Regulatory Mechanisms in Biosystems

ISSN 2519-8521 (Print)
ISSN 2520-2588 (Online)
Regul. Mech. Biosyst.

Effects of IGF2 genotypes on growth performance and meat productivity of three-way hybrid pigs

O. M. Tsereniuk*, A. M. Saienko*, I. O. Buhai*, V. O. Skrypnyk*,
I. O. Pchelnik**, O. G. Fesenko**, B. S. Shaferivskyi**, P. A. Vashchenko**

** Institute of Pig Breeding and Agroindustrial Production of National Academy of Agrarian Sciences of Ukraine, Poltava, Ukraine*
*** Poltava State Agrarian University, Poltava, Ukraine*

Article info

Received 18.03.2026
Received in revised form 13.04.2026
Accepted 24.05.2026

Institute of Pig Breeding and Agroindustrial Production of National Academy of Agrarian Sciences of Ukraine, Shvedska Mohyla St., 1, Poltava, 36000, Ukraine.
Tel.: +38-066-727-24-93.
E-mail: pigbreeding@ukr.net

Poltava State Agrarian University, Skovorody St., 1/3, Poltava, 36003, Ukraine.
Tel.: +38-096-944-98-12.
E-mail: pavlo.vashchenko@pdau.edu.ua

Tsereniuk, O. M., Saienko, A. M., Buhai, I. O., Skrypnyk, V. O., Pchelnik, I. O., Fesenko, O. G., Shaferivskyi, B. S., & Vashchenko, P. A. (2026). Effects of IGF2 genotypes on growth performance and meat productivity of three-way hybrid pigs. Regulatory Mechanisms in Biosystems, 17(4), e26084. doi:10.15421/0226084

The study investigated the association between IGF2 gene polymorphism and productive traits of commercial hybrid pigs obtained by crossing Danish Large White and Landrace sows with Duroc and Pietrain boars. The objective of the research was to evaluate the influence of IGF2 genotypes on fattening, carcass, meat productivity, and economic efficiency traits in modern commercial crossbreeding combinations. Genotyping was performed using PCR-RFLP analysis. Four hybrid combinations were studied: LWxLxD, LxLWxD, LWxLxP, and LxLWxP. Allele and genotype frequencies, Hardy–Weinberg equilibrium parameters, productive performance, carcass characteristics, and economic indicators were analyzed. The results demonstrated moderate heterozygosity (He = 0.42–0.492) and the absence of significant deviations from Hardy–Weinberg equilibrium in all experimental groups, indicating stability of the genetic structure at the IGF2 locus. Animals carrying AA and AB genotypes generally showed higher average daily gain, greater absolute weight gain, and shorter fattening periods compared with BB genotype carriers. Significant differences were observed for average daily gain, age at reaching 100 kg body weight, feed consumption, and absolute gain. The influence of the IGF2 polymorphism on carcass and meat traits was also established, particularly for preslaughter weight, transport weight, carcass length measured from the first cervical vertebra, carcass length measured from the first rib, and backfat thickness. In most cases, AA and AB genotypes were associated with better growth intensity and improved carcass quality, whereas BB animals tended to have thicker backfat. Economic evaluation showed that pigs with the AA genotype had the lowest production cost, the highest profitability level, and the greatest net profit per animal. The obtained results confirm the practical significance of the IGF2 locus as a promising marker for marker-assisted selection aimed at improving growth performance, meat productivity, and economic efficiency in commercial pig production systems.

Keywords: marker-assisted selection; insulin-like growth factor 2; Danish pig breeds; backfat thickness; average daily gain; economic efficiency; genetic diversity.

Introduction

The importance of implementing marker-assisted selection in animal breeding extends far beyond merely increasing productivity and economic efficiency of the livestock sector, as it is directly connected to addressing global environmental and socioeconomic challenges (Zos-Kior et al., 2020, 2021; Brockova et al., 2021). The application of MAS technologies facilitates the accelerated development of highly productive genotypes with improved feed conversion efficiency (Vashchenko et al., 2023), enhanced disease resistance (Vashchenko et al., 2022), and greater adaptability to climate change, thereby reducing the resource intensity of production and lowering greenhouse gas emissions per unit of output (McManus et al., 2020). In this context, the development of marker-assisted selection aligns with the achievement of the United Nations Sustainable Development Goals (SDGs), particularly SDG 2 “Zero Hunger” through ensuring food security and sustainable agriculture, SDG 12 “Responsible Consumption and Production” by promoting more efficient use of natural resources, and SDG 13 “Climate Action” through reducing the environmental impact of the agricultural sector while contributing to more efficient and sustainable land use (Goncharov et al., 2013; Zos-Kior et al., 2016; Bilan et al., 2017). Therefore, the integration of modern genetic technologies into breeding programs represents an important tool for establishing environmentally sustainable and competitive livestock production under conditions of ongoing global climate transformations.

Ensuring further progress in the pig industry requires improving pig productivity through the use of modern genetic resources and innovative technological solutions (Mote & Rothschild, 2020; Lykhach et al., 2022). Over the past 15–20 years, researchers have increasingly applied innovative approaches to breeding and selection programs involving a wide range of pig breeds, particularly Marker-Assisted Selection (MAS) technologies, which involve precise genotyping of animals at specific loci associated with the expression of economically important traits (Oliinychenko et al., 2019; Kirovych et al., 2023; Saienko et al., 2023). The subsequent use of obtained molecular genetic information is essential for accurate animal selection and breeding, optimal mating pair selection aimed at producing offspring of the desired type, or even pork products with preferred characteristics, such as lean meat or pork with increased intramuscular fat content (Johnsson, 2023; Rodrigues et al., 2024).

Insulin-like growth factor 2 (IGF2) is of considerable interest in modern pig breeding programs. It is a maternally imprinted growth factor that promotes skeletal muscle development by regulating cell proliferation and differentiation. A single nucleotide polymorphism (SNP) in intron 3 of the porcine IGF2 gene disrupts the binding site of BED-type zinc finger containing 6 (ZBED6), resulting in upregulation of IGF2 expression and exerting a significant effect on muscle growth, heart size, and backfat thickness. This favorable mutation is widespread in Western commercial pig populations (Duo et al., 2023). The IGF2 gene (also known as somatomedin A) is located on chromosome 2 (SSC2). It spans approximately 30 kbp and consists of nine exons, eight introns, and four promoters. Exons 7, 8, and 9 encode the IGF2 preproprotein (Amarger et al., 2002), whereas exons 1–6 are noncoding (O’Dell & Day, 1998). The IGF2 gene is considered one of the potentially important genetic markers associated with growth and carcass characteristics in pigs (Malgwi et al., 2022; Ampa-

pom et al., 2023), since IGF2 concentration is related to body weight in growing pigs (Lamberson et al., 1996; Wu et al., 2023).

Insulin-like growth factor 2 (IGF2), the first identified maternally imprinted growth factor in various species, is expressed exclusively from the paternal allele (Giannoukakis et al., 1993; Duo et al., 2023) under the control of several promoters. In particular, IGF2 is highly expressed during embryonic development and shows lower expression levels in the adult tissues (Van Laere et al., 2003; Criado-Mesas et al., 2019). It plays an important role in muscle growth by regulating myoblast proliferation, apoptosis, and differentiation (Saltiel & Kahn, 2001; Zanou & Gailly, 2013). In modern commercial pig breeds, the naturally occurring IGF2-intron3-G3072A substitution leads to a 5–6% increase in lean meat content, a 6–8% enlargement of the *longissimus dorsi* muscle area, a 5–8% increase in heart size, and a 6–12% reduction in backfat thickness (Jeon et al., 1999; Van Laere et al., 2003; Fontanesi et al., 2010). The importance of the ZBED6-IGF2 axis in regulating skeletal muscle growth has been demonstrated in several animal models (Oczkowicz et al., 2012; Younis et al., 2020), although its role in intramuscular fat deposition remains largely unclear (Duo et al., 2023).

The role of the IGF2 gene in the formation of meat productivity traits in pigs has been a subject of a considerable number of studies. However, little research has been conducted on the influence of different genotypes at this locus on a complex of economically important traits in modern commercial crossbreeding combinations involving Danish Large White and Landrace sows crossed with Duroc and Pietrain boars. Particular attention should be paid to evaluating productive traits depending on IGF2 polymorphism under intensive pork production systems, since the efficiency of genetic potential realization is largely determined by the interaction among genotype and feeding and housing conditions. Investigating associations between IGF2 genotypes and growth performance, fattening efficiency, and carcass traits is important for improving breeding programs, optimizing parental selection, and increasing the efficiency of modern genetic resource utilization. The obtained results may contribute to the implementation of more precise marker-assisted selection strategies in pig breeding, thereby improving animal productivity, enhancing pork quality, and strengthening the competitiveness of the pig industry under modern agricultural production conditions.

Materials and methods

During the study, all experimental procedures were carried out in accordance with the requirements of the Law of Ukraine "On Protection of Animals from Cruel Treatment" No. 3447-IV dated February 21, 2006, with amendments effective as of August 4, 2017. The Bioethics Commission of the Institute of Pig Breeding and Agro-Industrial Production of the National Academy of Agrarian Sciences of Ukraine approved the research methodology (protocol No. 4 dated 11/20/2022). Particular attention was paid to ensuring an appropriate level of animal welfare throughout the entire experimental period. Blood samples for genetic analyses were collected using procedures designed to minimize stress and reduce potential discomfort to the animals. In addition, the physiological condition and health status of the animals were continuously monitored, allowing timely responses to any changes and ensuring compliance with proper housing standards.

The study was conducted in accordance with the principles of the 3Rs (Replacement, Reduction, Refinement) established by *The European Convention for the Protection of Vertebrate Animals Used for Experimental and Other Scientific Purposes* (Strasbourg, 1985). In particular, the principle of replacement involved the use of only those procedures necessary to achieve the scientific objectives; the principle of reduction referred to optimizing the number of animals required to obtain statistically reliable results without excessive use of livestock; and the principle of refinement involved the implementation of methods aimed at minimizing pain, stress, and negative impacts on the animals. Adherence to these principles contributed not only to ensuring the ethical conduct of the research, but also to improving the reliability and scientific value of the obtained results.

According to the general experimental design (Fig. 1), during 2022–2026, molecular genetic studies were initially conducted in the Genetics Laboratory of the Institute of Pig Breeding and Agroindustrial Production of the National Academy of Agrarian Sciences of Ukraine, followed by experimental and production studies carried out under the conditions of LLC WEDA PODILLYA (Ternopil Oblast, Ukraine).

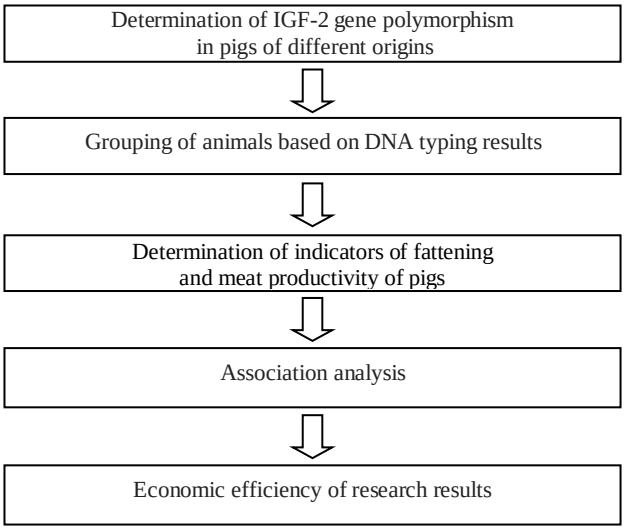

Fig. 1. Research organization scheme

According to the experimental design, four groups of Danish Large White and Landrace sows were formed, with 15 animals in each group. The first and third groups included purebred Danish Large White sows (LW), whereas the second and fourth groups consisted of their purebred Danish Landrace counterparts (L). Sows of groups II and IV were artificially inseminated with semen from Danish Large White boars (LW) of the same genetic origin. Their counterparts from groups I and III were inseminated with semen from Danish Landrace boars (L), also of Danish selection. At the final stage of hybridization, two-breed gilts from groups I and II were inseminated with semen from Duroc boars (D), whereas gilts from groups III and IV were inseminated with semen from Pietrain boars (P).

Housing conditions for the sows were identical throughout all stages of the reproductive cycle. Feeding conditions for all groups were also identical, based on complete and balanced compound feeds of in-house production formulated according to feeding standards (Ibatullin et al., 2016).

Feeding of the experimental pigs was organized according to their live body weight and physiological nutrient requirements. As body weight increased, the energy and nutritional value of the diets were gradually adjusted upward to support intensive growth and efficient fattening performance. For pigs weighing 40–50 kg, the daily ration provided 24.5 MJ of metabolizable energy and 1.80 kg of dry matter. The content of crude protein was 293 g, digestible protein 229 g, and lysine 14.7 g, while calcium and phosphorus levels amounted to 15.1 and 12.6 g, respectively. For pigs weighing 50–60 kg, dietary nutritional value was increased to 29.0 MJ of metabolizable energy and 2.13 kg of dry matter. Crude protein content increased to 347 g and digestible protein to 272 g. Lysine content reached 17.4 g, calcium 17.9 g, and phosphorus 14.9 g. In pigs weighing 60–70 kg, diets contained 32.4 MJ of metabolizable energy and 2.38 kg of dry matter. Crude and digestible protein levels reached 388 and 303 g, respectively. During this period, pigs received 19.4 g of lysine, 20.0 g of calcium, and 16.7 g of phosphorus per day. During the subsequent fattening stages (70–80 and 80–90 kg), the nutritional value of the diets continued to increase. Metabolizable energy content reached 34.8 and 38.2 MJ, while crude protein content amounted to 387 and 424 g, respectively. Mineral requirements also increased, with calcium levels ranging from 20.7 to 22.8 g and phosphorus levels from 17.2 to 18.8 g per animal per day. For pigs weighing 90–100 kg, the daily ration contained 40.7 MJ of metabolizable energy, 451 g of

crude protein, and 353 g of digestible protein. Lysine, calcium, and phosphorus contents reached 21.7, 24.2, and 20.0 g, respectively. At the final stage of fattening, when pigs reached 100–120 kg body weight, the nutritional value of the diets was the highest. Animals received 43.5 MJ of metabolizable energy, 3.20 kg of dry matter, 483 g of crude protein, and 378 g of digestible protein. Lysine content reached 23.2 g, calcium 25.9 g, and phosphorus 21.4 g. All animals received the same protein-mineral-vitamin supplement. This level of nutritional support ensured high productivity and intensive growth rates during the final fattening period.

Feed distribution in the pig housing facility was carried out automatically using a liquid feeding system manufactured by WEDA (Germany). The system provided automatic preparation, mixing, and delivery of feed mixtures according to predefined technological parameters. The use of liquid feeding enabled uniform distribution of nutrients within the diet, improved feed intake, and enhanced feed utilization efficiency. Automation of the feeding process ensured a stable feeding regime, minimized the influence of the human factor, and maintained appropriate sanitary and hygienic conditions in the facility by preventing feed residue accumulation (Fig. 2).

Fig. 2. Maintenance conditions of the experimental fattened pigs in the LLC WEDA PODILLYA (Ternopil Oblast, Ukraine).

Manure was removed through a slatted-floor system with subsequent storage in lagoons, which contributed to maintaining appropriate sanitary and hygienic conditions in the facility and ensured optimal housing conditions for the animals. The experimental pigs had unlimited access to drinking water throughout the entire study period. Water was supplied via automatic drinkers, the proper functioning of which was regularly monitored. Housing conditions were checked daily, including monitoring of microclimate parameters, the availability and condition of bedding, the operation of feeding and watering systems, as well as clinical observation of the animals' health status.

Before the beginning of the experiment, the housing facilities were thoroughly cleaned and disinfected in accordance with veterinary and sanitary requirements. In addition, the animals underwent preventive deworming to avoid parasitic diseases and to ensure uniform initial conditions for the study.

During the experimental period, the average air temperature in the pig housing facility was maintained at 19.92 ± 2.48 °C, while relative humidity ranged from 70% to 75%. Such microclimate parameters correspond to optimal conditions for pig fattening and contribute to maintaining physiological comfort, which is consistent with the findings reported by Lykhach et al. (2023).

Genetic analyses were carried out in the laboratory of the Institute of Pig Breeding and Agro-Industrial Production accredited in accordance with DSTU ISO 10012:2005, which holds Certificate of Accreditation No. 039-22 dated June 3, 2022, issued by the Ministry of Economic Development and Trade of Ukraine (State Enterprise "Poltava Regional Scientific and Technical Center for Standardization, Metrology and Certification"). Genomic DNA was isolated from bristles using Chelex 100 (Bio-Rad Laboratories Inc., USA) according to the method described by Walsh et al. (2013). For DNA typing, we used PCR-RFLP.

A fragment of the IGF2-in7-G162C (IGF2-NciI) gene located in intron 7 (NCBI sequence accession number AY242107), consisting of 336 base pairs, was amplified using the following specific primers: the forward primer 5'-CACAGCAGGTGCTCCATCGG-3' and the reverse primer 5'-GACAGGCTGTCATCCTGTGGG-3' (Vykoukalova et al., 2006). PCR reactions were performed in a final reaction volume of 25 μL containing 10–100 mg of genomic DNA, 200 nM of

each forward and reverse primer, 2.5 mM $MgCl_2$, 0.25 mM of each dNTP, and one unit of recombinant Taq DNA polymerase (Thermoscientific, EU).

The PCR amplification program included an initial denaturation step at 95 °C for 2 min, followed by 30 cycles of denaturation at 95 °C for 30 s, primer annealing at 62 °C for 30 s, extension at 72 °C for 60 s, and a final elongation step at 72 °C for 7 min. PCR amplification was performed using a Tertsik-2 thermocycler (DNA Technology, RF).

The amplified IGF2 fragment was digested with the restriction enzyme NciI (Thermo Fisher Scientific, Lithuania) at 37 °C for 3 h, resulting in restriction fragments specific for the following IGF2 genotypes: GG – 336 bp; CG – 336, 208, 100, and 28 bp; CC – 208, 100, and 28 bp. Electrophoretic analysis of amplification products was performed in a 2% agarose gel at a current of 76 mA and a voltage of 275 V. Visualization was carried out by staining the gel with ethidium bromide followed by examination under ultraviolet light using a transilluminator. According to electrophoresis results, the sizes of the obtained DNA fragments corresponded to the expected fragment sizes relative to the molecular weight marker pBR322 DNA-MspI Digest (Fig. 3).

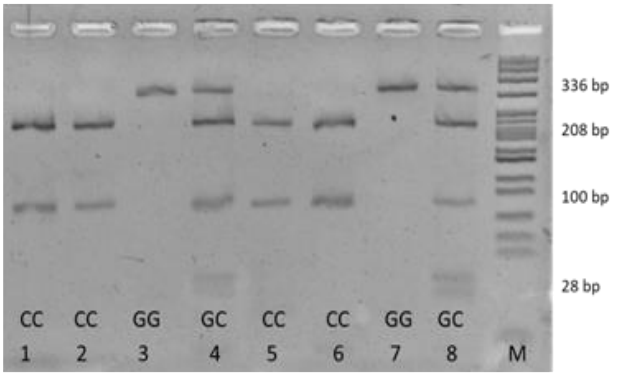

Fig. 3. Electrophoregram of TaqI restriction products of the IGF2 DNA locus in 3.5% agarose gel: lanes 1, 2, 5, and 6 correspond to experimental animals with the CC genotype; lanes 3 and 7 correspond to animals with the GG genotype; lanes 4 and 8 correspond to animals with the GC genotype; M represents the molecular weight marker pBR322 DNA-MspI Digest

For each group, expected genotype frequencies were calculated according to the Hardy–Weinberg law (p^2, 2pq, q^2). The GenAlEx 6.0 software package (Peakall, Australia, 2012) was used to calculate allele and genotype frequencies and to determine the level of heterozygosity (Peakall, 2012).

In the experimental animals, a complex of fattening and meat indicators was determined during the experiment. The weight of animals when placed and removed from fattening was determined by individual weighing on 150VP1-S electronic scales (Vahovymiriuvalni Systemy, Ukraine) with a division value of 0.05 kg and a maximum permissible weighing limit of 150 kg. Based on the data obtained, the average daily and absolute live weight gains for the fattening period were calculated, as well as the age of reaching a live weight of 100 kg. Additionally, feed consumption per head per day (kg) and feed conversion rates (%) were determined. After the completion of fattening, the preslaughter weight (kg), weight after transportation (kg), weight of steamed and chilled carcasses (kg) were taken into account. Morphometric indicators of the carcasses were determined in accordance with the requirements of the current DSTU 7158:2010 "Pigs for Slaughter. Technical Conditions". Carcass length was measured from the anterior edge of the first cervical vertebra to the anterior edge of the pubic symphysis using a measuring tape graduated in 1 mm increments. Carcass length from the first rib was measured from the anterior edge of the first rib to the anterior edge of the pubic symphysis using the same measuring tape. Backfat thickness at the level of the 6th–7th thoracic vertebrae was measured with a metal ruler with an accuracy of 1 mm. The loin eye area of the *longissimus dorsi* muscle was determined using a Placom planimeter (Placom, Japan).

Statistical processing of productive and morphological traits was performed using SAS/STAT® 15.1 (SAS Institute Inc., USA, 2018). The tables present the arithmetic means and their standard errors ($x \pm SE$). Differences among the groups were evaluated using one-way analysis of variance (ANOVA). The ratio of intergroup to intragroup variability was estimated with Fisher's F-test. Multiple comparisons were performed using Tukey's HSD test, and differences were considered statistically significant at $P < 0.05$.

Results

The results of the conducted studies revealed a moderate heterozygosity (He), which indicates a sufficient level of genetic diversity at the locus IGF2 (Table 1).

Table 1
Distribution of allele frequencies, genotypes and heterozygosity in four groups of three-breed pigs for the IGF2 gene, n = 15

Indicator	Group			
	LWxLxD	LxLWxD	LWxLxP	LxLWxP
Genotypes (AA/AB/BB), n	2 / 8 / 5	2 / 9 / 4	1 / 9 / 5	2 / 5 / 8
Genotype frequencies (AA/AB/BB)	0.133 / 0.533 / 0.333	0.133 / 0.600 / 0.267	0.067 / 0.600 / 0.333	0.133 / 0.333 / 0.533
Allele frequencies (A/B)	0.400 / 0.600	0.433 / 0.567	0.367 / 0.633	0.300 / 0.700
Expected genotype frequencies (E)	0.16 / 0.48 / 0.36	0.19 / 0.49 / 0.32	0.14 / 0.46 / 0.40	0.09 / 0.42 / 0.49
χ^2	0.186	0.730	1.297	0.657
Heterozygosity (He)	0.480	0.492	0.464	0.420

The groups where Duroc boars were used as the terminal sire line (LWxLxD, LxLWxD) were characterized by a higher frequency of allele A and greater heterozygosity compared with the groups in which Pietrain boars were used as the terminal sire line (LWxLxP, LxLWxP). Overall, allele B occurred more frequently than allele A, with a 1.31–2.33-fold difference. In all experimental groups, no statistically significant deviations from Hardy–Weinberg equilibrium were detected in genotype distributions ($P > 0.05$).

Based on pairwise comparisons of groups by IGF2 allele frequencies (Table 2), the null hypothesis of no differences was not rejected: In all cases, p-values exceeded the threshold of statistical significance ($P > 0.05$), indicating the absence of statistically significant differences between the studied groups. It was found that the allelic structure of the IGF2 locus is similar in all four groups, despite minor variations that may be due to breed characteristics. A moderate level of heterozygosity indicates a sufficient level of genetic diversity in the studied populations. In addition, no deviations from Hardy–Weinberg equilibrium were recorded in all groups, which indicates the stability of the genetic structure of the populations.

The analysis of variance revealed a significant effect of IGF2 gene polymorphism on certain fattening performance traits of growing pigs. The greatest number of significant intergroup differences was observed for average daily gain, age at reaching 100 kg live weight, daily feed intake, and absolute weight gain (Table 3).

Table 2
Pairwise comparison matrix of groups
based on IGF2 allele frequencies, χ^2 / P-value

Group	LWxLxD	LxLWxD	LWxLxP	LxLWxP
LWxLxD	–	0.000 / 1.000	0.000 / 1.000	0.293 / 0.588
LxLWxD	0.000 / 1.000	–	0.069 / 0.792	0.646 / 0.422
LWxLxP	0.000 / 1.000	0.069 / 0.792	–	0.075 / 0.784
LxLWxP	0.293 / 0.588	0.646 / 0.422	0.075 / 0.784	–

By the average daily gain, a significant advantage was established for animals of the LWxLxD combination with the AB genotype over young pigs of the LxLWxP combination with AB and BB genotypes. The difference between the AB groups amounted to 27 g, or 2.6%, while compared with the BB genotype the advantage reached 78 g, or 7.9%. Similarly, animals of the LxLWxD combination with the AB genotype exceeded young pigs of the LxLWxP combination with the AB genotype by 34 g, or 3.3%, and those with the BB genotype by 85 g, or 8.6%. Young pigs of the LWxLxP combination with the AB genotype were also characterized by higher growth intensity than animals of the LxLWxP combination. Their advantage over the AB genotype was 17 g, or 1.6%, while over the BB genotype it reached 68 g, or 6.9%.

Regarding the age of reaching a live weight of 100 kg, a significant difference was found between animals of the LWxLxD combination with the AB genotype and young pigs of the LxLWxP combination with the BB genotype. Animals of the first group reached a live weight of 100 kg 6.45 days earlier, corresponding to a 4.0% reduction in the fattening period. In terms of daily feed intake, a number of significant intergroup differences were identified. In particular, young pigs of the LWxLxD combination with the AB genotype consumed 0.134 kg/day more feed than animals of the LWxLxP combination with the BB genotype, or 5.6%, and 0.167 kg/day more than the LxLWxP combination with the AB genotype, or 7.1% ($P < 0.05$). Compared with young pigs of the LxLWxP combination with the BB genotype, the difference amounted to 0.289 kg/day, or 12.9%. Animals of the LWxLxD combination with the BB genotype also exceeded young pigs of the LxLWxP combination with the BB genotype in daily feed intake by 0.258 kg/day, or 11.5% ($P < 0.05$). A similar pattern was established for animals of the LWxLxP combination with the AB genotype, which consumed 0.155 kg/day, or 6.9% more feed than young pigs of the LxLWxP combination with the BB genotype ($P < 0.05$).

Regarding absolute gain, significant differences were found between young pigs of the LWxLxD combination with the AB genotype and animals of the LxLWxP combination with the BB genotype. The advantage of the first group amounted to 8.8 kg, or 13.6% ($P < 0.05$). A similar trend was observed between animals of the LWxLxP combination with the AB genotype and young pigs of the LxLWxP combination with the BB genotype, where the difference amounted to 7.8 kg, or 12.0% ($P < 0.05$). The results emphasize the practical importance of using the IGF2 genotype and optimal breed combinations for intensive pig production, particularly for reducing feed costs and shortening the period required to reach a live weight of 100 kg.

The influence of the IGF2 gene genotype on certain slaughter and meat productivity traits of young pigs from different breed combinations was established. The greatest number of significant intergroup differences was found for preslaughter weight, post-transportation weight, carcass length measured from the first cervical vertebra, carcass length measured from the first rib, and backfat thickness (Table 4).

Table 3

Association of IGF2 gene genotypes with productive indicators of fattening young animals (x ± SE)

Trait	Group / genotype IGF2											
	LWxLxD			LxLWxD			LWxLxP			LxLWxP		
	AA	AB	BB	AA	AB	BB	AA	AB	BB	AA	AB	BB
n	2	7	4	2	8	4	1	10	4	2	6	6
Initial body weight, kg	31.18	31.23 ± 0.53	31.25 ± 0.95	32.84	30.67 ± 0.39	30.68 ± 1.15	31.75	30.62 ± 0.38	30.33 ± 0.75	30.85	30.52 ± 0.24	30.12 ± 0.61
Average daily gain, g/day	1083	1063 ± 18^{a}	1053 ± 32^{a}	1044	1076 ± 14^{a}	1070 ± 41^{a}	1071	1068 ± 13^{a}	1053 ± 26^{a}	1071	1036 ± 8^{b}	985 ± 20^{b}
Age at reaching 100 kg live weight, days	153.7	154.72 ± 3.25^{a}	155.54 ± 4.45^{ab}	154.25	154.48 ± 2.75^{ab}	155.42 ± 6.76^{ab}	154.38	155.02 ± 6.18^{ab}	156.28 ± 7.67^{ab}	154.56	157.18 ± 2.28^{ab}	161.17 ± 1.57^{b}
Feed intake/day, kg/day	2.567	2.523 ± 0.033^{a}	2.492 ± 0.017^{ab}	2.500	2.492 ± 0.018^{ab}	2.445 ± 0.035^{ab}	2.455	2.434 ± 0.032^{ab}	2.389 ± 0.036^{b}	2.422	2.356 ± 0.056^{b}	2.234 ± 0.033^{c}
Feed conversion ratio, %	2.605	2.620 ± 0.019	2.652 ± 0.035	2.644	2.594 ± 0.035	2.626 ± 0.053	2.531	2.582 ± 0.016	2.676 ± 0.035	2.557	2.649 ± 0.033	2.861 ± 0.024
Absolute weight gain, kg	74.2	73.6 ± 1.5^{a}	72.7 ± 3.1^{ab}	72	73.4 ± 2.6^{a}	72.5 ± 2.6^{ab}	74	72.6 ± 2.2^{a}	70 ± 2.6^{ab}	72.5	70 ± 2.0^{ab}	64.8 ± 1.5^{b}

Notes: different letters within the same row indicate significant differences according to Tukey's test ($P < 0.05$); statistical analysis was not performed for groups with fewer than three animals ($n < 3$).

Table 4

Association of IGF2 polymorphism in different breed combinations with meat productivity indicators (x ± SE)

Feature	Group / Genotype IGF2											
	LWxLxD			LxLWxD			LWxLxP			LxLWxP		
	AA	AB	BB	AA	AB	BB	AA	AB	BB	AA	AB	BB
N	2	8	5	2	9	4	1	10	4	2	5	8
Preslaughter weight, kg	105.02	104.48 ± 0.92^{a}	103.44 ± 0.96^{a}	105.10	104.45 ± 1.05^{a}	102.54 ± 0.56^{a}	105.45	103.24 ± 1.28^{a}	101.46 ± 2.56^{ab}	105.53	102.16 ± 1.34^{ab}	97.58 ± 3.16^{b}
Post-transportation weight, kg	103.88	102.24 ± 1.04^{ab}	102.02 ± 1.42^{ab}	103.53	102.78 ± 0.89^{a}	101.45 ± 0.56^{ab}	102.00	100.12 ± 1.02^{b}	98.36 ± 2.16^{bcd}	102.55	99.2 ± 1.3^{c}	95.9 ± 2.1^{d}
Carcass weight, kg	78.25	78.28 ± 1.45	78.05 ± 2.67	78.75	77.56 ± 1.37	77.34 ± 2.67	78.15	75.65 ± 1.56	74.28 ± 1.44	79.57	75.35 ± 1.48	74.76 ± 1.52
Chilled carcass weight, kg	76.50	76.45 ± 1.45	75.88 ± 2.56	76.20	75.76 ± 1.67	75.42 ± 2.28	76.35	73.24 ± 1.52	72.62 ± 1.36	76.53	73.23 ± 1.67	72.14 ± 1.35
Carcass length measured from the first cervical vertebra, cm	85.45	85.92 ± 1.63^{ab}	88.78 ± 3.01^{a}	84.55	85.57 ± 1.89^{abc}	87.68 ± 0.78^{a}	85.60	84.72 ± 1.53^{bc}	83.82 ± 1.24^{bc}	85.26	82.67 ± 1.53^{c}	83.54 ± 1.67^{bc}
Carcass length measured from the first rib, cm	74.60	75.28 ± 1.63^{ab}	77.24 ± 2.91^{a}	73.53	74.24 ± 2.05^{ac}	75.81 ± 1.02^{a}	74.30	73.34 ± 1.35^{ac}	73.58 ± 1.44^{ac}	73.92	71.64 ± 1.52^{b}	72.48 ± 1.58^{bc}
Backfat thickness at the level of the 6th–7th thoracic vertebra, mm	18.30	19.41 ± 0.28^{a}	21.74 ± 0.39^{a}	16.80	19.34 ± 0.34^{a}	23.77 ± 0.37^{a}	20.00	17.42 ± 0.19^{ab}	15.18 ± 0.12^{b}	19.30	17.76 ± 0.23^{ab}	16.65 ± 0.17^{b}
Loin eye area, cm²	46.5	48.8 ± 2.6	45.8 ± 2.9	51.0	48.6 ± 3.6	45.3 ± 4.1	48.0	49.7 ± 2.2	51.0 ± 2.6	47.5	49.4 ± 3.7	50.9 ± 3.1

Notes: see Table 3.

A significant advantage in preslaughter weight was established for young pigs of the LWxLxD combination with AB and BB genotypes over animals of the LxLWxP combination with the BB genotype. In particular, animals with the AB genotype exceeded their counterparts of the LxLWxP combination with the BB genotype by 6.90 kg, or 7.1%, while the advantage of the BB genotype amounted to 5.86 kg, or 6.0%. Similarly, young pigs of the LxLWxD combination with AB and BB genotypes were characterized by higher pres-

laughter weight compared with animals of the LxLWxP combination with the BB genotype. The difference between the AB groups amounted to 4.58 kg, or 4.7%, and between the BB groups to 4.96 kg, or 5.1%. Animals of the LWxLxP combination with the AB genotype also exceeded young pigs of the LxLWxP combination with the BB genotype by 3.88 kg, or 4.0%.

A considerable number of significant intergroup differences were established for post-transportation weight. Young pigs of the LxLWxD combination with the AB genotype exceeded animals of the LWxLxP combination with the BB and AB genotypes by 4.42 kg (4.5%) and 2.66 kg (2.7%), respectively. Compared with young pigs of the LxLWxP combination with the AB and BB genotypes, the advantage amounted to 3.58 kg (3.6%) and 6.88 kg (7.2%), respectively. Animals of the LWxLxP combination with the AB genotype exceeded young pigs of the LxLWxP combination with the AB and BB genotypes by 0.92 kg (0.9%) and 4.22 kg (4.4%), respectively. In turn, young pigs of the LxLWxP combination with the AB genotype were characterized by higher post-transportation weight compared with the BB genotype of the same combination by 3.30 kg, or 3.4%.

Regarding carcass length, a significant advantage was established for animals of the LWxLxD combination with the BB genotype over young pigs of the LxLWxP combination with the AB genotype, measuring 6.11 cm, or 7.4%. Similarly, animals of the LxLWxD combination with the BB genotype exceeded young pigs of the LWxLxP combination with the AB and BB genotypes by 2.96 cm (3.5%) and 3.86 cm (4.6%), respectively, as well as animals of the LxLWxP combination with the AB genotype by 5.01 cm, or 6.1%.

A similar pattern was observed for carcass length measured from the first rib. Young pigs of the LWxLxD combination with the BB genotype exceeded animals of the LxLWxP combination with the AB and BB genotypes by 5.60 cm (7.8%) and 4.76 cm (6.6%), respectively. Animals of the LxLWxD combination with the BB genotype were also characterized by greater bacon half-carcass length compared with young pigs of the LxLWxP combination with the BB genotype by 3.33 cm, or 4.6%.

Regarding backfat thickness at the level of the 6–7th thoracic vertebra, we determined a significant effect of the IGF2 gene genotype on the meat productivity traits of young pigs. The highest values were observed in young pigs of the LxLWxD combination with the BB genotype, whose backfat thickness was 8.59 mm greater compared with animals of the LWxLxP combination with the BB genotype, or 56.6%. Compared with young pigs of the LxLWxP combination with the BB genotype, the difference amounted to 7.12 mm, or 42.8%.

Animals of the LWxLxD combination with the AB genotype were also characterized by greater backfat thickness than young pigs of the LWxLxP combination with the BB genotype and the LxLWxP combination with the BB genotype. The difference amounted to 4.23 mm, or 27.9%, and 2.76 mm, or 16.6%, respectively. A similar pattern was established for young pigs of the LxLWxD combination with the AB genotype, whose backfat thickness was 4.16 mm, or 27.4%, greater compared with animals of the LWxLxP combination with the BB genotype and 2.69 mm, or 16.2%, greater compared with young pigs of the LxLWxP combination with the BB genotype.

No significant difference was found for the loin eye area; only a tendency toward superiority of the AA and AB genotypes was observed, as they exceeded the minimum values in the sample by 8–12%.

The assessment of the economic efficiency of fattening final hybrid young pigs of different IGF2 gene genotypes indicated that, under identical feeding and housing conditions, the most efficient group consisted of animals with the IGF2-AA genotype (Table 5).

Table 5

Economic efficiency of fattening pigs with different genotypes according to the IGF2 gene per animal (x ± SE)

Indicator	Groups of animals with different IGF2 genotypes		
	AA (n = 7)	AB (n = 32)	BB (n = 21)
Fattening period, days	155	155	155
Average daily gain over the entire fattening period, g	912.50 ± 9.38[a]	914.84 ± 4.29[a]	867.86 ± 9.98[b]
Production output per animal for the entire fattening period, kg	105.00 ± 0.728[a]	103.88 ± 0.228[a]	100.29 ± 0.686[b]
Production cost per unit of output, UAH/kg	66.14	66.71	68.95
Total production costs for gross output, UAH	6945.0	6929.7	6914.6
Procurement price per unit of output, UAH/kg	82.00	82.00	82.00
Value of gross output at procurement prices, UAH	8610.2	8518.2	8223.8
Net profit per animal, UAH	1665.2	1588.5	1309.2
Additional profit obtained per animal, UAH	356.0	286.5	-
Profitability of producing 1 kg of gain, %	23.97	22.92	18.93

Notes. See Table 3.

Regarding the production cost per unit of output, it was established that in animals with the AA genotype this indicator was 0.57 UAH/kg, or 0.9%, lower compared with their counterparts with the AB genotype and 2.81 UAH/kg, or 4.1%, lower compared with the BB genotype. In turn, young pigs with the AB genotype were characterized by 2.24 UAH/kg, or 3.2%, lower production cost compared with animals with the BB genotype.

The value of gross output at procurement prices in animals with the AA genotype was 91.84 UAH, or 1.1%, higher compared with young pigs with the AB genotype and 386.22 UAH, or 4.7%, compared with the BB genotype. Similarly, animals with the AB genotype exceeded their counterparts with the BB genotype for this indicator by 294.38 UAH, or 3.6%.

In terms of net profit per animal, young pigs with the AA genotype exceeded animals with the AB genotype by 76.53 UAH, or 4.8%, and those with the BB genotype by 355.84 UAH, or 27.2%. The advantage of animals with the AB genotype over counterparts with the BB genotype amounted to 279.31 UAH, or 21.3%. The additionally obtained profit per animal in carriers of the AA genotype was higher compared with the AB genotype by 76.53 UAH, or 27.4%.

Regarding the profitability of producing 1 kg of gain, animals with the AA genotype showed an advantage of 1.05 percentage points over young pigs with the AB genotype and an advantage of 5.04 percentage points over those with the BB genotype. In turn, animals with the AB genotype exceeded their BB counterparts in profitability by 3.99 percentage points.

Thus, the results of the study indicate the feasibility of using the IGF2 AA genotype in breeding programs, as it ensures improvement in the main indicators of meat productivity and carcass quality. At the same time, the BB genotype may be of interest from the perspective of producing longer carcasses and bacon, which may be important depending on the production direction.

Discussion

The analysis of literature sources and the data obtained from our own studies demonstrated that the pig breeding industry has a considerable potential for further production growth through the targeted application of scientific and methodological approaches at both breeding and commercial farm levels. In order to provide the population with a sufficient amount of complete animal protein during the post-war reconstruction period, the pig industry may play a significant role. At the same time, it is necessary to take into account the specific characteristics of imported breeds that can be used in further breeding processes within domestic pig breeds in order to gradually increase their competitiveness and reduce dependence on imported breeding material. An important role in this process is assigned to marker-assisted selection (Sukhno et al., 2022; Sharma et al., 2024).

The study of IGF2 gene polymorphism in experimental hybrid pigs obtained by crossing Large White, Landrace, Duroc, and Pietrain breeds showed that χ^2 values ranged from 0.186 to 1.297, with $P > 0.05$ in all groups. This indicates the absence of significant deviation from Hardy–Weinberg equilibrium, suggesting the lack of strong within-group selection, uneven reproduction, or other factors that could alter allele composition. The obtained results indicate that the IGF2 gene is characterized by stability of allele distribution in different pig breed combinations and does not demonstrate signs of intrapopulation selection or structural shifts.

The absence of statistically significant intergroup differences and the Hardy–Weinberg equilibrium indicate a relatively uniform distribution of genetic variants within the studied populations. The observed level of heterozygosity was moderate and may be considered favorable for maintaining genetic diversity, which is important for future breeding programs. Thus, the IGF2 locus may be regarded as a stable genetic marker potentially suitable for use in marker-assisted selection programs aimed at improving pig productivity in different genotypic combinations.

Our findings are consistent with the data of other researchers who also did not detect signs of significant reduction in genetic variability at the IGF2 locus in modern industrial pig populations (Ojeda et al., 2008). In particular, an international study of haplotype variability of the IGF2 gene established that, despite intensive selection pressure for meat production traits, no general reduction in genetic variability between international and local European breeds was observed.

Similar to our results, the aforementioned study (Ojeda et al., 2008) demonstrated that even under directed selection aimed at increasing meatiness and the frequency of "desirable" IGF2 alleles, pig populations maintain a sufficient level of genetic variability and do not exhibit critical disturbances in population structure. The conformity of genotype distribution to Hardy–Weinberg equilibrium, established in our study, along with the absence of statistically significant intergroup differences, also confirms the absence of excessive selection pressure that could lead to narrowing of the genetic basis of the studied populations.

Moreover, the moderate heterozygosity identified in our studies is in good agreement with the conclusions of other authors regarding the preservation of genetic diversity in modern commercial and local pig populations. This indicates that the use of the IGF2 locus in marker-assisted selection programs can improve productive traits without substantial depletion of the genetic diversity of populations (Xu et al., 2020).

Our studies confirmed that IGF2 polymorphism affects such important quantitative traits as growth rate and backfat thickness, which is consistent with the opinion of researchers who state that these traits are controlled by multiple genes (Han et al., 2014; Lu et al., 2018; Ma et al., 2013). In addition, a considerable number of genes—including major genes as well as genes with moderate or minor effects—control overall meat quality.

Researchers have confirmed that RN, PRKAG3, RYR1, PHKG1, MC4R, and insulin-like growth factor 2 (IGF2) are the main genes influencing meat quality traits (Milan et al., 2000; Barbut et al., 2008; Zhukorskyi et al., 2022).

In our studies, we found that the IGF2 gene influences the development of the muscle tissue in hybrid pigs obtained by crossing the four main commercial breeds (Large White, Landrace, Duroc, and Pietrain). In general, carriers of the AA and AB genotypes were characterized by higher growth intensity, greater absolute gain, and a shorter period required to reach a live weight of 100 kg compared with animals with the BB genotype. At the same time, the effect of the gene was manifested through interaction with breed combination, indicating that the realization of genetic potential depends on the combination of parental forms.

It was established that animals with the AA and AB genotypes in most cases had higher average daily gains and absolute gains, whereas young pigs with the BB genotype were characterized by lower growth intensity and a longer fattening period. At the same time, the AA and AB genotypes were distinguished by a higher level of daily feed intake, which is probably associated with more intensive metabolic processes and more active formation of the muscle tissue. Our results are consistent with the studies conducted by other researchers on purebred Large White pigs (Kolaříková et al., 2003) and on other animal species (Younis et al., 2018).

Regarding meat production traits, an ambiguous nature of the IGF2 gene effect was established. In some breed combinations, the BB genotype was associated with increased backfat thickness, whereas carriers of the AA and AB genotypes were characterized by a tendency toward a larger loin eye area and a better ratio of muscle to fat tissue. The obtained results indicate that allelic variants of the IGF2 gene may be associated not only with growth intensity but also with the peculiarities of nutrient redistribution between the muscle and adipose tissues.

This is consistent with the opinion of other researchers, who state that among other genes, the insulin-like growth factor 2 gene (IGF2) belongs not only to the group of growth factors (including fattening traits), but also affects muscle tissue development (Carrodeguas et al., 2005). Considering that in modern commercial pig breeds the presence of the desirable IGF2 allele leads to improved meat quality traits (Jeon et al., 1999; Van Laere et al., 2003), the study of the productive performance of Danish-selected pigs under domestic conditions and the relationship between IGF2 DNA marker polymorphism and the subsequent growth and development of final hybrid young pigs will contribute to improving pig production systems and increasing their efficiency.

The results of our studies also emphasize the practical importance of using the IGF2 genotype and optimal breed combinations for intensive pig production, particularly for reducing feed costs and shortening the period required to reach a live weight of 100 kg.

Conclusions

The study established a significant influence of IGF2 gene polymorphism on fattening, carcass, and economic traits of terminal three-way hybrid pigs of Danish selection obtained using Large White, Landrace, Duroc, and Pietrain breeds. Animals carrying AA and AB genotypes generally demonstrated higher average daily gain, greater absolute gain, shorter periods required to reach 100 kg live weight, and improved economic efficiency compared with BB genotype carriers. The analysis of the genetic structure of the studied populations revealed moderate heterozygosity levels ($He = 0.42–0.492$) and the absence of significant deviations from Hardy–Weinberg equilibrium ($\chi^2 = 0.186–1.297$; $P > 0.05$), indicating sufficient genetic diversity and stability of the IGF2 locus in the investigated hybrid combinations.

The effect of IGF2 polymorphism on carcass characteristics was confirmed by significant differences in preslaughter weight, post-transportation weight, carcass length measured from the first cervical vertebra, carcass length measured from the first rib, and backfat thickness. In most cases, animals with the AA and AB genotypes were characterized by higher growth intensity and more favorable meat production traits, whereas BB genotype carriers tended to exhibit greater backfat thickness.

The economic assessment demonstrated that pigs with the AA genotype had the lowest production cost, the highest profitability level, and the greatest additional profit per animal, confirming the practical value of the IGF2 locus for marker-assisted selection programs aimed at improving growth performance, carcass quality, and production efficiency in commercial pig breeding systems.

The authors declare no conflicts of interest.

References

Amarger, V., Nguyen, M., Laere, A. S., Braunschweig, M., Nezer, C., Georges, M., & Andersso, L. (2002). Comparative sequence analysis of the INS–IGF2–H19 gene cluster in pigs. Mammalian Genome, 13, 388–398.

Ampaporn, K., Suwannasing, R., Phongphanich, P., Tunim, S., & Duangjinda, M. (2023). The variation of insulin like growth factor 2 maker is associa-

ted with growth traits in Thai Native (Kradon) pigs, Animal Bioscience, 36(9), 1350.
Barbut, S., Sosnicki, A. A., Lonergan, S. M., Knapp, T., Ciobanu, D. C., Gatcliffe, L. J., Huff-Lonergan, E., & Wilson, E. W. (2008). Progress in reducing the pale, soft and exudative (PSE) problem in pork and poultry meat. Meat Science, 79(1), 46–63.
Bilan, Y., Zos-Kior, M., Nitsenko, V., Sinelnikau, U., & Ilin, V. (2017). Projecting the social component of the efficient management of land resources. Journal of Security and Sustainability Issues, 7(2), 287–300.
Brockova, K., Rossokha, V., Chaban, V., Zos-Kior, M., Hnatenko, I., & Rubezhanska, V. (2021). Economic mechanism of optimizing the innovation investment program of the development of agro-industrial production. Management Theory and Studies for Rural Business and Infrastructure Development, 43(1), 129–135.
Carrodeguas, J. A., Burgos, C., Moreno, C., Sánchez, A. C., Ventanas, S., Tarrafeta, L., Barcelona, J. A., López, M. O., Oria, R., & López-Buesa, P. (2005). Incidence in diverse pig populations of an IGF2 mutation with potential influence on meat quality and quantity: An assay based on real time PCR (RT-PCR). Meat Science, 71(3), 577–582.
Criado-Mesas, L., Ballester, M., Crespo-Piazuelo, D., Castelló, A., Benítez, R., Fernández, A. I., & Folch, J. M. (2019). Analysis of porcine IGF2 gene expression in adipose tissue and its effect on fatty acid composition. PLoS One, 14(8), e0220708.
Duo, T., Liu, X., Mo, D., Bian, Y., Cai, S., Wang, M., Li, R., Zhu, Q., Tong, X., Liang, Z., Jiang, W., Chen, S., Chen , Y., & He, Z. (2023). Single-base editing in IGF2 improves meat production and intramuscular fat deposition in Liang Guang Small Spotted pigs. Journal of Animal Science and Biotechnology, 14, 141.
Fontanesi, L., Speroni, C., Buttazzoni, L., Scotti, E., Dall'Olio, S., Nanni Costa, L., & Russo, V. (2010). The insulin-like growth factor 2 (IGF2) gene intron3-g. 3072G> A polymorphism is not the only *Sus scrofa* chromosome 2p mutation affecting meat production and carcass traits in pigs: Evidence from the effects of a cathepsin D (CTSD) gene polymorphism. Journal of Animal Science, 88(7), 2235–2245.
Giannoukakis, N., Deal, C., Paquette, J., Goodyer, C. G., & Polychronakos, C. (1993). Parental genomic imprinting of the human IGF2 gene. Nature Genetics, 4(1), 98–101.
Goncharov, V. M., Zos-Kior, M., & Rakhmetulina Zhibek, B. (2013). The investment component of Ukrainian agrarian enterprises' development in conditions of land reform. Actual Problems of Economics, 10(148), 118–125.
Han, X., Yang, H., Jiang, T., Zhang, Q., Zeng, C., Fan, B., & Liu, B. (2014). Investigation of four candidate genes (IGF2, JHDM1A, COPB1 and TEF1) for growth rate and backfat thickness traits on SSC2q in Large White pigs. Molecular Biology Reports, 41(1), 309–315.
Ibatullin, I. I., Bashchenko, M. I., Zhukorskyi, O. M., Kandyba, V. M., Rudenko, Y. V., Ionov, I. A., Mykhalchenko, S. A., Tsvihun, A. T., Shapovalov, S. O., Zolotarov, A. P., Yeletska, L. M., Yurchenko, S. H., Kravchenko, Y. S., Saprykin, V. O., Haziiev, B. M., Kosov, M. O., Pomitun, I. A., Kosova, N. O., Tkachova, I. V., Vakulenko, I. S., Kostenko, V. I., & Boiarchuk, S. V. (2016). Dovidnyk z povnotsinnoyi hodivli sil's'kohospodars'kykh tvaryn [Handbook of balanced feeding of farm animals]. Ahrarna Nauka, Kyiv (in Ukrainian).
Jeon, J.-T., Carlborg, Ö., Törnsten, A., Giuffra, E., Amarger, V., Chardon, P., Andersson-Eklund, L., Andersson, K., Hansson, I., Lundström, K., & Andersson, L. (1999). A paternally expressed QTL affecting skeletal and cardiac muscle mass in pigs maps to the IGF2 locus. Nature Genetics, 21(2), 157–158.
Johnsson, M. (2023). Genomics in animal breeding from the perspectives of matrices and molecules. Hereditas, 160, 20.
Kirovych, N., Kytaieva, A., Riznychuk, I., Panikar, I., & Susol, R. (2023). Produktyvnist' svyney Pietren zalezhno vid al'ternatyvnykh variantiv heniv RYR1 ta MC4R [Productivity of Pietrain pigs depending on alternative variants of the RYR1 and MC4R genes]. Agrarian Bulletin of the Black Sea Littoral, 107, 105–114 (in Ukrainian).
Kolaríková, O., Putnová, L., Urban, T., Adámek, J., Knoll, A., & Dvorák, J. (2003). Associations of the IGF2 gene with growth and meat efficiency in Large White pigs. Journal of Applied Genetics, 44(4), 509–513.
Lamberson, W. R., Sterle, J. A., & Matteri, R. L. (1996). Relationships of serum insulin-like growth factor II concentrations to growth, compositional, and reproductive traits of swine. Journal of Animal Science, 74, 1753–1756.
Lu, H., Yan, H., Ward, M. G., Stewart, T., Adeola, O., & Ajuwon, K. M. (2018). Effect on Rendement Napole genotype on metabolic markers in Ossabaw pigs fed different levels of fat. Journal of Animal Physiology and Animal Nutrition, 102(1), e132–e138.
Lykhach, V. Y., Faustov, R. V., Shebanin, P. O., Lykhach, A. V., & Lenkov, L. H. (2022). Pidvyshchennia produktyvnosti svyney za vykorystannia suchasnoho henofondu ta innovatsiynykh tekhnolohichnykh rishen' [Increasing pig productivity using modern gene pool and innovative technological solutions]. Ilion, Kyiv (in Ukrainian).
Lykhach, V. Y., Povod, M. G., Shpetny, M. B., Nechmilov, V. M., Lykhach, A. V., Mikhalko, O. G., Barkar, E. V., Lenkov, L. G., & Kucher, O. O. (2023). Optymizatsiya tekhnolohichnykh rishen' utrymannia i hodivli svyney v umovakh promyslovoyi tekhnolohiyi [Optimization of technological solutions for keeping and feeding pigs in conditions of industrial technology]. Ilion, Mykolaiv (in Ukrainian).
Ma, J., Yang, J., Zhou, L., Zhang, Z., Ma, H., Xie, X., Cui, L., Yang, H., Liu, X., Duan, Y., Xiao, S., Ai, H., Ren, J., & Huang, L. (2013). Genome-wide association study of meat quality traits in a White Duroc× Erhualian F_2 intercross and Chinese Sutai pigs. PloS One, 8(5), e64047.
Malgwi, I. H., Halas, V., Grünvald, P., Schiavon, S., & Jocsak, I. (2022). Genes related to fat metabolism in pigs and intramuscular fat content of pork: A focus on nutrigenetics and nutrigenomics. Animals, 12(2), 150.
McManus, C. M., Rezende Paiva, S., & Faria, D. (2020). Genomics and climate change. Revue Scientifique et Technique, 39(2), 481–490.
Milan, D., Jeon, J. T., Looft, C., Amarger, V., Robic, A., Thelander, M., Rogel-Gaillard, C., Paul, S., Iannuccelli, N., Rask, L., Ronne, H., Lundström, K., Reinsch, N., Gellin, J., Kalm, E., Le Roy, P., Chardon, P., & Andersson, L. (2000). A mutation in PRKAG3 associated with excess glycogen content in pig skeletal muscle. Science, 288(5469), 1248–1251.
Mote, B. E., & Rothschild, M. F. (2020). Modern genetic and genomic improvement of the pig. In: Bazer, F. W., Lamb, G. C., & Wu, G. (Eds.). Animal agriculture. Sustainability, challenges and innovations. Academic Press, Amsterdam. Pp. 249–262.
O'Dell, S. D., & Day, I. N. M. (1998). Molecules in focus insulin-like growth factor II (IGF-II). The International Journal of Biochemistry and Cell Biology, 30, 767–771.
Oczkowicz, M., Tyra, M., Ropka-Molik, K., Mucha, A., & Żukowski, K. (2012). Effect of IGF2 intron3-g. 3072G> A on intramuscular fat (IMF) content in pigs raised in Poland. Livestock Science, 149(3), 301–304.
Ojeda, A., Huang, L.-S., Ren, J., Angiolillo, A., Cho, I.-C., Soto, H., Lemús-Flores, C., Makuza, S. M., Folch, J. M., & Pérez-Enciso, M. (2008). Selection in the making: A worldwide survey of haplotypic diversity around a causative mutation in porcine IGF2. Genetics, 178(3), 1639–1652.
Oliinychenko, Y. K., Vovk, V. O., Buslyk, T. V., Ilchenko, M. O., & Balatskyi, V. M. (2019). Henetychnyi ta asotsiatyvnyi analiz odnonukleotydnoho polimorfizmu g.22 G>C v heni katepsynu F svyney riznykh porid [Genetic and association analysis of the single nucleotide polymorphism g.22 G>C in the cathepsin F gene of pigs of different breeds]. Animal Science and Food Technology, 10(1), 21–26 (in Ukrainian).
Peakall, R., & Smouse, P. E. (2012). GenAlEx 6.5: Genetic analysis in Excel. Population genetic software for teaching and research – an update. Bioinformatics, 28, 2537–2539.
Rodrigues, G. P., Kiefer, C., Ullmann, L. S., da Rocha, G. H., Andrade, G. L., & Teixeira, S. A. (2024). Molecular markers and their importance for pig production and breeding: An overview. Caderno Pedagógico, 21(9), e8232–e8232.
Saienko, A., Peka, M., Tsereniuk, O., Babicz, M., Kropiwiec-Domańska, K., Onyshchenko, A., Vashchenko, P., & Balatsky, V. (2023). Analysis of polymorphism and development of a molecular-genetic system for genotyping by the telomerase reverse transcriptase (TERT) gene. Biosystems Diversity, 31(4), 436–443.
Saltiel, A. R., & Kahn, C. R. (2001). Insulin signalling and the regulation of glucose and lipid metabolism. Nature, 414(6865), 799–806.
Sharma, P., Doultani, S., Hadiya, K. K., George, L. B., & Highland, H. N. (2024). Overview of marker-assisted selection in animal breeding. Journal of Advances in Biology and Biotechnology, 27(5), 303–318.
Sukhno, V. V., Vashchenko, P. A., Saenko, A. M., Zhukorskyi, O. M., Tserenyuk, O. M., & Kryhina, N. V. (2022). Association of Fut1 and Slc11a1 gene polymorphisms with productivity traits of Large White pigs. Regulatory Mechanisms in Biosystems, 13(3), 225–230.
Van Laere, A. S., Nguyen, M., Braunschweig, M., Nezer, C., Collette, C., Moreau, L., Archibald, A. L., Haley, C. S., Buys, N., Tally, M., Andersson, G., Georges, M., & Anderss, L. (2003). A regulatory mutation in IGF2 causes a major QTL effect on muscle growth in the pig. Nature, 425(6960), 832–836.
Vashchenko, P. A., Zhukorskyi, O. M., Saenko, A. M., Khokhlov, A. M., Usenko, S. O., Kryhina, N. V., Sukhno, T. V., & Tsereniuk, O. M. (2023). The influence of feeding level on the growth of pigs depending on their genotype. Regulatory Mechanisms in Biosystems, 14(1), 112–117.
Vashchenko, P., Saienko, A., Sukhno, V., Tsereniuk, O., Babicz, M., Shkavro, N., Smołucha, G., & Łuszczewska-Sierakowska, I. (2022). Association of NRAMP1 gene polymorphism with the productive traits of the Ukrainian Large White pig. Medycyna Weterynaryjna, 78(11), 563–566.
Vykoukalova, Z., Knoll, A., Dvořák, J., & Čepica, S. (2006). New SNPs in the IGF2 gene and association between this gene and backfat thickness and

lean meat content in Large White pigs. Journal of Animal Breeding and Genetics, 123(3), 204–207.
Wakchaure, R., Ganguly, S., Praveen, P. K., Kumar, A., Sharma, S., & Mahajan, T. (2015). Marker assisted selection (MAS) in animal breeding: A review. Journal of Drug Metabolism and Toxicology, 6(5), e127.
Walsh, P. S., Metzger, D. A., & Higuchi, R. (2013). Chelex 100 as a medium for extraction of DNA for PCR-based typing from forensic material. Biotechniques, 54(3), 134–139.
Wu, Z., Hu, G., Zhang, Y., & Ao, Z. (2023). IGF2 may enhance placental fatty acid metabolism by regulating expression of fatty acid carriers in the growth of fetus and placenta during late pregnancy in pigs. Genes, 14(4), 872.
Xu, Y., Liu, X., Fu, J., Wang, H., Wang, J., Huang, C., Prasanna, B. M., Olsen, M. S., Wang, G., & Zhang, A. (2020). Enhancing genetic gain through genomic selection: From livestock to plants. Plant Communications, 1(1), 100005.
Younis, S., Naboulsi, R., Wang, X., Cao, X., Larsson, M., Sargsyan, E., Bergsten, P., Wels, N., & Andersson, L. (2020). The importance of the ZBED6-IGF2 axis for metabolic regulation in mouse myoblast cells. FASEB Journal, 34(8), 10250–10266.
Younis, S., Schönke, M., Massart, J., Hjortebjerg, R., Sundström, E., Gustafson, U., Björnholm, M., Krook, A., Frystyk, J., Zierath, J. R., & Andersson, L. (2018). The ZBED6–IGF2 axis has a major effect on growth of skeletal muscle and internal organs in placental mammals. Proceedings of the National Academy of Sciences, 115(9), E2048–E2057.
Zanou, N., & Gailly, P. (2013). Skeletal muscle hypertrophy and regeneration: Interplay between the myogenic regulatory factors (MRFs) and insulin-like growth factors (IGFs) pathways. Cellular and Molecular Life Sciences, 70(21), 4117–4130.
Zhukorskyi, O. M., Tsereniuk, O. M., Vashchenko, P. A., Khokhlov, A. M., Chereuta, Y. V., Akimov, O. V., & Kryhina, N. V. (2022). The effect of the ryanodine receptor gene on the reproductive traits of Welsh sows. Regulatory Mechanisms in Biosystems, 13(4), 367–372.
Zos-Kior, M., Hnatenko, I., Isai, O., Shtuler, I., Samborskyi, O., & Rubezhanska, V. (2020). Management of efficiency of the energy and resource saving innovative projects at the processing enterprises. Management Theory and Studies for Rural Business and Infrastructure Development, 42(4), 504–515.
Zos-Kior, M., Kuksa, I., Ilyin, V., & Chaikina, A. (2016). Land management prospects. Economic Annals-XXI, 9–10, 243–246.
Zos-Kior, M., Shkurupii, O., Fedirets, O., Shulzhenko, I., & Rubezhanska, V. (2021). Modeling of the investment program formation process of ecological management of the agrarian cluster. European Journal of Sustainable Development, 10(1), 571–583.