Conference Paper

DNA Markers for Meat Quality of Pigs

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Abstract

This paper presents the results of determining genotypes of 3-breed pig hybrids (Landrace x Yorkshire x Duroc) by marker genes MC4R (melanocortin receptor-4 gene), IGF2 (insulinoid growth factor-2), POU1F1 (pituitary transcription factor), H-FABP (protein gene binding fatty acids), GH (growth hormone gene), LEP (leptin gene) and their interrelation with meat productivity. Allele frequencies for the studied genes were determined (MC4R: A = 0.58, G = 0.42; IGF2: Q = 0.96, q = 0.04; POU1F1: E = 0.66, F = 0.34; H-FABP: D = 0.38, d = 0.62; GH: A = 0.26, G = 0.74; LEP: C = 0.27, T = 0.73). The study showed that 3-breed hybrids did not have the highest level of heterozygosity in most allelic genes. MC4R (AG = 48%), POU1F1 (EF = 68%) and H-FABP (Dd = 52%) genes had the greatest number of heterozygotes; IGF2 (QQ = 92%), GH (GG = 58%) and LEP (TT = 56%) genes had the greatest number of homozygotes. The data showed that the breeds used to obtain three-breed hybrids were selected for analogous (meat quality) traits and that they had a higher frequency of the desired Q (IGF2), G (GH) and T (LEP) gene alleles, which were lost from hybrids in the homozygous condition. We identified the most desirable genotypes for the studied genes (GGMC4R, AGMC4R, QQIGF2, EFPOU1F1, DDH-FABP, AAGH, CTLEP) which are recommended for pig selection as well as for selection of parent pairs for producing commercial hybrids with high meat productivity.

Keywords: gene-dependent selection, slaughter and meat qualities of pigs, marker genes, MC4R, IGF2, POU1F1, H-FABP, GH, LEP

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1. Introduction

In farm animal breeding new methods of estimation and selection along with the traditional ones are used. New methods of animal estimation include modern DNA technologies that allow identifying genes directly or indirectly related to economic traits.

By now there have been identified a number of DNA markers associated with economic traits or hereditary and other diseases. However the studies have not been finalized yet and need to be continued to clarify the action of promising gene markers and to search for the new ones that are optimal when used in breeding.

The study was intended to determine interrelation of genotypes of 3-breed pig hybrids (L x Y x D) by MC4R, IGF2, POU1F1, H-FABP, GH and LEP genes and their meat productivity.

2. Methods and Equipment

To conduct the research, samples of muscle tissue from 50 3-breed hybrids were taken after slaughter within the meat-processing plant “VEPOZ” (Rostov-on-Don). When estimating meat productivity we considered carcass weight (kg), length of the half carcass and bacon side (cm), fat depth (mm) - on the withers above spinous processes of the 6-7th thoracic vertebrae, above the last rib and the 1st, 2nd and 3rd sacral vertebrae.

DNA genotyping by the previously mentioned genes was carried out using traditional PCR techniques at the laboratory of molecular diagnostics and biotechnology of farm animals at Don State Agrarian University.

The findings were biometrically processed using conventional methods.

3. Results

MC4R gene (melanocortin receptor-4 gene) affects regulation of energy homeostasis, precocity, feed consumption and fatness. We established (refer to the table 1) that by MC4R gene 34% of the gilts had AA-genotype, 48% - AG, 18% - GG. A allele frequency is 0.58, G allele frequency is 0.42.

In AG-genotype (MC4R) the peak carcass weight is 0.88 and 1.43 kg heavier than in AA- and GG-pigs ($P<0.95$). GG- and AA-pigs had the largest length of the half carcass which was respectively 2.92 ($P>0.99$) and 2.55 cm ($P>0.99$) larger than that in AG-pigs. Length of the bacon side in GG-pigs was respectively 1.63 ($P>0.999$) and 5.08 cm ($P>0.999$) larger than that in AG- and AA-pigs and length of the bacon side in AG-gilts was 3.45 cm ($P>0.999$) larger than that in AA-pigs. Fat depth above the last rib in AG- and GG-gilts was respectively 2.26 ($P>0.90$) and 2.65 mm ($P>0.99$) shorter than that in AA-gilts.

Fat depth above sacrum in AA-gilts was longer than that in AG- and GG-gilts: above the 1st sacral vertebra respectively 3.05 (P>0.99) and 3.07 mm (P>0.99) longer; above the 2nd sacral vertebra respectively 2.72 (P>0.95) and 2.09 mm (P>0.90) longer; above the 3rd sacral vertebra respectively 4.39 (P>0.99) and 2.40 mm (P<0.90) longer. Fat length above the 3rd sacral vertebra in GG-gilts was 1.99 mm (P>0.90) longer than that in AG-gilts.

IGF-2 gene (insulinoid growth factor-2) ID: 396916 is one of the most promising markers of meat-fattening productivity. By IGF2 gene we identified only 2 genotypes: QQ - 92%, Qq - 8% of pigs. Q allele frequency is 0.96, q allele frequency is 0.04. Carcass in Qq-pigs was 3.43 kg (P>0.90) heavier than in QQ-pigs. According to other indicators the superiority of Qq of pigs is clearly unreliable.

POU1F1 gene (pituitary transcription factor) is a regulating transcription factor of the anterior pituitary gland which effectively stimulates gene expression of growth hormone, prolactin and thyrotropic hormone. It is a quantitative trait locus (QTL) of growth rate and fatness. Two genotypes of pigs were identified by POU1F1 gene - 32% EE and 68% EF. E allele frequency is 0.66, F allele frequency is 0.34. For most indicators, the EF-pigs were superior to their FF-counterparts, but the difference was unreliable (P <0.90).

One of the genes determining meat quality in pigs is protein gene H-FABP binding fatty acids which have three types of allelic polymorphism (H-FABP^{a} H-FABP^{D} H-FABP^{H}) and controls carcass structure, intramuscular fat deposits and fat depth. In our experiment by genotypes of H-FABP gene pigs were proportioned as follows: DD - 12%, Dd - 52%, dd – 36%. DD-gilts had respectively 5.53 (P>0.99) and 6.13 kg (P=0.98) heavier carcass weight than Dd- and dd-gilts.. Significantly, DD-genotype gilts had the shortest fat depth at all measured depth points.

GH (growth hormone gene) (Gene ID: 3968840). Growth hormone (GH) is of a great importance for regulating growth processes, cell proliferation and differentiation of all mammalian species and is connected with abdominal fat content (A. Korwin-Kossakowska et al., 2001). We have reported that GH gene was represented with 3 genotypes: AA – 10%, AG – 32%, GG – 58%. Frequency of A- allele = 0.26, G = 0.74.

AA-gilts exceeded their GG- and AG-herd-mates in carcass weight, half carcass length, bacon side length, fat depth on withers, above spinous processes of the 6-7th thoracic vertebrae, above the last rib and the 3rd sacral vertebra by 6.77 (P<0.95) and 8.65 cm (P<0.99); 1.56 (P>0.90) and 2.36 cm (P<0.95); 1.23 (P<0.90) and 1.62 cm (P<0.95); 2.17 (P<0.90) and 3.32 mm (P<0.90); 2.82 (P<0.90) and 3.44 mm (P>0.95); 1,59 (P<0,90) and 2.11 mm (P>0.98); 0.21 (P<0.90) and 0.80 mm (P<0.90) relatively. The fat depth above the 1st sacral vertebra in AA-gilts was respectively 0.15 (P<0.9) and

0.33 mm (P<0.90) longer than that of their AG- and GG-herd-mates. GG-homozygotes had 1.88 heavier carcass weight (P<0.90) than their AG-herd-mates, and relatively 0.68 (P<0.90) and 1.04 mm (P<0.90) longer fat depth above the 2nd sacral vertebra than their AA- and AG-herd-mates.

AG-heterozygotes had lighter carcass weight, shorter half carcass length and bacon side length, shorter fat depth on withers, above spinous processes of 6-7th thoracic vertebrae, above the last rib and the 2nd and 3rd sacral vertebrae than their AA- and GG-genotype herd-mates. GG-gilts had the shortest fat depth above the 1st sacral vertebra.

Table 1: Meat qualities in gilts of different genotypes by MC4R, IGF2, POU1F1, H-FABP, GH and LEP genes

Genotype by genes	Carcass weight, kg	Half carcass length, cm	Bacon side length, cm	Fat depth, mm					
				On the withers	Above spinous processes of the 6-7th thoracic vertebrae	Above the last rib	Above sacrum		
							Above the 1st vertebra	Above the 2nd vertebra	Above the 3rd vertebra
1	2	3	4	5	6	7	8	9	10
MC4R									
AA M±m n=17 δ Cv	78.82±2.18	100.3±0.71	79.59±0.58	35.24±1.17	22.94±0.88	20.76±0.71	15.18±0.79	15.76±0.88	19.18±1.08
	8.73	2.83	2.33	4.67	3.5	2.83	3.17	3.5	4.33
	11.08	2.82	2.93	13.25	15.26	13.36	20.88	22.21	22.58
AG M±m n=24 δ Cv	79,70±1,6	97.75±0.52	83.04±0.42	34.04±0.83	21.63±1	18.5±0.97	12.13±0.63	13.04±0.63	14.79±0.80
	7.68	2.5	2	4	4.83	4.67	3	3	3.83
	9.64	2.56	2.41	11.75	22.33	25.24	24.73	23.01	25.90
GG M±m n=9 δ Cv	78.27±2.69	100.67±0.82	84.67±0.65	36.44±1.30	23.78±1.47	18.11±0.59	12.11±0.50	13.67±0.53	16.78±0.71
	7.62	2.33	1.83	3.67	4.17	1.67	1.33	1.5	2
	9.74	2.31	2.16	10.07	17.54	9.22	10.98	10.97	11.92
IGF2									
QQ M±m n=46 δ Cv	78.37±1.92	99.24±0.66	84.09±0.58	34.80±0.93	22.37±0.90	19.24±0.74	13.22±0.72	14.07±0.76	17.20±0.93
	13.05	4.44	3.91	6.29	6.14	5.02	4.91	5.16	6.30
	16.65	4.48	4.66	18.07	27.43	26.10	37.16	36.67	36.63
Qq M±m n=4 δ Cv	81.8±1.66	98±1.16	83.5±0.87	33.5±2.31	23.5±2.50	18.75±1.54	12.5±1.54	14.25±1.54	17.5±2.02
	2.88	2	1.5	4	4.33	2.67	2.67	2.67	3.5
	3.27	2.04	1.80	11.94	18.43	14.24	21.36	18.74	20.00
POU1F1									
EE M±m n=16 δ Cv	76.02±1.74	98.88±0.60	83.5±0.47	35.44±0.73	23.06±0.86	19.06±0.52	13.81±0.47	15.38±0.65	18.5±0.65
	6.75	2.33	1.83	2.83	3.33	2	1.83	2.5	2.5
	8.88	2.36	2.19	7.99	14.44	10.49	13.25	16.25	13.51
1	2	3	4	5	6	7	8	9	10

Genotype by genes	Carcass weight, kg	Half carcass length, cm	Bacon side length, cm	Fat depth, mm					
				On the withers	Above spinous processes of the 6-7th thoracic vertebrae	Above the last rib	Above sacrum		
							Above the 1st vertebra	Above the 2nd vertebra	Above the 3rd vertebra
1	2	3	4	5	6	7	8	9	10
POU1F1									
	13.63	4.57	4.15	7.28	7.14	5.71	5.65	5.71	7.22
	16.91	4.61	4.93	21.04	32.18	29.65	43.98	42.40	42.70
H-FABP									
DD M±m n=6 δ Cv	84.23±1.16	97.83±0.97	83±0.67	34.67±1.42	21±1.26	18.17±1.04	11.67±1.04	12.83±1.34	16.17±1.42
	2.6	2.17	1.5	3.17	2.83	2.33	2.33	3	3.17
	3.09	2.22	1.81	9.14	13.48	12.82	19.97	23.38	19.60
Dd M±m n=26 δ Cv	78.70±1.52	98.88±0.6	83.85±0.57	34.85±0.8	22.77±0.83	19.54±0.77	13.15±0.53	14.15±0.57	17.77±0.67
	7.62	3	2.83	4	4.17	3.83	2.67	2.83	3.33
	9.68	3.03	3.38	11.48	18.31	19.60	20.30	20	18.74
dd M±m n=18 δ Cv	78.1±2.15	99.94±0.65	84.67±0.65	35±1.29	22.5±1.17	19.1±0.85	13.67±0.77	14.39±0.85	17.33±1.05
	8.85	2.67	2.67	5.33	4.83	3.5	3.17	3.5	4.33
	11.33	2.67	3.15	15.23	21.47	18.32	23.19	24.32	24.99
GH									
AA M±m n=5 δ Cv	85.84±2.54	100.8±0.84	85.4±0.59	37.2±1.84	25.2±1.25	20.8±0.59	13.4±0.25	13.8±1.25	17.8±0.59
	5.07	1.67	1.17	3.67	2.5	1.17	0.5	2.5	1.17
	5.91	1.66	1.37	9.87	9.92	5.63	3.73	18.12	6.57
AG M±m n=16 δ Cv	77.19±1.32	98.44±0.60	83.78±0.43	33.88±0.90	21.765±0.73	18.69±0.56	13.25±0.65	13.44±0.78	17±0.90
	5.12	2.33	1.67	3.5	2.83	2.17	2.5	3	3.5
	6.63	2.37	1.99	10.33	13.04	11.61	18.87	22.32	20.59
GG M±m n=29 δ Cv	79.07±1.67	99.24±0.60	84.17±0.53	35.03±0.85	22.38±0.91	19.21±0.88	13.07±0.66	14.48±0.69	17.59±0.79
	8.85	3.17	2.83	4.5	4.83	4.67	3.5	3.67	4.17
	11.19	3.19	3.36	12.85	21.58	24.31	26.78	25.35	23.71
LEP									
CC M±m n=5 δ Cv	84.12±2.17	99.8±0.25	84.2±0.25	38.6±1.00	25±2.09	22.6±1.5	15.2±1	17.6±1.42	21.6±1.5
	4.33	0.50	0.5	2	4.17	3	2	2.83	3
	5.15	0.50	0.59	5.18	16.68	13.74	13.16	16.08	13.89
TC M±m n=17 δ Cv	81.23±2.18	100.47±0.79	85.41±0.67	33.06±0.88	21.06±1.04	18.88±1	12.88±0.88	13.12±0.88	16.24±1.08
	8.73	3.17	2.67	3.5	4.17	4	3.5	3.5	4.33
	10.75	3.16	3.13	10.59	19.80	21.19	27.17	26.68	26.66
TT M±m n=28 δ Cv	76.81±1.44	98.21±0.48	83.18±0.42	35.32±0.90	22.86±0.67	18.79±0.54	12.96±0.48	14.04±0.48	17.39±0.51
	7.47	2.5	2.17	4.67	3.5	2.83	2.5	2.5	2.67
	9.73	2.55	2.61	13.22	15.31	15.06	19.29	17.81	15.35

Genotype by genes	Carcass weight, kg	Half carcass length, cm	Bacon side length, cm	Fat depth, mm					
				On the withers	Above spinous processes of the 6-7th thoracic vertebrae	Above the last rib	Above sacrum		
							Above the 1st vertebra	Above the 2nd vertebra	Above the 3rd vertebra
1	2	3	4	5	6	7	8	9	10

LEP gene is one of prospective candidate genes to estimate the growth and fat efficiency. Leptin produced primarily by adipocytes acts as a central regulator of fat content in the body by suppressing appetite and increasing energy consumption through decreasing the production of neuropeptide-Y in the arcuate nucleus of the hypothalamus. Leptin has a significant impact on gustatory cells. It may result in inhibiting eating.

We have found out that by LEP gene pigs were distributed according to the following genotypes: CC – 10%, CT – 34%, TT – 56%. C-allele rate = 0.27, T = 0.73. CC-pigs had 2.89 ($P<0.90$) and 7.31 kg ($P>0.99$) heavier carcass weight; 5.54 ($P>0.99$) and 3.28 mm ($P>0.95$) longer fat depth on withers; 3.94 ($P<0.90$) and 2.14 mm ($P<0.90$) above spinous processes of the 6-7th thoracic vertebrae; 3.72 ($P>0.90$) and 3.81 mm ($P>0.95$) above the last rib; 2.32 ($P>0.90$) and 2.24 mm ($P>0.95$) above the 1st sacral vertebra; 4.48 ($P>0.98$) and 3.56 mm ($P>0.95$) above the 2nd sacral vertebra; 5.36 ($P>0.99$) and 4.21 mm ($P>0.95$) above the 3rd sacral vertebra than their CT- and TT-herd-mates.

TT-gilts had the lightest carcass weight, the shortest half carcass length and bacon side length, fat depth above the last rib; CT-gilts – the shortest fat depth on withers above spinous processes of the 6-7th thoracic vertebrae, above the 1st, 2nd and 3rd sacral vertebrae.

4. Discussion

One can see that presented findings are not always in line with the published records.

Thus, we found out that GG (**MC4R**) genotype was associated with longer half carcass and bacon side length and longer withers fat depth; AG genotype was associated with greater carcass weight, AA genotype was associated with longer fat depth above the last rib and the 1st, 2nd and 3rd sacral vertebrae. AG-gilts had short fat depth (on the withers, above spinous processes of the 6-7th thoracic vertebrae, above the 2nd and 3rd sacral vertebrae). The above findings are in line with those of C.S. Bruun et al. [1]

showing that long fat depth in most of the studied breeds and hybrids is associated with AA (MC4R) genotype.

L. Getmantseva, M. Leonova, A. Usatov et al. in their experiment on 204 F_1 (♀ Landrace x ♂ Large White) gilts found out that GG genotype of MC4R gene was the best marker for body length and fat depth [2].

A. Van den Broeke, M. Alluwe, F.A. Tuyttens et al. estimated that pigs of AA (MC4R) genotype had longer fat depth ($P<0.001$) that resulted in lower meat content in the carcass ($P<0.001$) compared with pigs of GG genotype [3].

In our experiment Qq **(IGF2)**-gilts had greater carcass weight, longer fat depth (above spinous processes of the 6-7th thoracic vertebrae and above the 2nd and 3rd sacral vertebrae); QQ-gilts had longer half carcass and bacon side length, longer fat depth (on the withers, above the last rib and the 1st sacral vertebra).

D.L. Clark, B.M. Bohrer, M.A. Tavárez et al. state that single nucleotide polymorphism (SNP) in the regulatory region of intron 3 in IGF2 gene (IGF2 – G 3072 A) is associated with decreased fat deposition in pigs with A (A Pat) alleles compared with those inheriting G (G Pat) alleles from male parent. Despite of reduced subcutaneous fat depth extractable intramuscular lipid from LM was 0.64% units greater ($P=0.02$) in pigs with A Pat alleles compared with those having G Pat alleles [4].

According to T.V. Karpushina, O.V. Kostyunina, E.I. Sizareva and N.A. Zinovieva within Large White Breed QQ (IGF2)-gilts had the greatest live weight and the longest actual fat depth [5].

In the experiment of L.V. Getmantseva QQ (IGF2)-pigs of Large White Breed had shorter fat depth [6].

O.V. Kostyunina, S.S. Kramarenko, N.A. Svezhentseva et al. among other things found out that GG>AG>AA gilts and boars tended to increase live weight at the end of the fattening period and average fat depth (measured at 4 points) [7].

In our studies EF (**POU1F1**)-gilts had greater weight, longer half carcass length, longer bacon side length of the carcass and shorter fat depth (throughout the carcass).

L.V. Getmantseva estimated that among L x Y x D hybrids DDAG (POU1F1 and MC4R)-pigs had shorter fat depth [6].

Gye-Wong Kim, Jae-Young Yoo, Hack-Youn Kim while studying L x Y x D hybrids estimated that all 3 genotypes had significantly different carcass weight and other characteristics ($P<0.05$), fat depth being insignificantly different. The authors believe POU1F1 gene to affect carcass weight [8].

L. Getmantseva, A. Kolosov, M. Leonova et al. in their experiments on Landrace pigs (n=80), Duroc pigs (n=100) and Landrace x Large White hybrids (n=192) found out that Landrace pigs had significant polymorphism for carcass length in intron 1 of POU1F1 gene, and hybrids had significant polymorphism for carcass length and subcutaneous fat depth in intron 1 of POU1F1 gene [9].

Our findings showed that DD (**H-FABP**)-gilts had greater carcass weight and shorter fat depth; dd-gilts had longer half carcass and bacon side length, longer fat depth (on the withers, above the 1st and 2nd sacral vertebrae); Dd-gilts had longer fat depth (above spinous processes of the 6-7th thoracic vertebrae, above the last rib and the 3rd sacral vertebra).

M. Tyra, K. Ropka-Molic, R. Eckert et al. in their experiments on 5 popular polish breeds with different fat depth showed that H-FABP and LEPR genes were closely associated with the development and functioning of fat tissue [10].

In the experiment conducted by G. Goncharenko, N. Grishina pigs of dd (H-FABP) genotype had the shortest fat depth and pigs of Dd genotype had the longest fat depth [11].

O.N. Polozyuk, G.V. Maksimov, L.V. Getmantseva estimated that ddHH (H-FABP) pigs had the shortest fat depth above spinous processes of the 6-7th thoracic vertebrae and DdHh pigs - the longest [12].

Earlier we (G. Maximov, A. Maximov, N. Lenkova) estimated that dd-gilts had the greatest carcass weight and Dd-gilts had the longest fat depth [13].

We estimated that AA-gilts (**GH**) had the greatest carcass weight, the longest half carcass and bacon side length, the longest fat depth (on the withers, above spinous processes of the 6-7th thoracic vertebrae, above the last rib, the 1st and 3rd sacral vertebrae); AG-gilts had the shortest fat depth.

R. Bižiene, I. Miceikiene, L. Baltrenaite, N. Krasnopiorova estimated that pigs of GG genotype had less fat deposits and greater lean tissue yield than those of AG and AA genotypes [14].

V. Balatsky, I. Bankovska, N. Ramon et al. in their experiment on 72 pigs determined that *a* allele of GHRH gene (growth hormone — releasing hormone) was associated with lower intramuscular fat content [15].

In our experiment CC-gilts (**LEP**) had greater carcass weight and longer fat depth; CT-gilts had longer half carcass and bacon side length compared with TT-gilts, but shorter fat depth compared with CC-gilts.

D. Liu, Y. Hu, X. Yang et al. conducted the experiments on 780 Duroc, Yorkshire, Laiwu, Lulai Black pigs and Landrace × Yorkshire hybrids. All the pigs excepting Duroc and Yorkshire had 3 genotypes (GG, GA, AA) by LEP gene. G allele was the most frequent in western breeds and Landrace x Yorkshire hybrids and the least frequent in Laiwu pigs. It was estimated that Landrace x Yorkshire hybrids and Lulai Black pigs of GG genotype consistently tended to have longer fat depth than those of GA and AA genotypes. These findings proved that SNP G-2863A was a potential DNA marker for fat depth and played a regulatory role in leptin transcription [16].

D. Perez-Montarelo, A. Fernandez, J.M. Folch et al. state that sequencing LEP gene allowed one to identify 39 polymorphisms, 8 of which being new. 3 intronic polymorphisms LEP g. 1382 C>T, LEP g. 1387 C>T and LEP g. 1723 A>Г were genotyped, their association with pig productivity traits was found out. Analysis of LEP g. 1387 C>T and LEP g. 1382 C>T coaction proved their additive influence on live weight and carcass weight, as well as dominant influence on subcutaneous fat depth measured at several points. Polymorphism of LEP and LEPR has aggregate influence on both fatty acids composition in subcutaneous fat and fat depth. T alleles of both LEP g. 1387 C>T and LEPR c. 1987 C>T discovered in Iberian pigs determine increased growth, fat content and saturated fatty acids content in fat, that was probably due to greater feed intake [17].

D. Perez-Montarelo, A. Fernandez, C. Barragan et al. note that previous research proved significant influence of LEP and LEPR polymorphism on growth and fat deposition in pigs [18].

Analysis of our findings and those of other authors shows their diversity. Further investigations in this field are needed.

According to the centeric theory a gene though having a single function is complex in terms of its functioning as its general action is due to complex influence of its centers [19].

According to their effect, gene (point) mutations can be dominant or recessive. More often a mutant allele is recessive. According to the effect of mutant genes on the protein and enzyme biosynthesis 5 mutation types are distinguished: hypomorphic, hypermorphic, antimorphic, neomorphic and amorphic [19]. It may well be due to the mentioned gene effects as well as due to interaction of nonallelic genes that in different genotypes by the genes being studied certain traits responsible for meatness improve while others disimproved.

5. Conclusion

On the basis of these investigations we concluded that GG-gilts (MC4R) had 2.92 – 2.55 cm (P>0.09) longer half carcass length and 1.63 and 5.08 cm (P>0.999) longer bacon side length, longer fat depth on withers, above spinous processes of the 6-7th thoracic vertebrae; AG-gilts had heavier carcass weight; AA-gilts had 2.26 mm (P>0.90) and 2.65 mm (P>0.99) longer fat depth above the last rib, 3.05 – 3.07 mm (P>0.99) – above the 1st sacral vertebra; 2.09 mm (P>0.0) and 2.72 mm (P>0.95) – above the 2nd one; and 2.40 mm (P>0.90) and 4.39 mm (P>0.99) – above the 3rd sacral vertebra. AG-gilts had the shortest fat depth (on the sample) on withers, above the spinous processes of the 6-7th thoracic vertebrae, above the 2nd and 3rd sacral vertebrae.

Qq (IGE2)-genotype carriers had heavier carcass weight, longer fat depth above the spinous processes of the 6-7th thoracic vertebrae, above the 2nd and 3rd sacral vertebrae; and QQ-homozygotes had longer half carcass length and bacon side length, longer fat depth on withers, above the last rib and the 1st sacral vertebra. EF (POU1F1)-genotype carriers had heavier carcass weight, longer half carcass length and bacon side length and shorter fat depth on all portions of the carcass. DD-gilts (H-FABP) compared with other genotypes were characterized by 5.53 kg (P>0.99) and 6.13 kg (P = 0.98) heavier carcass weight, shorter fat depth on all portions. dd-gilts had longer half carcass length and bacon side length than their DD-herd-mates, longer fat depth on withers than their Dd- and DD-herd-mates, about the 1st and 2nd sacral vertebrae. Dd-heterozygotes had longer fat depth than their other herd-mates above the spinous processes of the 6-7th thoracic vertebrae, above the last rib and above the 3rd sacral vertebra. AA (GH)-genotype carriers had relatively 6.77 (P>0.95) and 8.65 cm (P>0.99), 1.56 (P<0.90) and 2.36 cm (P>0.95), 1.23 (P<0.95) and 1.62 cm (P>0.95) heavier carcass weight, longer half carcass length and bacon side length than their GG- and AG-herd-mates, had 2.17-3.23 mm (P<0.90) longer fat depth on withers, 2.82 mm (P<0.90) and 3.44 mm (P>0.95) above spinous processes of the 6-7th thoracic vertebrae, 1.59 mm (P<0.90) and 2.11 mm (P>0.98) above the last rib, above the 1st and 3rd sacral vertebrae. AG-gilts had the lightest carcass weight, the shortest half carcass length and bacon side length and also the shortest fat depth on every portion of the carcass (excepting above the 1st sacral vertebra). AA-gilts had 2.11 mm (P>0.98) longer fat depth above the last rib than AG-ones. CC(LEP)-pigs had relatively 2.89 kg (P<0.90) and 7.31kg (P>0.99) heavier carcass weight, 5.54 mm (P>0.999) and 3.28 mm (P>0.95) longer fat depth on withers, 3.72 mm (P>0.9) and 3.81 mm (P>0.95) – above spinous processes of 6-7th thoracic vertebrae, above the last rib, 2.32 mm (P>0.90) and 2.24 mm (P>0.95) – above the

1st sacral vertebra, 4.48 mm, P>0.98 and 3.56 mm, P>0.95 – above the 2nd sacral vertebra and 5.36 mm (P>0.99) and 4.21 mm (P>0.95) – above the 3rd sacral vertebra than their CT- and TT-herd-mates. CT-gilts had 2.26 cm (P>0.95) longer half carcass length and 2.23 cm (P>0.99) longer bacon side length than their TT-herd-mates, and had 5.54 mm (P>0.999) shorter fat depth on withers, 3.72 mm (P>0.90) – above the last rib, 2.32 mm (P>0.90) – above the 1st sacral vertebra, 4.48 mm (P>0.98) – above the 2nd sacral vertebra, 5.36 mm (P>0.99) – above the 3rd sacral vertebra, than their CC-herd-mates. TT-gilts had the lightest carcass weight (P>0.99), the shortest half carcass length (P>0.99), the shortest fat depth above the last rib (P>0.95).

Three-breed crosses didn't have a maximum level of heterozygosity (hybridity) of the allele gene generality. MC4R (AG = 48%), POU1F1 (EF = 68%), H-FABP (Dd = 52%) genes had the greatest number of heterozygotes, IGF2 (QQ = 92%), GH (GG = 58%), LEP (TT = 56%) genes had the greatest number of homozygotes. The data is likely to show that the breeds employed to obtain three-breed hybrids were selected for analogous (meat quality) traits and they had higher frequency of the desired Q (IGF2), G (GH) and T (LEP) gene alleles segregating from hybrids in homozygous condition.

This data to a certain extent is in line with V.D. Kabanov's conclusion (2001). He considers that mixing blood of different breed animals in multiple crossing results in division of hereditary and, consequently, its homogenization reducing, on the one hand, the likelihood of domination of any one particular breed traits and, on the other hand, developing the possibility of gene correlation in the process of clumping parent chromosomes and the possibility of emergence of new gene combinations including those with analogous traits.

The identified marker genes and genotypes (GG (MC4R), AG (MC4R), QQ (IGF2), EF (POUIFI), DD (H-FABP), AA (GH), CT (LEP) should be employed (along with conventional methods of farm animal estimation) in swine breeding and also when selecting parental pairs to obtain commercial hybrids with meat productivity.

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Conflict of Interest

The authors have no conflict of interest to declare.

References

[1] Bruun, C. S., *et al*. (2006). Evaluation of the Porcine Melanocortin 4 Receptor (MC4R) Gene as a Positional Candidate for a Fatness QTL in a Cross Between Landrace and Hampshire. *Animal Genetics,* vol. 37, issue 4, pp. 359-362.

[2] Getmantseva, L., *et al*. (2014). The Single and Combined Effect of MC4R and GH Genes on Productive Traits of Pigs. *American Journal of Agricultural and Biological Sciences,* vol. 12, issue 1, pp. 28-32.

[3] Van Den Broeke, A., *et al*. (2015). An Invention Study Demonstrates Effects of MC4R Genotype on Boar Taint and Performances of Growing-Finishing Pigs. *Journal of Animal Science,* vol. 93, issue 3, pp. 934-43.

[4] Clark, D. L., *et al*. (2014). Effects of the Porcine igf2 intron 3-g3072a Mutation on Carcass Cutability, Meat Quality, and Bacon Processing. *Journal of Animal Science*, vol. 92, issue 12, pp. 5778-5788.

[5] Karpushkina, T. V., *et al*. (2016). Production Traits of LW Pigs Related IGF2 and CTSD Genotype. *Achievements of Science and Technology AIC,* vol. 30, issue 6, pp. 82-85.

[6] Getmantseva, L. V. (2012). Influence of MC4R, IGF2 and POU1F1 on Production Traits of Pigs. (Thesis for a Master's degree in Agriculture, Persianovski Don State Agrarian University, 2012).

[7] Kostunina, O. V., Kramarenko, C. C. and Svezhentseva, N. A. (2015). IGF2 gene Association with Production Traits of LW Pigs (Sus Scrofa) with Regard to Sex Differentiation. *Agricultural Biology*, vol. 50, pp. 736-745.

[8] Kim, G. W., Yoo, J. Y. and Kim, H. Y. (2014). Association of Genotype of POU1F1 intron 1 with Carcass Characteristics in Crossbred Pigs. *Journal of Animal Science and Technology*, vol. 56, art. num. 25

[9] Getmantseva, L., *et al*. (2017). Effect of Polymorphisms in Intron 1 of the Swine POU1F1 Gene on Growth and Reproductive Traits. *Turkish Journal of Veterinary Animal Science*, vol. 41, pp. 643-647.

[10] Tyra, M., *et al*. (2011). H-FABP and LEPR Gene Expression Profile in Skeletal Muscles and Liver During Ontogenesis in Various Breeds of Pigs. *Domestic Animal Endocrinology,* vol. 40, issue 3, pp. 147-154.

[11] Goncharenko, G. and Grishina, N. (2010). Production Traits of Pigs Evaluated Through the Use of Immunogenetic and DNA-markers. *Chief Zoo Engineer*, vol. 3, pp. 10-13.

[12] Polozyuk, O. N., *et al*. (2014). Gene Markers Influencing Production of Pigs. *Swine Breeding*, vol. 4, pp. 35-36.

[13] Maksimov, G., Maksimov, A. and Lenkova, N. (2015). DNA-genotyping on RYRI, ESR and H-FABP alleles and Meat Production of pigs. *Chief Zoo Engineer,* vol. 1, pp. 24-31.

[14] Bižienė, R., *et al*. (2011). Association between Growth Hormone Gene Polymorphism and Economic Traits in Pigs. *VETERINARIJA IR ZOOTECHNIKA (Vet Med Zoot)*, vol. 56, issue 78, p. 27.

[15] Balatsky, V., Bankovska, I. and Ramona, N. (2016). Polymorphisms of the Porcine Cathepsins, Growth Hormone-Releasing Hormone and Leptin Receptor Genes and their Association with Meat Quality Traits in Ukrainian Large White breed. *Molecular Biology Reports,* vol. 43, pp. 517–526.

[16] Liu, D., *et al*. (2011). Identification and Genetic Effects of a Novel Polymorphism in the Distal Promoter Region of Porcine Leptin Gene. *Molecular Biology Reports,* vol. 38, issue 3, pp. 2051-7.

[17] Pérez-Montarelo, D., *et al*. (2012). Joint Effects of Porcine Leptin and Leptin Receptor Polymorphisms on Productivity and Quality Traits. *Animal Genetics,* vol. 43, issue 6, pp. 805-809.

[18] Pérez-Montarelo, D., *et al*. (2013*).* Transcriptional Characterization of Porcine Leptin and Leptin Receptor Genes. *PLoS One*. vol. 8 (6). doi: 10.1371/journal.pone.0066398

[19] Petuchov, V. L., *et al*. (2007). *Genetics*: *Textbook*. (2nd ed.). Novosibirsk: NSTU Publishing, p. 628.