Bulgarian Journal of Agricultural Science, 25 (No 4) 2019, 782–794

Determining genotypes of 3-breed pig hybrids by marker genes and their interrelation with meat productivity

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Abstract

Maximov, A., Vasilenko, V., Maximov, G., & Svinarev, I. (2019). Determining genotypes of 3-breed pig hybrids by marker genes and their interrelation with meat productivity. *Bulgarian Journal of Agricultural Science, 25*(4), 782–794

The paper presents the results of determining genotypes of 3-breed pig hybrids (Landrace × Yorkshire × Duroc) by MC4R, IGF2, POU1F1, H-FABP, GH, LEP marker genes and their interrelation with meat productivity. Allele frequencies for the studied genes have been determined. The studies proved that 3-breed hybrids did not have the highest level of heterozygosity in most allelic genes. There have been identified the most desirable genotypes for the studied genes (GG^{MC4R}, AG^{MC4R}, QQ^{IGF2}, EF^{POU1F1}, $DD^{H\text{-}FABP}$, AA^{GH}, CT^{LEP}) which are recommended for pig selection as well as for selection of parent pairs for producing commercial hybrids with high meat productivity. New methods of estimation and selection along with the traditional ones are used in farm animal breeding. The 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.

Keywords: genotyping; commercial; pig hybrids; slaughter qualities; meat qualities; gene-dependent selection; marker genes

Introduction

The study was intended to determine interrelation of genotypes of 3-breed pig hybrids (L × Y × D) by MC4R, IGF2 (Insulinoid Growth Factor 2), POU1F1, H-FABP, GH and LEP genes and their meat productivity.

Kim et al. (2006) found out that fat yield in pigs of GG-genotype (MC4R) was by 8% larger. Maximov and Getmantseva (2011) found out that in 3-breed hybrids (L × Y × D) AG-genotype (MC4R) was interrelated with better meat productivity.

Getmantseva (2012) showed that in pigs of Large White Breed, Danish Landrace and L × Y × D hybrids G allele (MC4R) frequency was 0.19; 0.60 and 0.40 respectively; and frequency of AA-, AG-, GG-genotypes in Large White pigs was 64.4; 33.9; 1.7%; in Danish Landrace – 0; 80; 20%; in L × Y × D hybrids – 25; 70; 5%. AG-genotype is desirable for fattening and meat trait selection. Fat depth in L × Y × D hybrids was 3.2 mm (13.2%) shorter.

According to Kostyunina et al. (2012) Landrace pigs had lower A allele (MC4R) frequency associated with greater precocity (10 – 66.8%, 34.4±5.7% on the average), Large White pigs (Large White, Edelschwein and Yorkshire) had higher A allele (MC4R) frequency (41.9 – 97.5%, 75.8±6.5% on the average), A allele (MC4R) frequency in LW × L hy-

brids was (42.4 – 52.2%). The highest A allele frequency was registered in LW pigs of French breeding (93.3%), the lowest A allele frequency – in Pietrain pigs (6.7%) that have relatively low precocity. High A allele frequencies are likely to be due to intensive pig selection for precocity.

Thus significant increase in A allele (MC4R) frequency in Landrace and Duroc pigs was also observed by Bruun et al. (2006) during the 12-year study, while decrease of A allele frequency in Yorkshire pigs was insignificant that suggested other loci being involved in selection for precocity. Dependence of productivity level on genotype by MC4R gene in purebred and hybrid pigs is ambiguous. Fat depth in purebred and hybrid pigs of AA-genotype by MC4R gene was longer than that of herd-average, differences in 2 groups of LW × L hybrids being significant (+0.5 and 1.41 mm) that was responsible for positive correlation between presence of A allele (MC4R) in genotype and level of this trait development ($r = 0.48$ and 0.41). The authors state that their findings are in line with available scientific data confirming that the effect of MC4R polymorphism on productive traits is not universal. For example, in most of the groups studied AA-pigs had longer fat depth and carcass length than GG-pigs.

Genetic potential of precocity and leanness when using MC4R marker has been experimentally established in L × Y × D hybrids by Chernukha et al. (2013). Frequency of desirable AG-genotype was 47.69%.

Lyadsky et al. (2011) found out that LW pigs of AG-genotype (MC4R) tended to form longer back fat depth.

Chernukha et al. (2015) identified 30 AA-homozygotes, 150 GG-heterozygotes and 142 AG-heterozygotes (MC4R) within the LLC "Ozersk Pig Complex". Purebred pigs had only GG-genotype and AG-heterozygotes, there were no AA-pigs. In Yorkshire pigs GG-genotype (60%) prevailed, in Landrace and Duroc pigs GG- and AG-genotypes were found in equal parts. AA-pigs were only among hybrids, their frequency in L × Y × D hybrids was 2.6 times higher than in Y × L hybrids. Frequency of A allele in the studied animals was 0.2 – 0.438, of G allele – 0.562 – 0.8, the highest G allele frequency being characteristic of purebred pigs and Y × L hybrids. L × Y × D hybrids had higher A allele frequency (0.438) compared to other breeds.

Raskatova et al. (2015) found out that AH-heterozygotes had larger body length (AG > GG at $P < 0.01$), but AA-pigs had longer fat depth ($P < 0.05$).

Lee et al. (2003), Jirtle (2004), Houston et al. (2005), Gilbert and Le Roy (2007), Hager et al. (2008), Sandor and Georges (2008) showed the effect of IGF2 mutation in the 3rd intron of the 13th chromosome – replacement of guanine by adenine at 3072 position (IGF2 – intron3 G 3072 A) – on the fat depth.

Karpushkina et al. (2016) within the LLC "Zmanensk Breeding Center" in Oryol Region found out that in the studied boar sample group in terms of allele and genotype frequency QQ-genotypes by IGF2 gene prevailed, their live weight being the heaviest: 3.1-9.4 kg heavier than that of Qq- and qq-boars. Average actual fat depth in QQ-boars (IGF2) was the longest: 0.2-0.5 mm longer than in Qq-boars ($P < 0.001$) and qq-boars ($P < 0.01$). At the same time average fat depth (adjusted to 100 kg weight) in QQ-boars (IGF2) was the shortest: 0.8 and 0.2 mm shorter than in Qq- and qq-boars ($P < 0.001$).

Van Laere et al. (2003) proved that mutation in gene IGF2 (q→Q) significantly affected growth rate and lipopexia in pigs.

Van den Maagdenberg et al. (2007), when studying the effect of proteolytic and lipolytic activity of enzymes, proved that pigs inheriting A allele from male parent had relatively heavier weight at slaughter that was likely to be due to decreased protein degradation.

The Canadian Center of Pig Industry Development proved that fat depth in QQ-pigs was 7.1 mm shorter. Genotyping of pigs bred in different countries revealed high frequencies of desirable Q allele in IGF2 gene in pigs of foreign breeding used both as male and female forms (Ernst & Zinoviyeva, 2000).

Ernst and Zinovieva (2008) within the CJSC (Closed Joint-Stock Company) stud farm "Zavolzhskoye" proved that fat depth in QQ-pigs was 3.5 mm shorter.

Gardan et al. (2008) proved that mutation in IGF2 gene contributed to the development of muscle hypertrophy and decreased fat cell development in subcutaneous tissue.

Loban (2010a; 2010b) discovered that using Belorussian Large White Breed with Qq- and QQ-genotype of IGF2 gene in boar reproduction allowed to improve fattening and meat quality and reduce fat depth by 0.7-1.8 mm. Frequency of desirable Q allele (IGF2) in Belorussian Large White Breed is 0.34.

Getmantseva (2012) found out that Q allele (IGF2) frequency in LW and DL pigs was 0.40 and 0.85 respectively and frequency of QQ-, Qq-, qq-genotypes in LW pigs was 27.1; 25.4; 47.5%, in L pigs – 80; 10; 10%. LW pigs of desirable QQ-genotype had better fattening qualities and 1.8 (7.8%) mm shorter fat depth than qq-pigs.

Kostyunina et al. (2008) within the Breeding Center "Zadneprovsky" in Vitebsk Region (Belarus) discovered that meat boars of foreign gene pool (Yorkshire, Duroc, Landrace) had the highest frequency of desirable Q allele (IGF2) (0.75-0.98) while sorusian Large White and Belorussian Meat boars had considerably lower frequency of desirable Q allele (IGF2) (0.34 – 0.36). Boar estimation with the elever

according to male parent genotype by IGF2 gene showed that in QQ-boars fat depth above spinous processes of the 6-7th vertebrae was 2.8 mm (11.3%) shorter and meatness by 3.6% greater than in qq-boars. Besides, it was observed that they tended to decrease fat depth above the 1st and 2nd lumbar vertebrae by 2.9 mm (16.2%) and increase depth of the rib eye by 3.29 mm (6.5%). The foresaid indices in Qq-boars were intermediate.

Estimation of young BLW pigs on fattening performance test showed that QQ-pigs had 1.8 mm (6.4%) shorter fat depth, by 0.7% greater dressing percentage, generally better meat and fattening qualities than qq-pigs.

Qq-heterozygotes had shorter fat depth, greater average daily gain and better meat qualities than qq-heterozygotes.

Kostyunina et al. (2009) recommend using IGF2 as a marker of fattening and meat traits in pigs. q-allele is undesirable.

Kostyunina et al. (2011) showed an increase in estimated breeding value (EBV) of fat depth (+0.44 mm) in boars of QQ (IGF2) / BB (ESR) genotype.

Kostyunina et al. (2015) in the experiment on 5908 progenies (5015 LW gilts and 893 LW boars) obtained from 20 boars of the given genotype by IGF2 gene established high frequencies of potentially desirable A allele and AA-genotype in a synthetic line of Body (0.986 and 0.971 respectively), Terminal Cross (0.977 and 0.955) and Duroc (0.960 and 0.921). The foresaid indices in LW Breed were intermediate (0.644 and 0.532). In Estonian Bacon, Belorussian Meat and Landrace Breeds A allele frequency ranged from 0.250 to 0.363, AA-genotype frequency ranged from 0.100 to 0.243. Livenskaya Breed had no A allele.

There has been established a tendency to increase live weight at the end of fattening period, average daily gain (in early and late fattening periods and for the whole fattening period), average actual fat depth (measured at 4 points) at the end of fattening period, fat depth for 100 kg and decrease precocity both in gilts and boars of genotypes GG > AG > AA. This tendency is stronger in boar. The authors recommend that selectionists bear these findings in view when developing programs of marker selection using IGF2 gene.

Raskatova et al. (2015) established that there were no differences in productivity level in pigs of different genotypes (IGF2), except for body length in the second fattening (Qq > QQ at $P < 0.01$), which was probably due to paternal effect of this marker. In case of obtaining 3-breed hybrids Duroc pigs are mainly used as male form, the frequency of desirable genotype in which can be as high as 100%.

Zinoviyeva (2010) noted that DD (POU1F1) pigs of 4 breeds and their hybrids had 2.9-4.8 mm longer fat depth than CC- and CD-herd-mates, and AA, AG (MC4R) 4-breed hybrids had 1.5-8.0 mm longer fat depth than GG-herd-mates.

Getmantseva (2012) proved that C allele (POU1F1) frequencies in LW, DL pigs and L × Y × D hybrids was 0.34, 0 and 0.15 respectively; frequency of CC-, CD- and DD-genotypes in LW pigs was 10.2, 49 and 40.8 respectively, in L pigs – 0, 0 and 100%, in L × Y × D hybrids – 0; 30 and 70%. Frequency of genotypes CCQQ, CCQq, CCqq, CDQQ, CDQq, CDqq, DDQQ, DDQq, DDqq by POU1F1 and IGF2 genes in LW pigs was 2.0, 4.1, 4.1, 8.2, 8.2, 3.06, 8.2, 12.2, 22.4% respectively. Pigs of desirable CDQQ-genotype had better fattening qualities and 2.2-2.85 mm longer fat depth (9.3 – 11.75%) than pigs of other genotypes. L × Y × D hybrids of DDAG-genotype by POU1F1 and MC4R genes had 2.55 (11%); 4.1 (16.5%); 2.0 mm (8.8%) shorter fat depth than L × Y × D hybrids of DDAA-, CDAA- and CDAG-genotypes.

Considering that H-FABP gene has a positive effect on intramuscular fat content (Zinoviyeva & Gladir, 2011) and its H-FABP^{D} and H-FABP^{d} allelic variants are responsible for decreasing fat depth by 3.5 to 10.5% (Arsiyenko, 2003), increasing hind quarter weight by 5.5 to 8.3%, rib eye area by 5.9 to 17.4%, this gene was suggested to be used as a genetic marker for pig selection for improving meat productivity traits.

Loban et al. (2004) within the Breeding Centre "Zadneprovski" (Belarus) determined that the presumptive desirable rate of dd (H-FABP) genotype in LW pigs was 49.3%, in Belorussian meat pigs – 34.8%, in HH genotype – 80.3 and 71.4% respectively. Frequency of undesirable D- and h-alleles in examined pig breeds was 0.32-0.34 and 0.14-0.17% respectively. dd- and HH-genotype pigs had significantly ($P < 0.05$) 4.1 and 8.0% shorter fat depth compared to DD- and hh-homozygotes. LW dd – HH and Dd – HH pigs had respectively 15.7 and 14.7% shorter fat depth than Dd – hh-pigs; Dd – HH-heterozygotes were intermediate. dd – HH and Dd – HH (H-FABP) pigs tended to have shorter fat depth than Dd – hh (fat depth – 22.4; 22.8 and 23.3 mm respectively).

Goncharenko and Grishina (2010) within the CJSC Agro-Industrial Complex "Inya", Novosibirsk region, have established that LW dd (H-FABP) pigs had the shortest fat depth (28.9 mm) and LW Dd-pigs had the longest one (33.3 mm). The difference amounted to 4.4 mm ($P < 0.05$).

The experiment was conducted within leading pig farming enterprises at the Stavropol Krai involving LWG (Large White Grigoropolis-1), Fast Growing Meat Breed-1, Landrace, Duroc breed pigs and their hybrids. Semyonov et al. (2013) have found out that H-FABP gene polymorphism is presented by two allelic variants – D and H. Allele frequen-

cy: D – 0.44 … 0.70 and d – 0.30 … 0.56; H – 0.53 … 0.72 and d – 0.28 … 0.47. ddHH and DdHH genotypes were better for meat pig breeding.

Chernukha et al. (2013) indicated that genotype frequency of H-FABP gene in 3-breed hybrids was: DD – 29.23; Dd – 30.77 and dd – 40% relatively.

Polozyuk et al. (2014) conducted an experiment on LW pigs (the CJSC stud farm "Jubileiny", Tyumen region) and Landrace pigs (the CJSC "Bataiskoye", Rostov region). Polozyuk et al. determined that DDHH, DdHh, ddhh, DDhh, ddHH, DdHH- genotypes at frequency 30.2; 18.6; 16.3; 13.9; 11.6; 4.6; 4.6% relatively were identified in Landrace pigs (H-FABP gene), and ddhh genotype was missing. Subsequent to the results of breeding ddHH pigs had the shortest fat depth above spinous processes of the 6-7th thoracic vertebrae (16.2 mm), and DdHh-boars had the longest (18.5 mm). The fat depth above the 1st-2nd lumber vertebrae in ddHH gilts was relatively 1.2; 1.0; 0.8 mm shorter than that of DdHH, DdHh, DDHh-gilts.

Earlier on we (Maksimov et al., 2015) conducted an experiment at the CJSC "Russkaya svinina" involving 40 LW x L pigs (average live weight 110 kg). We have determined rather high frequency of desirable dd-genotype – 42.5%, Dd-genotype (H-FABP) – 12.5%, DD – 45%. Dd-gilts had 1.9% heavier carcass weight than DD- homozygotes; they had 2.36% shorter carcass length ($P < 0.95$) and 2.03% longer one than their DD-herd-mates. Dd-pigs had 12.03% or 0.35 cm ($P < 0.95$) longer fat depth than DD-pigs.

Sayenko and Balatski (2009) have indicated that typing of GH (Growth Hormone) gene locus demonstrated various distribution of alleles and genotypes: in LB (Large Black) (n = 37) < < + > > = 0.89; ULW-1 (Ukrainian Large White) (n = 50) – < < + > > = 0.00, < < - > > = 1.00; LW (English, n = 47) – < < + > > = 0.16, < < - > > = 0.84; Pietrain (n = 9) – < < + > > = 0.78, < < - > > = 0.22; Meishan (n = 5) – < < + > > = 0.00, < < - > > = 1.00 and relatively < < +/ > > = 0.89, < < +/- > > = 0.00, < < - > > = 0.14, < < -/- > > = 0.77, < < +/+ > > = 0.80, < < +/- > > = 0.00, < < -/- > > = 0.20; < < +/+ > > = 0.00; < < +/- > > = 0.00, < < -/- > > = 1.00. The authors consider that in estimated populations animal traits to be influenced by GH are formed under the control of various gene allele variants. A specific polymorphism of GH gene enables marker-assisted inbreeding selection in these breeds.

Materials and Methods

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 the Don State Agrarian University.

The findings were biometrically processed using conventional methods.

Results and Discussion

MC4R gene (melanocortin receptor-4 gene) affects regulation of energy homeostasis, precocity, feed consumption and fatness. We established (refer to the table) 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 (Table 1).

There were no significant differences in withers fat depth among pigs of different genotypes by MC4R gene, however AG-gilts had the shortest withers fat depth and GG-gilts had the longest withers fat depth. The same was true for fat depth above spinous processes of the 6-7th thoracic vertebrae.

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 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. Length of the half carcass and bacon side in Qq-

pigs was respectively 1.24 ($P < 0.90$) and 0.59 cm ($P < 0.90$) longer than in Qq-gilts.

In QQ-pigs fat depth on the withers was 1.3 mm longer, fat depth above the last rib and above the 1st sacral vertebra was respectively 0.49 and 0.72 mm ($P < 0.90$) longer, fat depth above spinous processes of the 6-7th thoracic vertebrae and above the 2nd and 3rd sacral vertebrae was respectively 1.13, 0.18 and 0.3 mm ($P < 0.90$) shorter than in Qq-pigs.

POU1F1 gene (pituitary transcription factor) is a regulating transcription factor of the anterior pituitary gland which effectively stimulates gene expression of GH, 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. There were no FF-pigs.

EF-gilts had 4.6 gr heavier carcass weight, 0.38 cm longer half carcass length, 0.79 cm longer bacon side than EE-gilts ($P < 0.90$). But in EF-gilts fat depth on the withers was 0.82 mm shorter, above spinous processes of the 6-7th thoracic vertebrae – 0.88 mm shorter, above the 1st , 2nd and 3rd sacral vertebrae – respectively 0.96, 1.91 and 1.59 mm ($P < 0.90$) shorter than in EE-gilts. EF-gilts had 0.2 mm ($P < 0.90$) longer fat depth above the last rib than EE-gilts, the difference being insignificant.

One of the genes determining meat quality in pigs is protein gene H-FABP binding fatty acids which have three types of allelic polymorphism ($H\text{-}FABP^A$ $H\text{-}FABP^D$ $H\text{-}FABP^H$) 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.

Recessive homozygotes (dd) had 1.06 ($P < 0.90$) and 2.11 cm ($P > 0.90$) longer half carcass, 0.82 ($P < 0.90$) and 1.67 cm ($P > 0.90$) longer bacon half, 0.52 and 2.00 mm ($P < 0.90$) longer fat depth on the withers, 0.24 and 1.56 mm ($P < 0.90$) longer fat depth above the 1st and 2nd sacral vertebrae than Dd- and DD-herd-mates; and had 1.16 mm ($P < 0.90$) longer fat depth above the 3rd sacral vertebra than DD-herd-mates.

Dd-heterozygotes were characterized by a longer fat depth above spinous processes of the 6-7th thoracic vertebrae, above the last rib and the 3rd sacral vertebra by 0.27 and 1.77 mm ($P < 0.90$); 0.44 and 1.37 mm ($P < 0.90$); 0.44 and 1.6 mm ($P < 0.90$) respectively compared to dd- and DD-pigs. They had 1.48 mm ($P < 0.90$) longer fat depth above the 1st sacral vertebra then DD-pigs. Significantly, DD-genotype gilts had the shortest fat depth at all measured depth points.

(GH gene) (Gene ID: 3968840). The studies of 1990-s demonstrated the connection of its polymorphism with meat traits in different European breeds and lines. This fact allowed considering GH gene as a marker of meat pig productivity. 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 (Korwin-Kossakowska et al., 2004).

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.

LEP gene is one of prospective candidate gene 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. Leptin is also involved in inducing insulin resistance and may result in modification of the metabolic insulin effects, carried out through substrates of the insulin receptor. In fact, leptin may act through some components of insulin signaling cascade, sort of IRS-1 and IRS-2, PI-3-kinase and MAP-kinase (mitogen-activated protein kinase), and may modify the insulin-induced gene expression *in vitro* and *in vivo*.

Some mutations were identified in leptin gene. However, when carrying out the analysis on the effect of mutations on

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	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
n = 17 δ	8.73	2.83	2.33	4.67	3.5	2.83	3.17	3.5	4.33
Cv	11.08	2.82	2.93	13.25	15.26	13.36	20.88	22.21	22.58
AG M±m	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
n = 24 δ	7.68	2.5	2	4	4.83	4.67	3	3	3.83
Cv	9.64	2.56	2.41	11.75	22.33	25.24	24.73	23.01	25.90
GG M±m	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
n = 9 δ	7.62	2.33	1.83	3.67	4.17	1.67	1.33	1.5	2
Cv	9.74	2.31	2.16	10.07	17.54	9.22	10.98	10.97	11.92
IGF2									
QQ M±m	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
n = 46 δ	13.05	4.44	3.91	6.29	6.14	5.02	4.91	5.16	6.30
Cv	16.65	4.48	4.66	18.07	27.43	26.10	37.16	36.67	36.63
Qq M±m	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
n = 4 δ	2.88	2	1.5	4	4.33	2.67	2.67	2.67	3.5
Cv	3.27	2.04	1.80	11.94	18.43	14.24	21.36	18.74	20.00
POU1F1									
EE M±m	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
n = 16 δ	6.75	2.33	1.83	2.83	3.33	2	1.83	2.5	2.5
Cv	8.88	2.36	2.19	7.99	14.44	10.49	13.25	16.25	13.51
EF M±m	80.62±2.34	99.26±0.78	84.29±0.71	34.62±1.25	22.18±1.22	19.26±0.98	12.85±0.97	13.47±0.98	16.91±1.24
n = 34 δ	13.63	4.57	4.15	7.28	7.14	5.71	5.65	5.71	7.22
Cv	16.91	4.61	4.93	21.04	32.18	29.65	43.98	42.40	42.70

Table 1. Continued

1	2	3	4	5	6	7	8	9	10
H-FABP									
DD M±m	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
n = 6 δ	2.6	2.17	1.5	3.17	2.83	2.33	2.33	3	3.17
Cv	3.09	2.22	1.81	9.14	13.48	12.82	19.97	23.38	19.60
Dd M±m	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
n = 26 δ	7.62	3	2.83	4	4.17	3.83	2.67	2.83	3.33
Cv	9.68	3.03	3.38	11.48	18.31	19.60	20.30	20	18.74
dd M±m	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
n = 18 δ	8.85	2.67	2.67	5.33	4.83	3.5	3.17	3.5	4.33
Cv	11.33	2.67	3.15	15.23	21.47	18.32	23.19	24.32	24.99
GH									
AA M±m	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
n = 5 δ	5.07	1.67	1.17	3.67	2.5	1.17	0.5	2.5	1.17
Cv	5.91	1.66	1.37	9.87	9.92	5.63	3.73	18.12	6.57
AG M±m	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
n = 16 δ	5.12	2.33	1.67	3.5	2.83	2.17	2.5	3	3.5
Cv	6.63	2.37	1.99	10.33	13.04	11.61	18.87	22.32	20.59
GG M±m	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
n = 29 δ	8.85	3.17	2.83	4.5	4.83	4.67	3.5	3.67	4.17
Cv	11.19	3.19	3.36	12.85	21.58	24.31	26.78	25.35	23.71
LEP									
CC M±m	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
n = 5 δ	4.33	0.50	0.5	2	4.17	3	2	2.83	3
Cv	5.15	0.50	0.59	5.18	16.68	13.74	13.16	16.08	13.89
TC M±m	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
n = 17 δ	8.73	3.17	2.67	3.5	4.17	4	3.5	3.5	4.33
Cv	10.75	3.16	3.13	10.59	19.80	21.19	27.17	26.68	26.66
TT M±m	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
n = 28 δ	7.47	2.5	2.17	4.67	3.5	2.83	2.5	2.5	2.67
Cv	9.73	2.55	2.61	13.22	15.31	15.06	19.29	17.81	15.35

the economic traits, the replacement of cytosine to thymine at position 3469 in the 3rd exon turned out to be the major one. Polymorphism has a clear phenotypic expression that is characterized by increased accumulation of fat in the sacral part of the animal spine.

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.

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 Bruun et al. (2006) showing that long fat depth in most of the studied breeds and hybrids is associated with AA (MC4R) genotype. Lyadsky et al. (2011) observed that AG (MC4R)-gilts of Large White Breed tended to have short fat depth.

Getmantseva et al. (2014) 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.

Van den Broeke et al. (2015) 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.

The experiment of Raskatova et al. (2015) showed that AG (MC4R)-gilts had longer body length and AA-gilts had longer fat depth.

According to the findings of Octura et al. (2014) polymorphism in MC4R gene exercised no significant influence on the fat depth in Philippine local breeds. The authors believe that in the future researches should be carried out on larger sample group for further explanation of the influence of MC4R gene polymorphism on economic traits of Philippine local (native) pig breeds.

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).

Burgos et al. (2011) in their experiment on Landrace × Duroc hybrids estimated that progenies of pigs with G (IGF2) allele had both longer subcutaneous fat depth (subcutaneous fat depth was 23.1 mm compared with 19.1 mm back fat depth) and higher content of intermuscular fat.

Clark et al. (2014) 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.

According to Karpushina et al. (2016) within Large White Breed QQ (IGF2)-gilts had the greatest live weight and the longest actual fat depth. Earlier (Ernst & Zinoviyeva, 2008) it was estimated that pigs of QQ genotype had shorter fat depth.

In the experiment of Getmantseva (2012) QQ (IGF2)-pigs of Large White Breed had shorter fat depth. The same findings were received by Kostyunina et al. (2008).

Kostyunina et al. (2015) among other things found out that GG > AG > AA gilts and boars tended to increase live weight at the end of fattening period and average fat depth (measured at 4 points).

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).

According to Zinoviyeva (2010) DD (POU1F1)-pigs had longer fat depth than pigs of other genotypes.

Getmantseva (2012) estimated that among L × Y × D hybrids DDAG (POU1F1 и MC4R)-pigs had shorter fat depth.

Kim et al. (2014) while studying L × Y × D hybrids estimated that these 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.

Getmantseva et al. (2017) in their experiments on Landrace pigs (n = 80), Duroc pigs (n = 100) and Landrace × 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.

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).

Pang et al. (2006) in their experiment on Duroc, Large White, Landrace, Neijiang, Rongchang, Bamei, Hanjiang Black, Hanzhong White and wild pigs (n = 256) estimated that H-FABP genotypes significantly affected intramuscular fat content ($P < 0.05$); HH > Hh > hh, DD < Dd and AA < Aa < aa. Genetic effect was respectively 3.89; 3.42; 3.17; 2.27; 2.49; 2.91; 2.28; 2.70 and 2.95. HH, dd and aa genotypes had greater fat deposition in adipocytes.

Tyra et al. (2010) 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.

Arsiyenko (2003) estimated that D and d (H-FABP) alleles were responsible for reducing fat depth by 3.5-10.5%. Loban et al. (2004) established a tendency for shorter fat depth in pigs of dd – HH and Dd – HH (H-FABP) genotypes. In the experiment conducted by Goncharenko and Grishina (2010) pigs of dd (H-FABP) genotype had the shortest fat depth and pigs of Dd genotype had the longest fat depth.

Polozyuk et al. (2014) 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.

Earlier we (Maximov et al., 2015) estimated that dd-gilts had the greatest carcass weight and Dd-gilts had the longest fat depth.

Chen et al. (2014) analyzed distribution of polymorphism of H-FABP / (HinfI, MspI and HaeIII) and ACSL4 / PsaI and association of these 4 polymorphic loci with intramuscular fat content and fat depth in Yanan, Jinhua, Duroc, Landrace, Yorkshire pigs and Duroc × (Landrace × Yorkshire) hybrids. All 6 pig populations had polymorphism of H-FABP/HinfI. In ACSL4 / PsaI locus gilts of Duroc, Landrace, Yorkshire and Duroc × (Landrace × Yorkshire) had 3 genotypes and boars had only A and G haplotypes. Analysis of the discovered association showed that H-FABP/HinfI locus significantly affected intramuscular fat content in Duroc × (Landrace × Yorkshire) hybrids ($P < 0.05$) and Yanan pigs ($P < 0.001$). Hybrids with adH haplotype of polymorphic 3H-FABP loci had the highest intramuscular content (2.59%, $P < 0.05$). ACSL4 / PsaI locus was responsible for higher intramuscular fat content in gilts of GG genotype and boars of G haplotype compared with AA genotype (2.53 vs 2.10%, $P < 0.05$) or haplotype (2.48 vs 1.73%, $P < 0.01$) in polish pigs. The difference in fat depth in pigs of 4 polymorphic loci was insignificant ($P > 0.05$).

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.

Bižiene et al. (2011) estimated that frequency of AA, AG, GG genotypes by gene GH was respectively 0.121; 0.474; 0.405. Pigs of GG genotype had less fat deposits and greater lean tissue yield than those of AG and AA genotypes.

Balatsky et al. (2016) in their experiment on 72 pigs determined that *a* allele of GHRH gene (growth hormone — releasing hormone) was associated with lower intramuscular fat content.

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.

Peixoto et al. (2009) studied association of polymorphism of T2411C and T3266G haplonucleotides of LEP (SNPs) gene with carcass characteristics of F_2 local pigs that were hybrids of native brazilian Piau sows and Landrace, Large White, Rietrain.

T2411C SNP was among other things associated with fat depth above the last rib 6.5 cm from midline (P_2). T3266 G mutation was associated with average fat depth above the last and penult lumbar vertebrae and above the last rib, P_2. Phenotypic associations were also due to combining genotypes for both SNP associated with P_2 and carcass yield. The authors believe that SNP being analyzed can potentially be studied as markers of carcass characteristics.

Liu et al. (2011) 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 × Yorkshire hybrids and the least frequent in Laiwu pigs. It was estimated that Landrace × 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.

Uemoto et al. (2012) discovered polymorphism of LEPR in Duroc pigs (up to 953 pigs) and its influence on fat deposition. By using fine structure genetic mapping the authors discovered significant quantitative trait loci (QTL) for fat

depth, fat area coefficient and leptin concentration in serum (LEPC) near LEPR gene in the same region. This proves that c.2002 C > T SNP LEPR has strong effect on the traits being studied.

Perez-Montarelo et al. (2012) state that sequencing LEP gene allowed 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 > G 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.

Perez-Montarelo et al. (2013) noted that previous researches proved significant influence of LEP and LEPR polymorphism on growth and fat deposition in pigs.

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

According to the centeric theory (Petukhov et al., 2007) 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.

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 (Petukhov et al., 2007). It may well be due to the mentioned gene effects as well as due to interaction of non-allelic genes that in different genotypes by the genes being studied certain traits responsible for meatness improve while others disimprove.

Conclusion

On the basis of these investigations there should be 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 7.31 kg (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-herdmates. 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 the conclusion of Kabanov (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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Received: June, 29, 2018; *Accepted:* July, 31, 2018; *Published:* August, 31, 2019