



Reproductive performance traits and their discreteness in sows with different intrabreed differentiation by the melanocortin-4 receptor gene MC4R

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Abstract

The article presents the results of a study of reproductive performance traits and their discreteness in Large White sows of French breeding with different intrabreed differentiation according to the melanocortin-4 receptor gene MC4R. The experimental part of the study and data analysis were conducted at Agroprime-Holding LLC, Odesa Region, in the Laboratory of Genetics and the Laboratory of Pig Breeding and Selection of the Institute of Pig Breeding and Agroindustrial Production of NAAS, as well as in the Animal Husbandry Laboratory of the State Institution Institute of Grain Crops of NAAS. The reproductive performance of sows with different genotypes for the melanocortin-4 receptor gene MC4R (MC4R^{GG} – experimental group I; MC4R^{AG} – experimental group II) was evaluated using the following quantitative traits: total number of piglets born, head; number of piglets at weaning at 28 days of age, head; litter weight at weaning at 28 and 60 days of age, kg; and piglet survival to weaning, %. The coefficient of discreteness of quantitative traits in sows of experimental groups I and II was calculated according to the method of Siromolot V. V. and Sviatchenko S. I. (1984). It was established that Large White sows of French breeding were characterized by high reproductive performance. In terms of total number of piglets born and litter weight at weaning at 60 days of age, the animals exceeded the minimum requirements for the elite class by 11.29 and 24.24 %, respectively. The sow reproductive performance selection index in the monitored population ranged from 78.06 to 129.63 points. Significant differences between sows of experimental group I (MC4R^{GG}) and experimental group II (MC4R^{AG}) were found for the total number of piglets born (1.8 piglets), number of piglets at weaning at 28 days of age (0.8 piglets), litter weight at weaning at 28 days of age (11.4 kg), litter weight at weaning at 60 days of age (25.1 kg), and the sow reproductive performance selection index (13.70 points). The highest piglet survival rate to weaning at 28 days of age (95.4 ± 2.32 %) was recorded in sows of experimental group II (MC4R^{AG}). The coefficients of discreteness (D) of reproductive performance traits in sows with different genotypes for the melanocortin-4 receptor gene MC4R were relatively high and ranged from 0.302 to 0.599. The maximum increase in additional production was obtained from sows of experimental group I (MC4R^{GG}), amounting to +6.28 %, with an economic value of +303.50 UAH per sow per farrowing.

Keywords: sow; breed; melanocortin-4 receptor gene MC4R; breeding value; reproductive performance; discreteness coefficient; value of additional production.

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1. Introduction

Modern pig production is characterized by a high intensity of production and continuously increasing requirements for the productive and reproductive traits of animals (Mar-tyshuk et al., 2020; Khalak et al., 2025; Mykhalko et al.,

2026). The efficiency of the industry largely depends on the genetic potential of the breeding female stock, since the reproductive capacity of sows directly determines the number of offspring obtained, piglet survival, the formation of technological groups, and the overall economic efficiency of pork production. In this regard, systematic evaluation of the

breeding value of pigs, identification of the most productive genotypes, and their targeted use in breeding programs are of considerable importance (Khalak et al., 2023, 2024).

The results of studies by Ukrainian and foreign researchers, as well as the practical experience of breeding farms, indicate that improving the efficiency of breeding work in pig production requires a comprehensive evaluation of animals according to origin, individual performance, reproductive traits, selection indices, and progeny performance. In modern breeding programs, traditional methods of phenotypic evaluation are increasingly combined with molecular genetic technologies, which makes it possible to characterize the genetic potential of animals more accurately and to improve the efficiency of selection.

Reproductive traits deserve particular attention because they have a complex genetic basis and are generally characterized by low to moderate heritability. Based on the analysis of 19,036 reproductive records from 4,986 Large White sows, Yu et al. (2022) estimated genetic parameters for such traits as total number born, number born alive, litter weight at birth, average piglet birth weight, gestation length, age at first insemination, and age at first farrowing. The authors emphasized the advisability of the integrated use of these indicators in systems for evaluating the breeding value of sows.

The complex nature of reproductive traits necessitates the use of modern genomic methods. Nonneman and Lents (2023) noted that the low to moderate heritability of reproductive traits in pigs does not preclude the achievement of substantial genetic progress through genomic selection. Current approaches in the functional genomics of reproduction include the use of single nucleotide polymorphism panels, genome-wide association studies, transcriptomic analyses, resequencing, and functional validation of candidate genes.

The potential of this approach is supported by the results of genome-wide association studies in Large White pigs. Chang Wu et al. (2022), after examining 695 animals, identified genomic regions associated with total number born, number born alive, number of piglets weaned, litter weight, and other indicators of reproductive performance. Among the candidate genes identified by the authors were TUSC3, THRB, and STT3B. These findings confirm the feasibility of using molecular genetic markers for a more detailed differentiation of sows according to a set of reproductive traits.

The importance of considering both genetic and environmental factors was also confirmed in a large-scale study by Yang et al. (2023), in which reproductive traits of Duroc, Landrace, and Yorkshire pigs were analyzed. The authors used data from 1,887 litters of Duroc sows, 21,787 litters of Landrace sows, and 74,796 litters of Yorkshire sows and evaluated 11 reproductive traits. These results indicate the need to account simultaneously for the genetic component and the conditions of housing and reproduction when assessing reproductive performance in sows.

Recent studies also confirm the effectiveness of genomic approaches specifically in Large White pig populations. Zhang et al. (2024) applied genome-wide association analysis and phenotype prediction approaches to reproductive traits in Large White pigs. Their findings expand current knowledge of the genetic architecture of reproductive performance and support the potential value of genomic information for improving pig breeding programs.

One of the promising approaches to improving breeding work is marker-assisted selection, which involves the use of

polymorphisms in individual genes as additional selection criteria. Among the candidate genes of considerable interest in pig breeding, particular attention has been given to the melanocortin-4 receptor gene MC4R. This receptor is involved in the regulation of energy balance, feed intake, and processes associated with body weight gain and fat deposition (Kim et al., 2006).

The functional significance of the Asp298Asn polymorphism in the MC4R gene has been confirmed experimentally. Zhang et al. (2020) found that the Asp298Asn substitution may affect the constitutive activity of the receptor, its expression on the cell surface, and intracellular signaling. In particular, the MC4R^{Asn} variant was characterized by lower basal activity and reduced cell-surface expression compared with MC4R^{Asp}, indicating the functional significance of this polymorphism and its potential use as a selection marker.

The association of MC4R polymorphism with productive traits in pigs was also demonstrated by Calta et al. (2022). In a study involving 439 commercial crossbred pigs fed ad libitum and 119 animals under restricted feeding, differences among genotypes were found in average daily gain, feed conversion ratio, carcass weight, dressing percentage, lean meat content, and backfat thickness. The authors also indicated a possible interaction between the MC4R genotype and feeding level.

At the same time, most current studies of the MC4R gene are focused primarily on growth traits, feed intake, carcass composition, and fat deposition, whereas its possible association with the complex of reproductive traits in sows has been studied to a much lesser extent. This determines the need for further investigations in specific breeds and populations with simultaneous consideration of animal genotype and actual reproductive performance.

Another important component of breeding evaluation is the assessment of variability and consolidation of economically important traits. Analysis of the coefficient of discreteness makes it possible to characterize the degree of differences between individual genotype groups and the overall population based on a set of quantitative traits. In the present study, this coefficient was calculated for total number born, number of piglets at weaning, and litter weight at 28 and 60 days of age.

Thus, combining traditional evaluation of reproductive traits, index selection, and molecular genetic differentiation of animals is a promising approach to improving breeding work in pig production. Of both scientific and practical interest is the identification of specific patterns in the manifestation of reproductive traits in sows with different MC4R genotypes, the determination of the level of discreteness of the traits studied, and the evaluation of the economic efficiency of using the respective genotype groups.

The aim of this study was to investigate reproductive traits and the level of their discreteness in Large White sows of French breeding with different genotypes for the melanocortin-4 receptor gene MC4R and, based on the data obtained, to substantiate the economic efficiency of using the experimental groups of animals.

2. Materials and methods

The study and data analysis were conducted at the breeding farm for Large White and Landrace pigs of Agroprime-Holding LLC, Odesa Region, at the Animal Husbandry

Laboratory of the State Institution Institute of Grain Crops of NAAS, and at the Laboratory of Pig Breeding and Selection of the Institute of Pig Breeding and Agroindustrial Production of NAAS.

The polymorphism of the melanocortin-4 receptor gene (MC4R) was studied in Large White sows of French breeding from AXIOM (n = 40) in collaboration with researchers from the Genetics Laboratory of the Institute of Pig Breeding and Agroindustrial Production of NAAS (Creative Co-operation Agreement No. 1/25-DN-P; Protocol of Genetic

Studies on Animal Testing Using DNA Markers No. 4/26-DN dated January 21, 2026). DNA was extracted from biological samples using Chelex-100 ion-exchange resin (Walsh et al., 1991).

For DNA typing of the animals, the polymerase chain reaction (PCR) technique and the restriction fragment length polymorphism (RFLP) method were used to analyze the MC4R gene locus (Kim et al., 2006; Muñoz et al., 2011). Photodocumentation was performed using a Canon digital camera (Fig. 1).

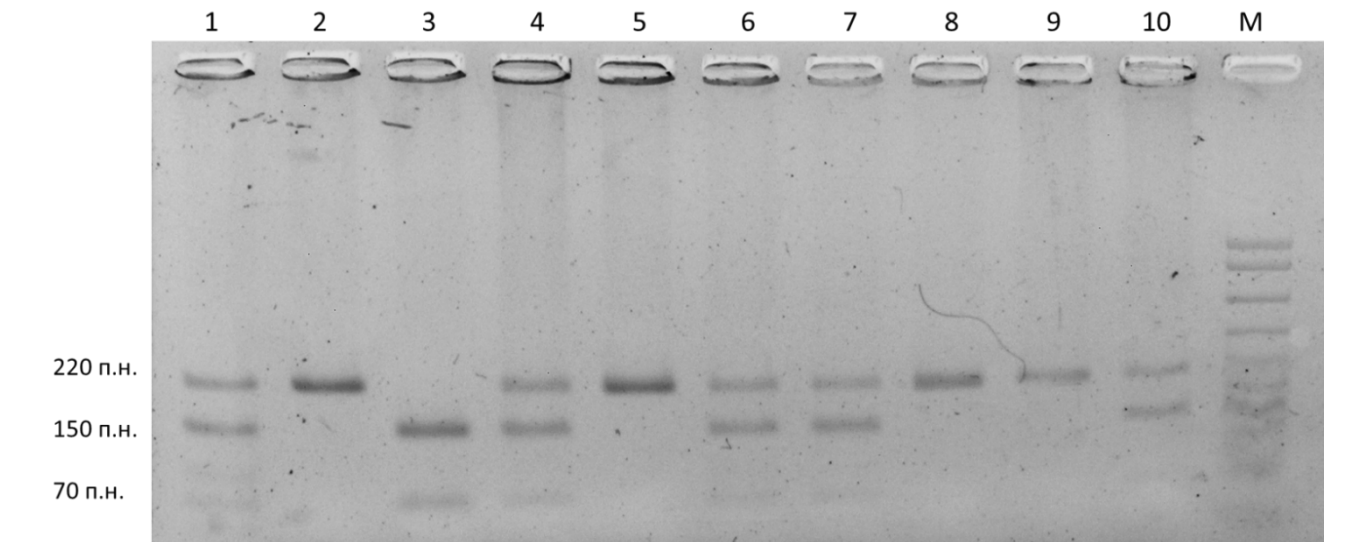


Fig. 1. Electrophoresis of MC4R gene restriction fragments in a 2 % agarose gel. Lanes 1, 4, 6, and 7 – AG genotype; lanes 2, 5, 8, and 9 – AA genotype; lane 3 – GG genotype. M – molecular weight marker pBR322/MspI (Saienko A. M., Lobchenko O. V., Khalak V. I., 2026)

The reproductive performance of sows with different genotypes for the melanocortin-4 receptor gene MC4R (MC4R^{GG} – experimental group I; MC4R^{AG} – experimental group II) was evaluated using the following quantitative traits: total number of piglets born, head; number of piglets at weaning at 28 days of age, head; litter weight at weaning at 28 and 60 days of age, kg; and piglet survival to weaning, %.

Litter weight at weaning at 60 days of age was determined using a calculation method (Khalak, 2022) (Table 1).

The sow reproductive performance selection index (SRPSI) and the coefficient of discreteness of quantitative traits in sows of experimental groups I and II were calculated using the following mathematical models:

$$SRPSI = (6,0 \times X_1) + \left[9,34 \times \left(\frac{X_2}{X_3} \right) \right] \tag{1}$$

where: SRPSI – sow reproductive performance selection index, points; X₁ – total number of piglets born, head; X₂ – litter weight at weaning, kg; X₃ – age at weaning, days (Tsereniuk et al., 2010);

$$D = 1 - \frac{S_1 \times S_2 \dots \times S_m}{\sigma_1 \times \sigma_2 \dots \times \sigma_m} \tag{2}$$

where: S₁, S₂ ... S_m – standard deviation within the group; σ₁, σ₂ ... σ_m – standard deviation of the total sample.

The economic efficiency of using Large White sows of French breeding with different breeding values was calculated according to the methodology described by Ladyka et al. (2023).

Table 1
Correction coefficients for adjusting litter weight at weaning to 60 days of age

Age at weaning, days	Coefficient	Age at weaning, days	Coefficient
21	3.000	41	1.708
22	2.976	42	1.656
23	2.952	43	1.604
24	2.928	44	1.552
25	2.904	45	1.500
26	2.880	46	1.460
27	2.804	47	1.420
28	2.728	48	1.380
29	2.652	49	1.340
30	2.500	50	1.300
31	2.428	51	1.275
32	2.356	52	1.250
33	2.284	53	1.225
34	2.212	54	1.200
35	2.140	55	1.150
36	2.064	56	1.120
37	1.988	57	1.090
38	1.912	58	1.060
39	1.836	59	1.030
40	1.760	60	1.000

Biometric processing of the obtained data was performed according to the methods described by Kovalenko et al. (2010) and Kramarenko et al. (2019).

3. Results and discussion

It was established that in Large White sows of French breeding, the frequencies of the A and G alleles were 0.09 and 0.91, respectively, while the frequencies of the AG and GG genotypes were 0.13 and 0.87, respectively.

Analysis of the primary zootechnical records (Form 2-SV "Breeding Sow Card", Form 4-SV "Journal of Mating (Insemination) Records of the Sow Herd", and Form 5-SV "Journal of Sow Farrowing and Piglet Records") and the results of our study showed that the total number of piglets born in Large White sows of French breeding ($n = 40$) was 12.4 ± 0.26 head; the number of piglets at weaning at 28 days of age was 11.6 ± 0.15 head; litter weight at weaning at 28 days of age was 89.8 ± 1.49 kg; litter weight at weaning at 60 days of age was 237.6 ± 3.88 kg; piglet survival to weaning at 28 days of age was 93.6 ± 0.45 %; and the sow

reproductive performance selection index (SRPSI) was 103.38 ± 2.036 points.

The coefficient of variation (C_v , %) of the above quantitative traits ranged from 8.58 to 13.71 % (Table 2).

Taking into account intrabreed differentiation by the melanocortin-4 receptor gene (MC4R), it was established that sows of experimental group I (MC4R^{GG}) outperformed their counterparts of experimental group II (MC4R^{AG}) in total number of piglets born by 1.8 piglets ($td = 3.05$, $P < 0.01$), number of piglets at weaning at 28 days of age by 0.8 piglets ($td = 2.67$, $P < 0.05$), litter weight at weaning at 28 days of age by 11.4 kg ($td = 3.73$, $P < 0.001$), litter weight at weaning at 60 days of age by 25.1 kg ($td = 3.81$, $P < 0.001$), and the sow reproductive performance selection index (SRPSI) by 13.70 points ($td = 2.97$, $P < 0.01$) (Table 3).

The highest piglet survival rate to weaning at 28 days of age (95.4 ± 2.32 %) was recorded in sows of experimental group II (MC4R^{AG}).

Table 2

Variability indicators of reproductive traits in Large White sows of French breeding, $n = 40$

Traits, units of measurement	Biometric indicators	
	$\sigma \pm S\sigma$	$C_v \pm SC_v$, %
Total number of piglets born, head	1.69 ± 0.189	13.71 ± 1.534
Number of piglets at weaning, head	0.99 ± 0.111	8.58 ± 0.960
Litter weight at weaning at 28 days of age, kg	9.47 ± 1.060	10.55 ± 1.180
Litter weight at weaning at 60 days of age, kg	24.59 ± 2.751	10.35 ± 1.158

Table 3

Reproductive performance of sows with different genotypes for the melanocortin-4 receptor gene MC4R

Traits, units of measurement	Biometric indicators	MC4R ^{GG}	MC4R ^{AG}
		Group I	Group II
	n	37	3
Total number of piglets born, head	$\bar{X} \pm Sx$	12.5 ± 0.26	10.7 ± 0.53
	$\sigma \pm S\sigma$	1.60 ± 0.186	1.87 ± 0.767
	$C_v \pm SC_v$, %	12.82 ± 1.491	17.50 ± 7.173
Difference from the elite class, head	–	+1.5	–0.3
Number of piglets at weaning, head	$\bar{X} \pm Sx$	11.6 ± 0.16	10.2 ± 0.26
	$\sigma \pm S\sigma$	0.68 ± 0.079	0.77 ± 0.316
	$C_v \pm SC_v$, %	5.90 ± 0.686	7.60 ± 3.115
Litter weight at weaning at 28 days of age, kg	$\bar{X} \pm Sx$	90.7 ± 1.48	79.3 ± 2.67
	$\sigma \pm S\sigma$	6.05 ± 0.704	7.78 ± 3.189
	$C_v \pm SC_v$, %	6.70 ± 0.779	9.90 ± 4.058
Litter weight at weaning at 60 days of age, kg	$\bar{X} \pm Sx$	239.5 ± 3.89	214.4 ± 5.32
	$\sigma \pm S\sigma$	23.71 ± 2.757	24.27 ± 9.947
	$C_v \pm SC_v$, %	9.90 ± 1.152	11.40 ± 4.673
Difference from the elite class, kg	–	+59.50	+34.40
Piglet survival to weaning, %	$\bar{X} \pm Sx$	92.8 ± 0.44	95.4 ± 2.32
	$\sigma \pm S\sigma$	104.40 ± 2.000	90.70 ± 4.161
	$C_v \pm SC_v$, %	12.16 ± 1.414	14.61 ± 5.988
Sow reproductive performance selection index (SRPSI), points	$\bar{X} \pm Sx$	11.67 ± 1.357	16.10 ± 6.599
	$\sigma \pm S\sigma$		

The calculated coefficients of discreteness (D) for reproductive performance traits in sows of the experimental groups are presented in Table 4.

It was established that the coefficients of discreteness (D) for reproductive performance traits in sows with different genotypes for the melanocortin-4 receptor gene MC4R were relatively high and ranged from 0.302 to 0.599. This indicates a high degree of consolidation of reproductive performance traits in sows of the studied population.

The results of calculating the value of additional produc-

tion obtained from sows with different genotypes for the melanocortin-4 receptor gene MC4R are presented in Table 5.

It was established that the maximum increase in additional production, based on the indicator "litter weight at weaning at 28 days of age, kg", was obtained from sows of experimental group I (MC4R^{GG}). The increase amounted to +6.28%, and its economic value was +303.50 UAH per head per farrowing.

Table 4

Coefficient of discreteness (D) of reproductive performance traits in sows of the experimental groups

Traits, units of measurement	Standard deviation	<i>MC4R</i> ^{GG}	<i>MC4R</i> ^{AG}
		Group I	Group II
	<i>n</i>	37	3
Total number of piglets born, head	<i>S</i> ₁	1.60	1.87
	<i>σ</i> ₁	1.69	1.69
Number of piglets at weaning, head	<i>S</i> ₂	0.68	0.77
	<i>σ</i> ₂	0.99	0.99
Litter weight at weaning at 28 days of age, kg	<i>S</i> ₃	6.05	7.78
	<i>σ</i> ₃	9.47	9.47
Litter weight at weaning at 60 days of age, kg	<i>S</i> ₄	23.71	24.27
	<i>σ</i> ₄	24.59	24.59
D		0.599	0.302

Note: S – standard deviation within the group; σ – standard deviation of the total sample

Table 5

Efficiency of the study results

Group	Genotype	<i>n</i>	Litter weight at weaning at 28 days of age, kg	Increase in additional production, %	Value of additional production, UAH/head/farrowing*
II	<i>MC4R</i> ^{AG}	3	79.3 ± 2.67	–6.70	–323.81
I	<i>MC4R</i> ^{GG}	37	90.7 ± 1.48	+6.28	+303.50

*Note: * the selling price of young pigs at the time of the study was 75.8 UAH per 1 kg of live weight

The results obtained in the present study indicate that intrabreed differentiation of Large White sows according to the melanocortin-4 receptor gene (*MC4R*) was associated with differences in a number of reproductive performance traits. Sows with the *MC4R*^{GG} genotype demonstrated higher values for total number of piglets born, number of piglets at weaning, litter weight at 28 and 60 days of age, and the sow reproductive performance selection index compared with animals carrying the *MC4R*^{AG} genotype. At the same time, the highest piglet survival rate to weaning was recorded in the *MC4R*^{AG} group. These results suggest that the relationship between *MC4R* genotype and reproductive performance may be trait-specific and should not be interpreted solely in terms of an overall advantage of one genotype over another.

The predominance of the G allele in the studied population is also noteworthy. In the examined Large White sows, the frequencies of the A and G alleles were 0.09 and 0.91, respectively, whereas the frequencies of the AG and GG genotypes were 0.13 and 0.87. This resulted in a markedly unequal distribution of animals between the experimental groups, with 37 sows in the *MC4R*^{GG} group and only 3 sows in the *MC4R*^{AG} group. Therefore, although statistically significant differences were detected for several traits, the limited number of *MC4R*^{AG} animals should be taken into account when interpreting the results. Further studies on larger and more balanced genotype groups are needed to confirm the observed associations.

The reproductive traits analyzed in this study are known to have a complex genetic background and to be influenced by both genetic and environmental factors. Yu et al. (2022) demonstrated that reproductive traits in Large White pigs generally have low to moderate heritability, which limits the efficiency of selection based exclusively on phenotypic records. Similar conclusions were reached by Yang et al. (2023), who showed that reproductive performance in commercial pig populations is affected by both genetic and non-genetic factors. These findings support the use of combined

approaches in which traditional reproductive records are supplemented with molecular genetic information.

Genome-wide studies have further demonstrated that reproductive performance in pigs is controlled by multiple genomic regions and candidate genes rather than by a single major locus. Chang Wu et al. (2022) identified several genomic regions associated with litter size, number of piglets weaned, and litter weight in Large White pigs, while Zhang et al. (2024) confirmed the complex genetic architecture of reproductive traits using genome-wide association and phenotype prediction approaches. Thus, the differences observed in the present study between *MC4R* genotypes should be interpreted as part of a broader polygenic background rather than as evidence that *MC4R* alone determines reproductive performance.

The biological relevance of the *MC4R* gene is well established in relation to energy homeostasis, feed intake, growth, and fat deposition. Kim et al. (2006) demonstrated associations between *MC4R* polymorphism and growth and fatness traits in pigs, whereas Zhang et al. (2020) provided functional evidence that the Asp298Asn polymorphism may alter receptor activity and cell-surface expression. Calta et al. (2022) also reported differences among *MC4R* genotypes in average daily gain, feed conversion, carcass weight, lean meat content, and backfat thickness. These findings indicate that *MC4R* may influence physiological pathways associated with energy metabolism, which could indirectly affect reproductive performance through body condition, nutrient partitioning, and metabolic status.

However, most previous studies of *MC4R* in pigs have focused primarily on growth, feed efficiency, carcass composition, and fat deposition, whereas its possible association with reproductive performance in sows has been investigated much less extensively. Therefore, the present findings provide additional information on the potential relationship between *MC4R* polymorphism and reproductive traits in Large White sows of French breeding. Nevertheless, because reproductive performance is a complex trait deter-

mined by numerous genes and environmental factors, the observed associations should be considered preliminary and require validation in independent populations.

An important feature of the present study was the evaluation of the discreteness of reproductive traits. The coefficients of discreteness ranged from 0.302 to 0.599, indicating a relatively high degree of consolidation of the studied reproductive traits within the investigated population. The higher coefficient observed in the MC4R^{GG} group suggests greater uniformity of this genotype group for the analyzed reproductive characteristics. From a breeding perspective, such consolidation may be valuable because it reflects a more stable expression of economically important traits within a selected group.

The observed differences also had an economic dimension. Sows of the MC4R^{GG} genotype showed a higher litter weight at weaning at 28 days of age, which was associated with an increase in additional production of 6.28 % and an estimated economic benefit of 303.50 UAH per sow per farrowing. In contrast, the MC4R^{AG} group showed a reduction in additional production of 6.70 %. These data demonstrate that reproductive differences associated with genotype may have practical consequences for the economic efficiency of pig production.

Overall, the results support the potential value of combining traditional reproductive performance evaluation, selection indices, and molecular genetic markers in breeding programs. At the same time, MC4R should be considered as a complementary marker rather than an independent selection criterion. Further studies involving larger populations, more balanced genotype frequencies, and additional genetic markers are required to determine the stability of the observed associations and to assess whether MC4R can be reliably incorporated into marker-assisted or genomic selection programs for reproductive performance in Large White pigs.

4. Conclusions

Large White sows of French breeding were characterized by high reproductive performance. In terms of total number of piglets born and litter weight at weaning at 60 days of age, they exceeded the minimum requirements for the elite class by 11.29 and 24.24 %, respectively. The sow reproductive performance selection index (SRPSI) in the studied population ranged from 78.06 to 129.63 points.

Considering the intrabreed differentiation of sows by the melanocortin-4 receptor gene MC4R, significant differences were established between animals of experimental group I (MC4R^{GG}) and experimental group II (MC4R^{AG}) in total number of piglets born (1.8 piglets), number of piglets at weaning at 28 days of age (0.8 piglets), litter weight at weaning at 28 days of age (11.4 kg), litter weight at weaning at 60 days of age (25.1 kg), and the sow reproductive performance selection index (13.70 points). The highest piglet survival rate to weaning at 28 days of age (95.4 ± 2.32 %) was recorded in sows of experimental group II (MC4R^{AG}).

The coefficients of discreteness (D) of reproductive performance traits in sows with different genotypes for the melanocortin-4 receptor gene MC4R were relatively high and ranged from 0.302 to 0.599.

The maximum increase in additional production was obtained from sows of experimental group I (MC4R^{GG}). It

amounted to +6.28 %, with an economic value of +303.50 UAH per head per farrowing.

Conflict of interest

The authors declare no conflicts of interest.

References

- Calta, J., Zadinová, K., Čítek, J., Kluzáková, E., Okrouhlá, M., Stupka, R., Tichý, L., Machová, K., Stratil, A., & Vostrý, L. (2022). Possible effects of the MC4R Asp298Asn polymorphism on pig production traits under ad libitum versus restricted feeding. *Journal of Animal Breeding and Genetics*, 140(2), 207–215.
[Crossref] [Google Scholar]
- Chang Wu, Z., Wang, Y., Huang, X., Wu, S., & Bao, W. (2022). A genome-wide association study of important reproduction traits in large white pigs. *Gene*, 838, 146702.
[Crossref] [Google Scholar]
- Khalak, V. I., Bordun, O. M., Hutyi, B. V., Usenko, S. O., Ilchenko, M. O., Fesenko, O. H., & Shaferivskyi, B. S. (2026). Adaptivno-produktyvni yakosti svynomatok velykoi biloi porody frantsuzkoi selektsii ta yikh otsiniuvannia za novoiu matematychnoiu modeliui selektsiinoho indeksu [Adaptive-productive qualities of sows of a large white breed of French selection and their evaluation according to a new mathematical model of the selection index]. *Visnyk ahrarnoi nauky*, 2(875), 22–31 (in Ukrainian).
[Crossref] [Google Scholar]
- Khalak, V. I., Gutyj, B. V., & Bordun, O. M. (2024). Some innovations in pig farming and their zootechnical assessment. *Ukrainian Journal of Veterinary and Agricultural Sciences*, 7(2), 50–54.
[Crossref] [Google Scholar]
- Khalak, V. I., Gutyj, B. V., Bordun, O. M., Kucher, S. D., Fesenko, O. G., & Shaferivskyi, B. S. (2025). Sow's operating value: a new evaluation method and its effectiveness for selecting highly productive animals. *Scientific and Technical Bulletin of State Scientific Research Control Institute of Veterinary Medical Products and Fodder Additives and Institute of Animal Biology*, 26(1), 236–245.
[Crossref] [Google Scholar]
- Khalak, V. I. (2022). Reproductive qualities of sows of different types of adaptation and the level of their phenotype consolidation. *Animal Breeding and Genetics*, 64, 164–172.
[Crossref] [Google Scholar]
- Khalak, V., Kostenko, O., Rodchenko, L., Gutyj, B., Martyshuk, T., & Vus, U. (2025). Physicochemical properties of muscle tissue of young pigs of the large white breed of foreign origin, their variability, and correlation with biochemical parameters of blood serum. *Scientific Messenger of LNU of Veterinary Medicine and Biotechnologies. Series: Veterinary Sciences*, 27(118), 133–140.
[Crossref] [Google Scholar]
- Khalak, V., Tsereniuk, O., Khmelnychi, L., Kozak, A., Gutyj, B., & Bordun, O. (2025). Selection index of reproductive qualities of sows (SIRQS): calculation algorithm and mechanism for selecting highly productive animals. *Scientific Messenger of LNU of Veterinary Medicine and Biotechnologies. Series: Agricultural Sciences*, 27(102), 3–9.
[Crossref] [Google Scholar]
- Khalak, V., Voloshchuk, V., Gutyj, B., Zasucha, L., Onyshchenko, A., Ilchenko, M., Ofilenko, N., Pokhyl, V., Pundyk, V., Bezalychna, O., & Stadnytska, O. (2023). Young pig fattening and meat quality due to varying formation intensities in early ontogenesis and two genotypes of the melanocortin receptor 4 (Mc4r) gene. *Veterinarska Stanica*, 54(6), 613–624.
[Crossref] [Google Scholar]

- Kim, K. S., Lee, J. J., Shin, H. Y., Choi, B. H., Lee, C. K., Kim, J. J., Cho, B. W., & Kim, T. H. (2006). Association of melanocortin 4 receptor (MC4R) and high mobility group AT-hook 1 (HMGA1) polymorphisms with pig growth and fat deposition traits. *Animal genetics*, 37(4), 419–421. [\[Crossref\]](#) [\[Google Scholar\]](#)
- Kovalenko, V. P., Khalak, V. I., Nezhlukchenko, T. I., & Papakina, N. S. (2010). Biometrychnyi analiz minlyvosti oznak silskohospodarskykh tvaryn i ptytsi [Biometric analysis of the variability of characteristics of agricultural animals and poultry]. Navchalnyi posibnyk z henetyky silskohospodarskykh tvaryn. Kherson: Oldi (in Ukrainian). [\[Google Scholar\]](#)
- Kramarenko, S. S., Luhovoi, S. I., Lykhach, A. V., & Kramarenko, O. S. (2019). Analiz biometrychnykh danykh u rozvedenni ta selektsii tvaryn: navchalnyi posibnyk [Analysis of Biometric Data in Animal Breeding and Selection: A Study Guide]. Mykolaiv: MNAU (in Ukrainian). [\[Google Scholar\]](#)
- Ladyka, V. I., Khmelnychiy, L. M., Povod, M. G. [etc.] (2023). Tekhnolohiia vyrobnytstva ta pererobky produktiv tvarynnytstva: pidruchnyk dlia aspirantiv [Technology of production and processing of livestock products: a textbook for graduate students]. Odesa: Oldi+ (in Ukrainian). [\[Google Scholar\]](#)
- Martyshuk, T. V., Gutyj, B. V., Zhelavskiy, M. M., Midyk, S. V., Fedorchenko, A. M., Todoriuk, V. B., Nahirniak, T. B., Kisera, Ya. V., Sus, H. V., Chemerys, V. A., Levkivska, N. D., & Iglitskej, I. I. (2020). Effect of Butaselmavit-Plus on the immune system of piglets during and after weaning. *Ukrainian Journal of Ecology*, 10(2), 347–352. [\[Abstract\]](#) [\[Google Scholar\]](#)
- Muñoz, G., Alcázar, E., Fernández, A., Barragán, C., Carrasco, A., de Pedro, E., Silió, L., Sánchez, J. L., & Rodríguez, M. C. (2011). Effects of porcine MC4R and LEPR polymorphisms, gender and Duroc sire line on economic traits in Duroc × Iberian crossbred pigs. *Meat science*, 88(1), 169–173. [\[Crossref\]](#) [\[Google Scholar\]](#)
- Mykhalko, O., Shpyrna, I., Shpetnyi, M., Opara, V., Gutyj, B., Borshchenko, V., Verbelchuk, S., Kovalchuk, Y., Shcherbatiuk, N., Yaremchuk, O. (2026). Economic efficiency of rearing and fattening lowweight piglets at early weaning with the addition of a pork meal substitute in the first week of rearing. *Scientific Papers Series Management, Economic Engineering in Agriculture and Rural Development*, 26(2), 509–526. [\[Abstract\]](#) [\[Google Scholar\]](#)
- Nonneman, D. J., & Lents, C. A. (2023). Functional genomics of reproduction in pigs: Are we there yet?. *Molecular reproduction and development*, 90(7), 436–444. [\[Crossref\]](#) [\[Google Scholar\]](#)
- Tsereniuk, O. M., Khvatov, F. I., & Stryzhak, T. A. (2010). Efektyvnist selektsiinykh i otsinovykh indeksiv materynskoj produktyvnosti svynei [Effectiveness of breeding and evaluation indices of maternal productivity of pigs]. *Naukovo-tekhnichnyi biuleten Instytutu tvarynnytstva NAAN*, 102, 173–183 (in Ukrainian). [\[Google Scholar\]](#)
- Walsh, P. S., Metzger, D. A., & Higuchi, R. (1991). Chelex 100 as a medium for simple extraction of DNA for PCR-based typing from forensic material. *BioTechniques*, 10(4), 506–513. [\[Abstract\]](#) [\[Google Scholar\]](#)
- Yang, Y., Gan, M., Yang, X., Zhu, P., Luo, Y., Liu, B., Zhu, K., Cheng, W., Chen, L., Zhao, Y., Niu, L., Wang, Y., Zhang, H., Wang, J., Shen, L., & Zhu, L. (2023). Estimation of genetic parameters of pig reproductive traits. *Frontiers in Veterinary Science*, 10, 1172287. [\[Crossref\]](#) [\[Google Scholar\]](#)
- Yu, G., Wang, C., & Wang, Y. (2022). Genetic parameter analysis of reproductive traits in Large White pigs. *Animal bioscience*, 35(11), 1649–1655. [\[Crossref\]](#) [\[Google Scholar\]](#)
- Zhang, H., Bao, S., Zhao, X., Bai, Y., Lv, Y., Gao, P., Li, F., & Zhang, W. (2024). Genome-Wide Association Study and Phenotype Prediction of Reproductive Traits in Large White Pigs. *Animals*, 14(23), 3348. [\[Crossref\]](#) [\[Google Scholar\]](#)
- Zhang, J., Li, J., Wu, C., Hu, Z., An, L., Wan, Y., Fang, C., Zhang, X., Li, J., & Wang, Y. (2020). The Asp298Asn polymorphism of melanocortin-4 receptor (MC4R) in pigs: evidence for its potential effects on MC4R constitutive activity and cell surface expression. *Animal genetics*, 51(5), 694–706. [\[Crossref\]](#) [\[Google Scholar\]](#)