

Part 1. Biotechnology

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SNP L127V OF GROWTH HORMONE GENE IN BREEDING HERD OF ABERDEEN ANGUS IN KHARKIV REGION, EASTERN UKRAINE

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Summary. Bovine growth hormone (*bGH*) effects on animal growth and metabolism. Therefore, it plays a vital role in regulation of body weight, fertility and lactation performance of cattle. This enables *bGH* gene to be used as a candidate marker for improving growth, meat or milk production and for marked-assisted selection programs of cattle too. The aim of this study is analyzing the polymorphic variant L127V of *bGH* gene in Aberdeen-Angus bred in Kharkiv region and comparing of obtained result with commercial herds from other countries.

PCR-RFLP methods were set up for the SNP genotyping. Testing deviation from the Hardy-Weinberg equilibrium was performed using Pearson's chi-squared test. Pearson's correlation coefficient *r* was used to measure the strength of association between two characteristics.

The allele and genotype frequencies of SNP L127V (rs41923484; g.2141C>G) are: L — 0.319 and V — 0.681; LL — 8.6%, LV — 46.6% and VV — 44.8% (n=58), population is in Hardy-Weinberg equilibrium. The studied population is close to beef herds of Russian selection. It was found a positive correlation of L-allele with birth weight within the moderate climatic zone (*r*=0.93).

Keywords: Aberdeen-Angus breed, growth hormone gene, SNP L127V

Introduction. Bovine growth hormone (*bGH*) belongs to a family of somatotrophic hormones. It is a single polypeptide chain with 190 or 191 amino acids and molecular weight 22 kDa (Salces et al., 2011). Growth hormone has an effects on growth and metabolism by interacting with specific receptor on the surface of target cells. *bGH* gene is located in 19 BTA and consists of five exons separated by four introns (Hadi et al., 2015). *bGH* plays a vital role in regulation of body weight, fertility and lactation performance of cattle. Therefore, SNPs in *bGH* gene can be used as predictors of growth, meat or milk production traits for supporting marked-assisted selection programs in cattle.

To date there are following SNPs of *bGH* gene investigated in cattle: four (253 C>T, 303 C>T, 502 C>T, and 559 G>A) in the promoter, one (679 C>T) in exon 1, one (1,692 T>C) in intron 3 four (2141 C>G, 2258 C>T, 2277 C>T, and 2291 A>C) in exon 5 (Lee et al., 2013) and one (C/T in 40.5 Mb locus) in intron 4, which could be used to differentiate humped (*B. indicus*) from humpless (*B. taurus*) cattle (Thomas et al., 2007).

Considering a multiple effect of *bGH* on growth and lactation processes SNPs of *bGH* gene was studied

both in beef and dairy breeds: Aberdeen Angus — in Japan, USA, Brazil (Chikuni et al., 1991; Ge et al., 2003; Vasconcellos et al., 2003), Simmental and Hereford — in Lithuania (Krasnopiorova et al., 2012), Charolais — in Lithuania, Brazil (Krasnopiorova et al., 2012; Kemenes et al., 1999; Regitano et al., 1999), Limousin — in Lithuania, Indonesia (Krasnopiorova et al., Hartatik, 2013), Holstein — in Japan, Germany, Hungary, Poland, Lithuania, Iran (Chikuni et al., 1991; Hradecka et al., 2008; Balogh et al., 2009; Krasnopiorova et al., 2012; Hadi et al., 2015), Jersey — in Italy, Poland (Dario et al., 2008; Komisarek et al., 2011), Brangus — in Mexico (Thomas et al., 2007), Nellore — in Brazil (Kemenes et al., 1999), as well as endemic cattle breeds — in Philippines (Salces et al., 2011) and Korea (Lee et al., 2013). These *bGH* SNPs are associated with birth weight, weight gain, constitution, milk yield, fat, protein, fertility.

Studies of *bGH* SNP L127V in Ukrainian breeds were carried out in small populations of Aberdeen-Angus, Southern Beef, Polissian Beef (Kopylova et al., 2009; Kostenko, Starodub, 2011), Ukrainian Grey (Podoba et al., 2009; Mokhnachova et al., 2016), Volinian Beef (Bochkov et al., 2009), Holstein (Kopylova et al., 2009;

Hyl et al., 2011; Nekrasov et al., 2016), Ukrainian Black-and-White Dairy (Nekrasov et al., 2016), Ukrainian Red-and-White Dairy and Ukrainian Red Dairy (Kopylova et al., 2009).

The purpose of the study was to conduct a comparative analysis of the alleles and genotypes frequencies distribution for SNP *L127V* in the Aberdeen-Angus breeding herd in Kharkiv region and to compare obtained result with similar parameters of commercial herds from other countries.

Material and methods. The study object was Aberdeen-Angus breeding herd (n=58; cows: n=52, bulls: n=6) bred at PE 'Agrofirma Svitanok' (Kharkiv region, Ukraine). Evaluation of growth dynamics was conducted via the control weighing at birth and at the age of 8, 12, 15, 18 months, and 2, 3, 4, 5 years.

DNA was extracted from blood samples using DNA extraction kits 'Diatom DNA Prep 100' (Isogene, Russian Federation). PCR-RFLP methods were set up for the SNP genotyping using primer pairs (Lee et al., 2013) and restriction endonuclease AluI ('Fermentas', Lithuania). The digested fragments were electrophoresed on 2.0% agarose gel.

The genetic distance between the studied population and data known from the literature was determined according to Nei (1972). The deviation of allele frequencies from Hardy-Weinberg equilibrium was tested using Pearson's chi-squared test. Normality test assessment was used for data distribution. Pearson's correlation coefficient *r* was used to measure the strength of association between two characteristics. Means for more than two groups were compared by ANOVA. The statistical hypotheses were tested on the significance level of 0.05 (Atramentova, Utevskaia, 2008).

Results. According to the literature the preferred allele is *L-allele*, as it is associated with higher birth weight (Lee et al., 2013; Thomas et al., 2007) and mature weight, marbling (Gill et al., 2009).

Allele and genotype frequencies of SNP *L127V* and its deviation from the Hardy-Weinberg equilibrium for studied Aberdeen-Angus herd are given in Table 1.

Table 1 – Allele and genotype frequencies of SNP *L127V* in the Aberdeen-Angus herd in Kharkiv region

Parameter	<i>L127V</i>		
	<i>L</i>	<i>V</i>	
Allele frequencies			
Cows (n=52)	0.333	0.667	
Bulls (n=6)	0.167	0.833	
Total (n=58)	0.319	0.681	
Genotype frequencies	<i>LL</i>	<i>LV</i>	<i>VV</i>
Cows (n=52)			

<i>n_{act.}</i>	5	25	22
%	9.6	48.1	42.3
<i>n_{exp.}</i>	5.9	23.2	22.9
%	11.3	44.6	44.1
Statistics	$\chi^2_{act.} = 0.16; p > 0.05$		
Bulls (n=6)			
<i>n_{act.}</i>	0	2	4
%	0.0	33.3	66.7
<i>n_{exp.}</i>	0.2	1.7	4.1
%	2.8	27.8	69.4
Statistics	$\chi^2_{act.} = 0.20; p > 0.05$		
Total (n=58)			
<i>n_{act.}</i>	5	27	26
%	8.6	46.6	44.8
<i>n_{exp.}</i>	5.9	25.2	26.9
%	10.2	43.4	46.4
Statistics	$\chi^2_{act.} = 0.15; p > 0.05$		

Note: df=2, $\Sigma\chi^2_{st.0.05} = 5.99$.

Data given in Table 1 suggest that studied population was found to be in equilibrium state. Consequently, there are no evidence of increasing preferred allele frequency without targeted selection.

Three genotype groups separated by SNP *L127V* were compared via body weight dynamics from birth to the age of five years (Table 2).

Table 2 – Body weight dynamics in Aberdeen-Angus by SNP *L127V*, $x \pm s_x$

Age	Weight, kg		
	<i>L127V</i>		
	<i>LL</i>	<i>LV</i>	<i>VV</i>
Birth	35.2±1.3*	30.4±1.0*	29.9±0.9*
Average daily gain, kg/day	0.763±0.54	0.771±0.15	774±19
8 months	220.8±15.3	213.3±4.7	208.7±4.1
12 months	288.8±18.6	280.4±4.4	272.8±6.0
15 months	342.0±19.8	324.0±4.9	318.9±4.4
18 months	380.8±24.9	369.1±6.2	362.6±4.1
2 years	421.4±19.0	416.2±6.6	413.1±7.1
3 years	460.3±22.8	446.9±8.5	446.8±10.3
4 years	505.0±18.1	488.7±9.8	479.9±10.9
5 years	588.0±40.0	557.0±19.8	579.8±21.8

Note: $x \pm s_x$ — mean ± standard error; * — differences are significant at $p < 0.05$

Table 3 – Genotype and allele frequencies at SNP *L127V* in the beef cattle populations by climate zones (longitudinal length)

Breed	Breed characteristics	Country	Longitudinal length	n	Genotypes, %				Alleles			HWE	Reference	D
					LL	LV	VV	L	L	V				
Beef or beef-dairy breeds														
Aberdeen-Angus	CLM=500–700 kg BLM=750–1000 kg BW=16–25 kg	Ukraine	49° N	58	8.6	46.6	44.8	0.319	0.681	0.681	E	Present study	—	
		Ukraine	49° N	9	11.1	55.6	33.3	0.389	0.611	0.611	E	Kostenko et al., 2011	0.005	
		Ukraine	49° N	10	60.0	40.0	0.0	0.800	0.200	0.200	E	Kopylova et al., 2009	0.428	
		USA	40° N	468	34.4	55.1	10.5	0.620	0.380	0.380	DE	Geet et al., 2003	0.163	
		Japan	35° N	6	33.3	50.0	16.7	0.590	0.410	0.410	E	Chikuniet al., 1991	0.130	
		Brazil	11° S	52	—	—	—	0.770	0.230	0.230	—	Vasconcellos, 2003	0.378	
Auliekol	CLM=540–560 kg BLM=950–1050 kg	Kazakhstan	48° N	50	—	—	—	0.640	0.360	0.360	—	Beysnova et al., 2016	0.188	
Charolais	CLM=600–700 kg BLM=1000–1200 kg BW=40–45 kg	Lithuania	55° N	—	75.0	20.0	5.0	0.850	0.150	0.150	E	Krasnopiorova et al., 2012	0.516	
		Brazil	11° S	32	—	—	—	0.720	0.280	0.280	—	Kemenes et al., 1999	0.299	
		Brazil	11° S	36	—	—	—	0.736	0.264	0.264	—	Regitanoet al., 1999	0.323	
Hanwoo	CLM=550–600 kg	South Korea	36° N	231	84.8	11.7	3.5	0.907	0.093	0.093	E	Lee et al., 2013	0.622	
Hereford	CLM=650–850 kg BLM=900–1350 kg BW=28–35 kg	Lithuania	55° N	—	90.0	0.0	10.0	0.900	0.100	0.100	DE	Krasnopiorova et al., 2012	0.608	
		Japan	35° N	10	70.0	20.0	10.0	0.800	0.200	0.200	E	Chikuni et al., 1991	0.428	
Indigenous Philippine Cattle	CLM=300–400 kg	Philippines	13° N	55	20.0	45.0	35.0	0.430	0.570	0.570	E	Salces et al., 2011	0.017	
Kalmyk	CLM=420–480 kg BLM=750–950 kg BW=20–25 kg	Russia	60° N	60	1.7	20.0	78.3	0.117	0.883	0.883	E	Sulimova et al., 2011	0.057	
		Russia	60° N	79	5.1	31.6	63.3	0.209	0.791	0.791	E	Sulimova et al., 2011	0.021	
Kazakh White-headed	CLM=540–580 kg BLM=850–950 kg BW=27–30 kg	Lithuania	55° N	—	58.3	11.1	30.6	0.639	0.361	0.361	DE	Krasnopiorova et al., 2012	0.186	
		Indonesia	5° S	6	66.67	33.33	0.0	0.830	0.170	0.170	E	Hartatik et al., 2013	0.480	
Limousin	CLM=550–600 kg BLM=1000–1100 kg BW=34–42 kg	Indonesia	5° S	81	81.5	18.5	0.0	0.910	0.090	0.090	E	Hartatik et al., 2013	0.627	

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Limousin-Ongole crossbred	—	Indonesia	5° S	56	78.6	21.4	0.0	0.890	0.110	E	Hartatik et al., 2013	0.590
Madura	BLM=250–300 kg	Indonesia	5° S	65	100.0	0.0	0.0	1.000	0.000	—	Hartatik et al., 2013	0.802
Mongolian cattle (beef-dairy)	—	Russia	60° N	47	0.0	25.0	75.0	0.125	0.875	E	Sulimova et al., 2011	0.053
Polissian Beef	CLM=550–600 kg BLM=900–1000 kg BW=28–32 kg	Ukraine	49° N	13	69.2	23.1	7.7	0.807	0.193	E	Kostenko et al., 2011	0.440
Simmental	CLM=550–900 kg BLM=850–1300 kg BW=34–36 kg	Lithuania	55° N	—	50.0	12.5	37.5	0.563	0.438	DE	Krasnopiorova et al., 2012	0.102
Southern Beef	CLM=550–650 kg BLM=950–1100 kg BW=25–30 kg	Ukraine	49° N	8	87.5	12.5	0.0	0.937	0.063	E	Kostenko et al., 2011	0.679
		Ukraine	49° N	21	61.9	38.1	0.0	0.810	0.190	E	Kopylova et al., 2009	0.445
Ukrainian Grey	CLM=450–500 kg BLM=800–850 kg BW=27–30 kg	Ukraine	49° N	84	98.0	2.0	0	0.980	0.020	E	Mokhnachova et al., 2016	0.763
		Ukraine	49° N	51	—	—	—	0.706	0.294	—	Podoba et al., 2009	0.278
Volinian Beef (breeding herd)	CLM=500–550 kg	Ukraine	49° N	27	56.0	44.0	0.0	0.778	0.222	E	Bochkov et al., 2009	0.391
Volinian Beef (production herd)	BLM=950–1050 kg BW=28–32 kg	Ukraine	49° N	41	34.0	44.0	22.0	0.561	0.439	E	Bochkov et al., 2009	0.101
Wagyu	CLM=450–500 kg	Japan	35° N	25	24.0	40.0	36	0.440	0.560	E	Chikuni et al., 1991	0.020
Zeboid hybrid	—	Russia	60° N	95	3.2	37.9	58.9	0.222	0.778	E	Sulimova et al., 2011	0.018

Note: CLW — cow live weight, BLW — bull live weight, BW — birth weight; HWB — Hardy-Weinberg equilibrium; E — equilibrium, DE — disequilibrium; D — Nei's genetic distance.

The differences between the groups in birth weight were 4.8–5.2 kg or 14.6–16.1% ($p < 0.05$). Group *LL* was superior to *LV* or *VV* growth at each time point, although the growth dynamics between groups was comparable. The differences in the live weight decreased over time and were 3–25 kg or 1–5% between *LL* and *LV* groups, and 10–25 kg, or 2–7% between *LL* and *VV* groups.

Our findings are consistent with the results obtained by Lee et al. (2013) and Thomas et al. (2007): birth weight of *LL*-animals was eventually greater. In beef cattle *L*-allele was associated with a higher body weight and marbling score (Gill et al., 2009).

Literature data on beef cattle populations in the world are summarized in Table 3.

Mostly, literature data suggest that analyzed populations were in a state of equilibrium, except Simmental, Limousine, Hereford in Lithuania and Aberdeen-Angus in USA. Observed disequilibrium may be a consequence of an unbalanced number of heterozygous animals.

The different breeds in Russia show a low frequency of allele *L* (Sulimova et al., 2011), presumably, to be determined by long-term selection in indigenous isolated populations. Alternatively, the *L*-allele frequency in different breeds within equatorial zone is high (Hartatik et al., 2013, Lee et al., 2013). Smaller animal size, being characteristic for this climate zone according to the Bergman's rule, can therefore support a size increasing due to long-term selection, resulting to *L*-allele frequency increase.

Since the *L*-allele is associated with a higher body weight, correlation analysis for this allele frequency vs. different species birth and mature weight within a single

zone climate was carried out. A positive correlation of *L*-allele with birth weight ($r = 0.93, p < 0.05$) was established for different breeds within the moderate climatic zone. In general, Ukrainian breeds are similar for mature weight (the differences do not exceed 50–100 kg) and the *L*-allele frequency. The last observation is supported by our data on growth dynamics, where effect of *bGH* is mostly pronounced before till two-year age.

There was a trend to increasing *L*-allele frequency with decreasing latitude for Limousine and Aberdeen-Angus breeds, while the reverse trend was observed for Charolais and Hereford breeds. That is the last larger breeds (average CLW=650 kg, BLW=1200 kg) in the warmer climate show decrease in *L*-allele frequency being associated with decrease of animal body size in warm climate. Smaller breeds, Limousine and Aberdeen-Angus, (up to CLW=600 kg, BLW=800–1000 kg) demonstrate more stable allele frequencies with a tendency to a slight increase. Regardless of the region, the breed (being introduced worldwide) demonstrates stable *L*-allele frequency to be typical for the breed.

Nei's genetic distances showed that the closest to the studied population was the Ukrainian Aberdeen-Angus population (Kostenko et al., 2011) and some breeds of Russian selection (Sulimova et al. 2011). The highest differences, over 0.65, are observed for breeds of Ukrainian selection — Southern Beef and Ukrainian Grey, as well as for Madura (Hartatik et al., 2013).

Conclusion. The preferred allele frequency of SNP *L127V* was 0.319. The studied population is close to beef herds of Russian selection. It was found a positive correlation of *L*-allele with birth weight within the moderate climatic zone ($r = 0.93$).

References

- Atramentova, L. A. and Utevskaia, A. M. (2008) *Statistical methods in biology [Statisticheskie metody v biologii]*. Gorlovka: Likhtar. ISBN 9789662129267. [in Russian].
- Balogh, O., Kovács, K., Kulcsár, M., Gáspárdy, A., Zsolnai, A., Kátai, L., Pécsi, A., Fésüs, L., Butler, W. R. and Huszenicza, G. (2009) 'AluI polymorphism of the bovine growth hormone (GH) gene, resumption of ovarian cyclicity, milk production and loss of body condition at the onset of lactation in dairy cows', *Theriogenology*, 71(4), pp. 553–661. doi: 10.1016/j.theriogenology.2008.06.032.
- Beyshova, I. S., Nametov, A. M. and Terletskiy, V. P. (2016) 'Development of genetic markers for productivity traits in beef pedigree cattle of Auliekol and Kazakh white head breeds' [Razrabotka geneticheskikh markerov dlya priznakov myasnoy produktivnosti plemennogo krupnogo rogatogo skota Auliekol'skoy i Kazakhskoy belogolovoy porod], *Veterinary, Zootechnics and Biotechnology [Veterinariya, zootekhnika i biotekhnologiya]*, 1, pp. 36–42. Available at: <http://elibrary.ru/download/71223733.htm>. [in Russian].
- Bochkov, V. M., Luniova, A. E., Tarasiuk, S. I. and Nasyrova, I. A. (2009) 'Genetic structure of Volynian beef breed of cattle by the somatostatin polymorphic variant' [Henetychna struktura za polimorfizmom somatotropnogo hormonu volynskoi m'iasnoi porody velykoi rohatoi khudoby], *Scientific Bulletin of National University of Life and Environmental Sciences [Naukovyi visnyk Natsionalnoho universytetu bioresursiv i pryrodokorystuvannia Ukrainy]*, 138, pp. 332–336. Available at: http://www.nbu.gov.ua/old_jrn/Chem_Biol/nvnu/2009_138/09bvm.pdf. [in Ukrainian].
- Chikuni, K., Terada, F., Kageyama, S., Koishikawa, T., Kato, S. and Ozutsumi, K. (1991) 'Identification of DNA sequence variants for amino acid residues 127 of bovine growth hormone using the polymerase chain reaction method', *Animal Science and Technology [Nihon Chikusan Gakkaiho]*, 62(7), pp. 660–666. doi: 10.2508/chikusan.62.660. [in Japanese].
- Dario, C., Carnicella, D., Ciotola, F., Peretti, V. and Bufano G. (2008) 'Polymorphism of growth hormone GH1-AluI in

- Jersey Cows and its effect on milk yield and composition, *Asian-Australasian Journal of Animal Sciences*, 21(1), pp. 1–5. doi: 10.5713/ajas.2008.60586.
- Ge, W., Davis, M. E., Hines, H. C., Irvin, K. M. and 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), pp. 641–648. doi: 10.2527/2003.813641x.
- Gill, J. L., Bishop, S. C., McCorquodale, C., Williams, J. L. and Wiener, P. (2009) 'Association of selected SNP with carcass and taste panel assessed meat quality traits in a commercial population of Aberdeen Angus-sired beef cattle', *Genetics Selection Evolution*, 41(1), pp. 36. doi: 10.1186/1297-9686-41-36.
- Hadi, Z., Atashi, H., Dadpasand, M., Derakhshandeh, A. and Ghahramani Seno, M. M. (2015) 'The relationship between growth hormone polymorphism and growth hormone receptor genes with milk yield and reproductive performance in Holstein dairy cows', *Iranian Journal of Veterinary Research*, 16(3), pp. 244–248. Available at: <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4782692/pdf/ijvr-16-244.pdf>.
- Hartatik, T., Volkandari, S. D., Rachman, M. P. and Sumadi (2013) 'Polymorphism leu/val of growth hormone gene identified from limousin cross local cattle in Indonesia', *Procedia Environmental Sciences*, 17, pp. 105–108. doi: 10.1016/j.proenv.2013.02.017.
- Hradecká, E., Čítek, J., Panicke, L., Řehout, V. and Hanusová, L. (2008) 'The relation of GH1, GHR and DGAT1 polymorphisms with estimated breeding values for milk production traits of German Holstein sires', *Czech Journal of Animal Science*, 53(6), pp. 238–245. Available at: <http://www.agriculturejournals.cz/publicFiles/01545.pdf>.
- Hyl, M. I., Horodna, O. V., Kramarenko, S. S. and Smetana, O. Yu. (2011) 'Analysis of cow milk production dependence on polymorphic variants of separate structure genes' [Analiz zalezhnosti molochnoi produktyvnosti koriv vid polimorfizmu okremykh strukturnykh heniv], *Scientific Bulletin of National University of Life and Environmental Sciences [Naukovyi visnyk Natsionalnoho universytetu bioresursiv i pryrodokorystuvannia Ukrainy]*, 160(2), pp. 285–293. Available at: http://www.nbu.gov.ua/old_jrn/Chem_Biol/nvnau_tvpp/2011_160_2/11gmi.pdf. [in Ukrainian].
- Kemenes, P. A., Regitano, L. C. de A., Rosa, A. J. de M., Packer, I. U., Razook, A. G., Figueiredo, L. A. de, Silva, N. A., Etchegaray, M. A. L. and Coutinho, L. L. (1999) 'k-Casein, b-lactoglobulin and growth hormone allele frequencies and genetic distances in Nelore, Gyr, Guzerá, Caracu, Charolais, Canchim and Santa Gertrudis cattle', *Genetics and Molecular Biology*, 22(4), pp. 539–541. doi: 10.1590/s1415-47571999000400012.
- Komisarek, J., Michalak, A. and Walendowska, A. (2011) 'The effects of polymorphisms in DGAT1, GH and GHR genes on reproduction and production traits in Jersey cows', *Animal Science Papers and Reports*, 29(1), pp. 29–36. Available at: <http://archiwum.ighz.edu.pl/files/objects/7501/66/strona29-36.pdf>.
- Kopylova, K. V., Kopylov, K. V. and Arnaut, K. O. (2009) 'Genetic structure characteristics of cattle by Quantitative traits loci (QTL)' [Osoblyvosti henetychnoi struktury riznykh porid velykoi rohatoi khudoby za lokusamy kilkisnykh oznak (QTL)], *Scientific Bulletin of National University of Life and Environmental Sciences [Naukovyi visnyk Natsionalnoho universytetu bioresursiv i pryrodokorystuvannia Ukrainy]*, 138, pp. 239–245. Available at: http://www.nbu.gov.ua/old_jrn/Chem_Biol/nvnau/2009_138/09kkv.pdf. [in Ukrainian].
- Kostenko, S. O. and Starodub, L. F. (2011) 'Prediction of beef breeds bulls productivity based on cytogenetic and molecular genetic markers' [Prohnoz produktyvnosti buhava miasnykh porid na osnovi tsytohetychnykh ta molekuliarno-henetychnykh markeriv], *Scientific Bulletin of National University of Life and Environmental Sciences [Naukovyi visnyk Natsionalnoho universytetu bioresursiv i pryrodokorystuvannia Ukrainy]*, 160(2), pp. 266–273. Available at: http://www.nbu.gov.ua/old_jrn/Chem_Biol/nvnau_tvpp/2011_160_2/11slv.pdf. [in Ukrainian].
- Krasnopiorova, N., Baltreinaite, L. and Miceikiene, I. (2012) 'Growth hormone gene polymorphism and its influence on milk traits in cattle bred in Lithuania' *Veterinarija ir Zootechnika*, 58, pp. 42–46. Available at: <http://vetzoo.lsmuni.lt/data/vols/2012/58/pdf/krasnopiorova.pdf>.
- Lee, J.-H., Lee, Y.-M., Oh, D.-Y., Jeong, D.-J. and Kim, J.-J. (2013) 'Identification of single nucleotide polymorphisms (SNPs) of the bovine growth hormone (*bGH*) gene associated with growth and carcass traits in Hanwoo', *Asian-Australasian Journal of Animal Sciences*, 26(10), pp. 1359–1364. doi: 10.5713/ajas.2013.13248.
- Mokhnachova, N., Suprovich, T., Dobrynska, M. and Fursa, N. (2016) 'Characteristics of Ukrainian Grey cattle by DNA-markers' [Kharakterystyka Siroi ukrainskoi porody velykoi rohatoi khudoby za DNK-markerany], *Animal Breeding and Genetics [Rozvedennia i henetyka tvaryn]*, 51, pp. 283–289. Available at: http://digest.iabg.org.ua/images/digest/51/Animal_breeding_and_genetics_51.pdf. [in Ukrainian].
- Nei, M. (1972) 'Genetic distance between populations', *The American Naturalist*, 106(949), pp. 283–292. doi: 10.1086/282771.
- Nekrasov, A. A., Popov, A. N., Popov, N. A. and Fedotova, E. G. (2016) 'Impacts of milk protein and hormone gene polymorphisms on energy for growth of Holstein Black-and-White heifers' [Vliyanie polimorfizma genov molochnykh belkov i gormonov na energiyu rosta telok Chernopestroy Golshtinskoy porody], *Tavric Scientific Review [Tavricheskiy nauchnyy obozrevatel']*, 5(2), pp. 91–95. Available at: <http://elibrary.ru/download/12725655.pdf>. [in Russian].
- Podoba, B. Ye., Arnaut, K. O., Kovtun, S. I. and Shcherbak, O. V. (2009) 'Study of Ukrainian Grey breed by genetic markers and embryotechnological approaches' [Doslidzhennia henofondu siroi ukrainskoi porody za henetychnymy markeramy ta embriotekhnologichnymy

pidkhodamy], *Scientific Bulletin of National University of Life and Environmental Sciences [Naukovyi visnyk Natsionalnoho universytetu bioresursiv i pryrodokorystuvannia Ukrainy]*, 138, pp. 234–239. Available at: http://www.nbu.gov.ua/old_jrn/Chem_Biol/nvnau/2009_138/09pbe.pdf. [in Ukrainian].

Regitano, L. C. A., Azevedo, J. L., Vencovsky, R., Packer, I. U., Barbosa, P. F., Rosa, A. J. M., Silva, N. A., Etchegaray, M. A. L. and Coutinho, L. L. (1999) 'Selection for breed-specific growth hormone and IGF-I alleles in a synthetic beef cattle cross, Canchim', *Genetics and Molecular Biology*, 22(4), pp. 531–537. doi: 10.1590/s1415-47571999000400011.

Salces A. J., Icalia, P. J. C., Mendioro, M. S. and Sevilla, C. C. (2014) 'SNP analysis of the growth hormone gene in indigenous Philippine cattle, Ilocos genetic group by PCR-RFLP', *Proceedings of the 10th World Congress on Genetics Applied to Livestock Production*, 17–22 August, 2014, Vancouver, BC, Canada, pp. 515. Available at: <https://asas.confex.com/asas/WCGALP14/webprogram/Paper10015.html>.

Sulimova, G. E., Fedunin, A. A., Klimov, E. A. and Stolpovski, Yu. A. (2011) 'Evaluation of cattle genetic potential of for traits of good quality meat on the basis of DNA-markers' [Otsenka geneticheskogo potentsiala otechestvennogo skota po priznakam vysokogo kachestva myasa na osnove DNK-markernykh sistem], *Problems of productive animal biology [Problemy biologii produktivnykh zivotnykh]*, 1, pp. 62–64. Available at: <http://elibrary.ru/item.asp?id=16092146>. [in Russian].

Thomas, M. G., Enns, R. M., Shirley, K. L., Garcia, M. D., Garrett, A. J. and Silver, G. A. (2007) 'Associations of DNA polymorphisms in growth hormone and its transcriptional regulators with growth and carcass traits in two populations of Brangus bulls', *Genetics and Molecular Research*, 6(1), pp. 222–237. Available at: <http://www.funpecrp.com.br/gmr/year2007/vol1-6/pdf/gmr0277.pdf>.

Vasconcellos, L. P. de M. K., Tambasco-Talhari, D., Pereira, A. P., Coutinho, L. L. and Regitano, L. C. de A. (2003) 'Genetic characterization of Aberdeen Angus cattle using molecular markers', *Genetics and Molecular Biology*, 26(2), pp. 133–137. doi: 10.1590/s1415-47572003000200005.