N., Bag-

- nicka, E., & Krzyzewski, J. (2006). Effect of polymorphism in IGF-1 gene on production traits in Polish Holstein-Friesian cattle. *Anim Sci Pap Rep*, 24 (3), 225-37.
- Silveira, P. A. S., Butler, W. R., da Silva, T. C., Barros, C. C., Corrêa, M. N., & Schneider, A. (2019). Association of polymorphisms in the IGF-I, GHR and STAT5A genes with serum IGF-I concentration and reproductive performance of Holstein dairy cows. *Animal reproduction science*, 211, 106206.
- Sönmez, Z., Özdemir, M., Bayram, B., & Aksakal, V. (2018). Holstein ineklerde GH/AluI polimorfizmi ile baz süt verim özellikleri arasındaki ilişkiler. *Türk Tarım-Gıda Bilimve Teknoloji Dergisi*, 6 (5), 602-606.
- Szewczuk, M., Bajurna, M., Zych, S., & Kruszyński, W. (2013). Association of insulin-like growth factor I gene polymorphisms (IGF1/TasI and IGF1/SnaBI) with the growth and subsequent milk yield of Polish Holstein-Friesian heifers. *Czech Journal of Animal Science*, 58 (9), 404-411.
- Szewczuk, M. (2016). Analysis of the relationship between insulin-like growth factor 1 receptor gene polymorphisms in Montbeliarde cows and the birth weight of their calves. *Acta Veterinaria Brno*, 85 (1).
- Ulyanov, V. A., Kubekova, B. Z., Beishova, I. S., Belaya, A. V., & Papusha, N. V. (2021). Preferred and undesirable genotypes of bGH and bIGF-1 genes for the milk yield and quality of black-and-white breed. *Veterinary World*, 14 (5), 1202.
- Yardibi, H., Hosturk, G. T., Paya, I., Kaygısız, F., Çiftçioğlu, G., Mengi, A., Oztabak, K., 2009. Associations of growth hormone gene polymorphism with milk production traits in South Anatolian and East Anatolian Red cattle. *J Anim Vet Adv*, 8, 1040-1044.
- Yazdanpanah A, Hedayatollah R, Khalil M, Morteza M, Saber K. 2013. Polymorphism of insulin-like growth factor 1 in Najdi cattle populations. *American JBiochem Biotech*. 9:300-306
- Yeh, F. C., Yang, R. C., & Boyle, T. (1999). PopGene: Microsoft Windows-based freeware for population genetic analysis, version 1. 31. University of Alberta: Edmonton, Canada.
- Zhang W, Gao X, Zhang Y, Zhao Y, Zhang J, Jia Y, Zhu B, Xu L, Zhang L, Gao H, Li J and Chen Y (2018). Genome-wide assessment of genetic diversity and population structure insights into admixture and introgression in Chinese indigenous cattle. *BMC Genet*. 19 (1): 1-12. <https://doi.org/10.1186/s12863-018-0705-9>.
- Zhang, H. M., Brown, D. R., Denise, S. K., & Ax, R. L. (1993). Rapid communication: polymerase chain reaction-restriction fragment length polymorphism analysis of the bovine somatotropin gene. *Journal of Animal Science*, 71 (8), 2276-2276.
- Zhou G, Zhu Q, Jin H G, Guo S L, 2006. Genetic variation of growth hormone gene and its relationship with milk production traits in China Holstein cows. *Asian-Australasian J. of Anim. Sci*. 19 (3):315-318.