

UDC 575.22:636.082:636.4(477)

GENETICS IN PIG BREEDING: A REVIEW OF UKRAINIAN RESEARCH IN INTERNATIONAL SCIENTIFIC PUBLICATIONS

M. Yu. Peka

V. N. Karazin Kharkiv National University
4 Svobody Sq, Kharkiv, Ukraine, 61022
<https://ror.org/03ftejk10>

Peka M. Yu. ✉

pekapoltava@gmail.com

<https://orcid.org/0000-0003-0612-1164>

Manuscript was received/

Рукопис надійшов

16.04.2026

Received after review/

Після рецензування

28.04.2026

Accepted for printing/

Прийнято до друку

22.06.2026

Available online/

Доступно онлайн

30.06.2026

Declaration of conflicts of interest/

Декларування конфлікту інтересів:

Not necessary/

Не потрібно

Ethical approval/

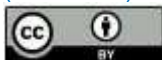
Етичне схвалення:

Not applicable/

Не застосовується



Attribution Licens 4.0 International
(CC BY 4.0)



Objective. The aim of this study was to systematically analyze publications on pig genetics authored by Ukrainian researchers and indexed in the Scopus database, with emphasis on identifying the main research directions, methodological approaches, frequently studied genetic polymorphisms, and pig breeds. An additional objective was to assess how Ukrainian research in pig breeding genetics is represented within the international scientific space. **Methods.** A systematic literature search was conducted in the Scopus database. The selection process included identification, screening of titles and abstracts, and eligibility assessment based on full-text analysis. Inclusion criteria comprised original research articles and reviews focused on pig genetics with at least one Ukrainian-affiliated author. Exclusion criteria included conference abstracts, studies not directly related to pig genetics and those violating ethical standards. Data analysis focused on genetic markers, breeds, traits studied, and methodological approaches. **Results.** The initial search yielded 126 records, of which 39 publications met the inclusion criteria after screening and eligibility assessment. The dataset demonstrated thematic heterogeneity, with 29 studies directly addressing molecular genetic variability, predominantly through analysis of single nucleotide polymorphisms. The most frequently studied gene was *MC4R*, followed by *RYR1*, *ESR1*, *PRLR*, *LEP*, and *LEPR*. Research was primarily conducted on Ukrainian Large White pigs, with limited representation of other breeds. The main areas of investigation included growth traits, reproductive performance, and meat quality characteristics. Methodologically, the majority of studies employed PCR-based approaches, especially PCR-RFLP, while genome-wide approaches such as sequencing and GWAS were absent. The analysis also indicated a relatively small number of Scopus-indexed publications compared to the broader range of national research. **Conclusions.** Ukrainian research in pig genetics, as represented in internationally indexed literature, is characterized by a focus on candidate and causal gene polymorphisms and marker-assisted selection. However, its international visibility remains limited, and methodological approaches lag behind current global trends. Future development requires both the adoption of genome-wide technologies and increased integration into international scientific publishing to enhance the accessibility and impact of Ukrainian research.

Keywords: pig genetics, pig breeding, Ukraine, polymorphism, SNP, marker-assisted selection, candidate genes, Scopus, PCR-RFLP.

Для цитування (за ДСТУ 8302:2025):

Пека М. Ю. Genetics in Pig Breeding: a Review of Ukrainian Research in International Scientific Publications. *Свинарство і агропромислове виробництво* : міжвідом. темат. наук. зб. / Ін-т свинарства і АПВ НААН. Полтава, 2026. Вип. 7(85). С. 42–57. [https://doi.org/10.37143/2786-7730-2026-7\(85\)4](https://doi.org/10.37143/2786-7730-2026-7(85)4)

Introduction. The intensification of animal production systems in the context of global food security has positioned genetic improvement as a central determinant of efficiency, sustainability, and product quality in livestock industries. In pig breeding, advances in molecular genetics have enabled a transition from phenotype-driven selection toward genotype-informed strategies, thereby accelerating genetic gain and enhancing the precision of breeding programs [1, 2]. Among these approaches, the identification and utilization of DNA polymorphisms, the development of reliable genotyping platforms, and the implementation of marker-assisted selection (MAS) have become important tools [3]. While genomic selection has emerged as a dominant paradigm in leading breeding systems worldwide [4–8], its adoption remains uneven, particularly in countries where infrastructural, financial, and institutional constraints limit large-scale genomic integration.

Within this global landscape, Ukrainian research in pig genetics represents a distinctive case shaped by both strong scientific traditions in animal breeding [9] and systemic challenges affecting the visibility and dissemination of research outputs. Historically, Ukrainian scientists have contributed to the study of genetic polymorphisms associated with economically important traits in pigs, including growth performance, meat quality, and reproductive efficiency. These investigations have primarily relied on candidate gene approaches, with particular attention to polymorphic variants in genes such as *MC4R*, *RYR1*, *ESR1*, *PRLR*, and others. The application of polymerase chain reaction (PCR)-based methods, restriction fragment length polymorphism (RFLP) analysis, and related genotyping techniques has enabled the characterization of allelic diversity within both local and commercial pig breeds [10–12].

Despite these efforts, the international visibility of Ukrainian research in this domain remains limited. A substantial proportion of scientific findings has traditionally been disseminated through national journals and other locally oriented publication channels that are not indexed in major international databases. As a result, the global scientific community has only partial access to the Ukrainian body of research. Publications indexed in Scopus constitute a key interface through which Ukrainian studies become accessible to an international readership, effectively shaping the external perception of national research activity in pig genetics.

In this context, the present systematic review is designed to address several interrelated objectives. First, it **aims** to identify and systematize Scopus-indexed publications authored by Ukrainian researchers that focus on the genetics of pigs. The review seeks to characterize the spectrum of studied genetic polymorphisms, the methodological approaches employed for genotyping, and the extent to which MAS is represented. Particular emphasis is placed on determining which pig breeds have been investigated, how frequently specific candidate genes and polymorphisms appear in the literature, and how research efforts are distributed across different scientific groups and institutions.

In addition, the review aims to examine how Ukrainian research in pig genetics is presented within the international scientific space. By focusing exclusively on Scopus-indexed publications, it seeks to delineate the subset of studies that are visible to researchers who do not have access to Ukrainian-language sources. This approach is intended to provide a structured basis for evaluating the thematic priorities, methodological orientations, and scope of

Ukrainian contributions as they are communicated to a global audience. Through these objectives, the review is positioned to contribute to a clearer understanding of both the content and the international representation of Ukrainian research in pig breeding genetics.

Methods. The methodology of this systematic review was designed to ensure transparent, reproducible, and targeted identification of internationally visible publications on pig genetics authored by Ukrainian researchers. The primary source of bibliographic data was the Scopus database, and the search strategy was constructed to capture publications at the intersection of pig breeding and genetics while simultaneously limiting results to those affiliated with Ukrainian institutions and published after 1990. The final search string was formulated as: TITLE-ABS-KEY((pig OR swine OR porcine OR boar OR sow OR piglet OR gilt) AND (gene OR genetic OR genome OR genotyping OR polymorphism OR mutation)) AND AFFILCOUNTRY(Ukraine) AND PUBYEAR > 1990 AND PUBYEAR < 2026

The analysis was conducted in several sequential stages, conceptually aligned with standard systematic review workflows [13–15]. At the identification stage, all records retrieved from the database were compiled. During the initial screening stage, titles and abstracts were evaluated to exclude publications not directly related to pig genetics. In the subsequent eligibility assessment, full-text articles were examined, where necessary, to confirm their relevance to the objectives of the review. Inclusion criteria encompassed original research articles and reviews focused on pig genetics that included at least one author affiliated with a Ukrainian institution. Exclusion criteria comprised conference abstracts, studies unrelated to pig genetics, and articles violating ethical standards. Following the selection process, the final dataset of publications was subjected to data analysis.

1. Structure of the literature dataset and its content

The search query yielded 122 unique scientific publications (after removal of two duplicates identified in the Scopus database), while four additional publications were identified in the Scopus database through manual review of the author profiles of researchers included in the original dataset; these records were not retrieved in the initial search due to missing country information in the Scopus metadata. Following title and abstract screening, 52 publications were retained, while the remaining records were excluded due to lack of relevance. Excluded studies primarily focused on other biological objects (e.g., humans or guinea pigs), belonged to unrelated scientific domains in which pigs were only indirectly mentioned, or addressed aspects of pig production not related to genetics (e.g., infectious diseases). Subsequent full-text assessment, including evaluation of content relevance and compliance with ethical standards, resulted in 39 publications deemed eligible for further analysis.

The final dataset exhibited notable heterogeneity in both scope and research focus. Specifically, three publications [16–18] addressed pig genetic resources in a broad context, one study focused on cytogenetics [19], and two publications represented reviews of individual pig genes [20, 21]. Two studies investigated gene expression at the mRNA level [22, 23], while the other two [24, 25] were exclusively *in silico* analyses without laboratory research. The remaining

29 publications constituted molecular genetic studies of pig genetic variability. Within this subset, one study [26] examined microsatellite loci, one focused on mitochondrial DNA [27], and one presented a comparative study of pig somatotropin forms coded by different genes [28], while the majority (26 studies) investigated single nucleotide polymorphisms (SNPs) in one or several genes [29–51].

2. Main directions of genetic research in pig breeding in Ukraine

Publications investigating genetic variability in pigs within the framework of population and association studies are of particular relevance. A substantial proportion of these studies focuses on the distribution of SNPs in candidate and causal genes across different pig breeds and their associations with economically important traits. Consolidated information on the genes studied by Ukrainian research groups (as well as Ukrainian scientists participating in international collaborations), the pig breeds analyzed, and the productive traits evaluated is presented in Table 1.

Table 1. Main studied genes, pig breeds and associations with productive traits

Gene	Breed	Studied associations with productive traits	Source
CTSB	Ukrainian Large White, English Large White, Large Black, Landrace, Ukrainian Steppe Spotted, Ukrainian Steppe White, Myrhorod, Poltava Meat, Meishan, Pietrain	N/A (population study)	[10]
	Ukrainian Large White	Meat quality parameters	[11]
CTSD	Ukrainian Large White	Meat quality parameters	[12]
CTSF	Ukrainian Large White	Meat quality parameters	[12]
CTSK	Ukrainian Large White, English Large White, Large Black, Landrace, Ukrainian Steppe Spotted, Ukrainian Steppe White, Myrhorod, Poltava Meat, Meishan, Pietrain	N/A (population study)	[10]
	Ukrainian Large White	Meat quality parameters	[11]
CTSL	Ukrainian Large White, English Large White, Large Black, Landrace, Ukrainian Steppe Spotted, Ukrainian Steppe White, Myrhorod, Poltava Meat, Meishan, Pietrain	N/A (population study)	[10]
	Ukrainian Large White	Meat quality parameters	[11]
CTSS	Ukrainian Large White, English Large White, Large Black, Landrace, Ukrainian Steppe Spotted, Ukrainian Steppe White, Myrhorod, Poltava Meat, Meishan, Pietrain	N/A (population study)	[10]
	Ukrainian Large White	Meat quality parameters	[11]
ESR1	Ukrainian Large White	Reproductive traits	[29]
	Ukrainian Large White, English Large White, Large Black, Landrace, Ukrainian Steppe Spotted, Ukrainian Steppe White, Myrhorod, Poltava Meat, Meishan, Pietrain	N/A (population study)	[10]
	Myrhorod, Poltava Meat	Reproductive traits, selection indices	[30]
FUT1	Ukrainian Meat Breed	N/A (population study)	[31]
	Ukrainian Large White	Growth traits, backfat thickness	[32]

Continuation of the tabl.

Gene	Breed	Studied associations with productive traits	Source
GH	Ukrainian Large White, Myrhorod	N/A (methodological study)	[33]
	Ukrainian Large White, English Large White, Large Black, Landrace, Ukrainian Steppe Spotted, Ukrainian Steppe White, Myrhorod, Poltava Meat, Meishan, Pietrain	N/A (population study)	[10]
GHRH	Ukrainian Large White	Meat quality parameters	[11]
IGF2	Ukrainian Large White, English Large White, Large Black, Landrace, Ukrainian Steppe Spotted, Ukrainian Steppe White, Myrhorod, Poltava Meat, Meishan, Pietrain	N/A (population study)	[10]
	Ukrainian Large White	Meat quality parameters	[12]
LEP	Ukrainian Large White	Growth traits, backfat thickness	[34]
	Ukrainian Large White	Meat quality parameters	[35]
	French Large White, Belgian Large White, French × Belgian crossbreed	N/A (population study)	[36]
LEPR	Ukrainian Large White	Meat quality parameters	[11]
	Ukrainian Large White	Growth traits, backfat thickness	[34]
	Ukrainian Large White	Meat quality parameters	[35]
MC4R	Ukrainian Large White	Backfat thickness	[37]
	Ukrainian Large White, English Large White, Large Black, Landrace, Ukrainian Steppe Spotted, Ukrainian Steppe White, Myrhorod, Poltava Meat, Meishan, Pietrain	N/A (population study)	[10]
	Ukrainian Large White	Growth traits, backfat thickness, selection indices	[38]
	Ukrainian Large White	Growth traits, backfat thickness, selection indices	[39]
	Ukrainian Large White	Growth traits, backfat thickness, blood biochemical parameters	[40]
	Ukrainian Large White	Growth traits, backfat thickness, selection indices	[41]
	Ukrainian Large White	Reproductive traits	[42]
	Myrhorod	N/A (population study)	[43]
	Ukrainian Large White × Landrace crossbreed	Growth traits, backfat thickness	[44]
	N/A	N/A (<i>in silico</i> study)	[24]
MUC4	Ukrainian Meat Breed	N/A (population study)	[31]
NR6A1	N/A	N/A (<i>in silico</i> study)	[24]
PRKAG3	N/A	N/A (<i>in silico</i> study)	[24]
PRLR	Ukrainian Large White, English Large White, Large Black, Landrace, Ukrainian Steppe Spotted, Ukrainian Steppe White, Myrhorod, Poltava Meat, Meishan, Pietrain	N/A (population study)	[10]
	Myrhorod, Poltava Meat	Reproductive traits, selection indices	[30]

Continuation of the tabl.

Gene	Breed	Studied associations with productive traits	Source
<i>RYR1</i>	Ukrainian Large White, Myrhorod, Poltava Meat	Viability of piglets	[46]
	Ukrainian Large White, English Large White, Large Black, Landrace, Ukrainian Steppe Spotted, Ukrainian Steppe White, Myrhorod, Poltava Meat, Meishan, Pietrain	N/A (population study)	[10]
	Landrace	Reproductive traits, selection indices	[47]
	Welsh	Reproductive traits, selection indices	[48]
	Myrhorod	N/A (population study)	[43]
	N/A	N/A (<i>in silico</i> study)	[24]
	French Large White, Belgian Large White, French × Belgian crossbreed	N/A (population study)	[36]
<i>SCD</i>	Duroc	Intramuscular fat content	[49]
<i>SLC11A1 (NRAMP1)</i>	Ukrainian Large White	Growth traits, backfat thickness	[50]
	Ukrainian Large White	Growth traits, backfat thickness	[32]
<i>SYNGR2</i>	N/A	N/A (<i>in silico</i> study)	[24]
<i>TERT</i>	N/A	N/A (<i>in silico</i> study)	[25]
	Ukrainian Large White	N/A (methodological study)	[51]

Note. N/A – not available (corresponding data is not available from the study).

The most extensively studied gene in pigs by Ukrainian researchers is *MC4R* (melanocortin 4 receptor). This gene was addressed in 11 of the studies included in the present review [10, 24, 37–45]. All of these investigations focused on the same SNP, rs81219178 (c.1426G>A), a missense polymorphism resulting in the amino acid substitution D298N in the encoded protein [24]. This variant has been analyzed for associations with a broad spectrum of productive traits, including litter size (total number of piglets born and number born alive), litter weight, birth weight, average daily gain, number of piglets at weaning, litter weight at weaning, age at reaching 100 kg body weight, backfat thickness, body length, selection indices, and certain biochemical blood parameters. Most association studies were conducted in Large White pigs of various origins, although population-level data for this polymorphism are available for a wider range of breeds. Despite inconsistent evidence regarding its association with specific traits, this polymorphism has remained a sustained focus of multiple research groups over time.

Another frequently studied gene is *RYR1* (ryanodine receptor 1) [10, 24, 36, 43, 46–48], particularly the missense polymorphism rs344435545 (g.1843C>T), which results in the R615C substitution in the receptor protein [24]. This variant is widely regarded as causal for Porcine Stress Syndrome and is associated with malignant hyperthermia [46], which underpins its continued research relevance. However, among the Scopus-indexed publications analyzed in this review, only several studies assessed its association with viability of piglets [46], reproductive traits (including number of piglets born alive, total number born, and litter weight), or selection indices [47, 48]. The remaining studies primarily addressed population-genetic distributions or theoretical aspects of this polymorphism [10, 24, 36, 43].

SNPs in the *ESR1* (estrogen receptor 1) and *PRLR* (prolactin receptor) genes have been examined in several studies [29, 30] for their associations with reproductive traits in pigs, including the number of piglets born alive, total number of piglets born, number of piglets at weaning, and litter weight at weaning. These traits are hypothesized to be influenced by genetic variation in the respective loci. Association analyses have been conducted primarily in Ukrainian Large White, Myrhorod, and Poltava Meat breeds [29, 30], with additional population-level data reported for several other breeds [10]. However, the overall strength of evidence supporting these associations remains limited, largely due to constraints on the number of available studies with strong associations.

Polymorphisms in a range of genes have also been investigated in relation to meat quality parameters, including intramuscular fat content, protein, ash, water content, pH, and other physicochemical characteristics of pork [11, 12, 35]. These studies have focused on genes encoding cathepsins (e.g., *CTSB*, *CTSD*, *CTSF*, *CTSK*, *CTSL*, and *CTSS*), as well as *LEP* (leptin) and its receptor *LEPR*, *GHRH* (growth hormone-releasing hormone), and *IGF2* (insulin-like growth factor 2). Notably, these investigations [11–12, 35] have predominantly been conducted in Ukrainian Large White pigs and are largely attributable to a single research group, with results disseminated across multiple publications.

Several additional genes have been addressed in isolated studies. For instance, polymorphisms in *MUC4*, *FUT1*, and *SLC11A1*, which are considered candidates for influencing resistance to infectious diseases, have been investigated in several works [31, 32, 50]. However, these studies primarily report population genetic characteristics or associations with growth traits and backfat thickness, while direct analyses of disease resistance phenotypes remain absent. Similarly, recent studies [24, 25] have employed *in silico* approaches to predict the functional relevance of polymorphisms in genes such as *TERT*, *PRKAG3*, *SYNGR2*, and *NR6A1*. Nevertheless, association studies linking these variants to productive traits in Ukrainian pig populations have not yet been reported in Scopus-indexed publications.

3. Current status of genetic research in pig breeding in Ukraine: issues and prospects

The majority of genetic studies in pig breeding, as represented in Scopus-indexed publications, have been conducted by research groups affiliated with several key scientific institutions. Leading positions are held by the Institute of Pig Breeding and Agroindustrial Production of the National Academy of Agrarian Sciences of Ukraine (Poltava, Ukraine); Poltava State Agrarian University (Poltava, Ukraine); and the Institute of Grain Crops of the National Academy of Agrarian Sciences of Ukraine (Dnipro, Ukraine), among others. At the level of individual contributions, the most prolific authors include Balatsky Viktor (14 publications), Saienko Artem (14 publications), Tsereniuk Oleksandr (10 publications), and Vashchenko Pavlo (8 publications), who frequently appear as co-authors in overlapping collaborations.

The vast majority of studies have been conducted on the Ukrainian Large White pig breed, as well as on Large White populations of other geographical origins. Other breeds, including Myrhorod, Landrace, and Poltava Meat pigs, are represented far less frequently. Consequently, most association data are

available for Ukrainian Large White pigs. The principal focus of these studies includes growth performance traits, reproductive characteristics of sows, and meat quality parameters.

A key limitation is the relatively small number of studies available in Scopus-indexed sources. At the same time, analysis of reference lists within these publications indicates that the actual volume of research on pig genetics in Ukraine is substantially larger. A significant proportion of studies appears to have been published in journals not indexed in Scopus, resulting in fragmented international visibility and limited accessibility for the global scientific community. As a consequence, for certain genes and breeds, only population-level studies without association analyses were identified within this review. It is plausible that complementary association studies exist outside the indexed publications or that some research efforts did not progress beyond the population-genetic stage.

A positive trend is the increase in the number of publications in the analyzed dataset during the 2020s, suggesting improved international representation of recent Ukrainian research in pig genetics. However, a major methodological limitation remains evident. Most studies rely on PCR-based approaches, particularly PCR-RFLP. While these methods are suitable for analyzing individual polymorphisms in candidate or causal genes and can support MAS, they are limited in scope [52, 53]. Notably, this methodological framework in pig genetics in Ukraine has remained largely unchanged from the early 2000s to the present.

In contrast, none of the analyzed studies employed sequencing technologies (including Sanger sequencing or next-generation sequencing), microarray-based genotyping, or genome-wide association studies (GWAS), which are standard in contemporary international research [54–58]. This methodological gap constrains the ability to investigate genetic variability at the genome-wide level and limits the implementation of genomic selection approaches, which are generally more effective than marker-assisted strategies [2, 5, 59]. Accordingly, an important prospect for the development of pig genetics research in Ukraine is the transition toward large-scale, genome-wide methodologies. The adoption of advanced genomic tools would enable more comprehensive analyses of genetic architecture and facilitate alignment of Ukrainian research with current international standards in animal breeding science.

Conclusions. This systematic review summarizes pig genetics research conducted by Ukrainian scientists and represented in the Scopus database, reflecting the segment of national research visible to the international scientific community. The analyzed studies are predominantly focused on candidate gene approaches, particularly single nucleotide polymorphisms in genes such as *MC4R*, *RYS1*, *ESR1*, *PRLR*, *LEP*, *LEPR*, and others in relation to growth, reproductive, and meat quality traits. Most investigations are focused on the Ukrainian Large White breed, while the thematic structure of the studies reflects a consistent orientation toward MAS, supported by PCR-based genotyping methodologies.

At the same time, the overall number of Scopus-indexed publications remains relatively small, which constrains the international visibility of Ukrainian research. This limited representation does not fully reflect the actual volume of scientific work conducted within the country, as a substantial proportion of studies is disseminated through non-indexed sources. As a result, the global scientific

community has access only to a partial and potentially fragmented view of Ukrainian research in pig genetics.

Methodologically, the orientation of most studies on individual candidate genes, without integration of genome-wide approaches, including sequencing and GWAS, highlights a gap relative to current global standards and constrains the implementation of genomic selection. Overall, further development of the field requires both methodological advancement toward genome-scale analyses and increased integration into international publication practices to enhance the visibility and impact of Ukrainian research in pig breeding genetics.

REFERENCES

1. Margeta, V., Škorput, D., Djurkin Kušec, I., Kralik, Z., Kušec, G., & Gvozdanović, K. (2025). A Comprehensive Review: Molecular and Genealogical Methods for Preserving the Genetic Diversity of Pigs. *Applied Sci*, 15(6), 3394. <https://doi.org/10.3390/app15063394>
2. Panigrahi, M., Rajawat, D., Nayak, S. S., Bose, A., Bharia, N., Singh, S., Sharma, A., & Dutt, T. (2025). Advancements in Animal Breeding: From Mendelian Genetics to Machine Learning. *Intern J of molecular Sci*, 26(23), 11352. <https://doi.org/10.3390/ijms262311352>
3. Krupa, E., Moravčíková, N., Krupová, Z., & Žáková, E. (2021). Assessment of the Genetic Diversity of a Local Pig Breed Using Pedigree and SNP Data. *Genes*, 12(12), 1972. <https://doi.org/10.3390/genes12121972>
4. Samorè, A. B., Buttazzoni, L., Gallo, M., Russo, V., & Fontanesi, L. (2015). Genomic selection in a pig population including information from slaughtered full sibs of boars within a sib-testing program. *Animal : an Intern J of Animal Biosci*, 9(5), 750–759. <https://doi.org/10.1017/S1751731114002924>
5. Samorè, A. B., & Fontanesi, L. (2016). Genomic selection in pigs: state of the art and perspectives. *Italian J of Animal Sci*, 15(2), 211–232. <https://doi.org/10.1080/1828051X.2016.1172034>
6. Su, R., Lv, J., Xue, Y., Jiang, S., Zhou, L., Jiang, L., Tan, J., Shen, Z., Zhong, P., & Liu, J. (2025). Genomic selection in pig breeding: comparative analysis of machine learning algorithms. *Genetics, Selection, Evolution : GSE*, 57(1), 13. <https://doi.org/10.1186/s12711-025-00957-3>
7. Biscarini, F., Nicolazzi, E. L., Stella, A., Boettcher, P. J., & Gandini, G. (2015). Challenges and opportunities in genetic improvement of local livestock breeds. *Frontiers in Genetics*, 6, 33. <https://doi.org/10.3389/fgene.2015.00033>
8. Misztal, I., Aguilar, I., Lourenco, D., Ma, L., Steibel, J. P., & Toro, M. (2021). Emerging issues in genomic selection. *J of Animal Sci*, 99(6), skab092. <https://doi.org/10.1093/jas/skab092>
9. Voitenko, S. L. (2024). Pigs of meat breeds in Ukraine and the need for the revival of pig breeding. *Animal Breeding and Genetics*, 67, 29–45. <https://doi.org/10.31073/abg.67.04>
10. Balatsky, V. N., Saienko, A. M., Pena, R. N., Buslyk, T. V., & Gibolenko, O. S. (2015). Genetic diversity of pig breeds on ten production quantitative traits loci. *Cytology and Genetics*, 49(5), 299–307. <https://doi.org/10.3103/S0095452715050023>
11. Balatsky, V., Bankovska, I., Pena, R. N., Saienko, A., Buslyk, T., Korinnyi, S., & Doran, O. (2016). Polymorphisms of the porcine cathepsins, growth hormone-releasing hormone and leptin receptor genes and their association with meat quality traits in Ukrainian Large White breed. *Molecular Biology Reports*, 43(6), 517–526. <https://doi.org/10.1007/s11033-016-3977-z>
12. Balatsky, V. N., Oliynychenko, Y. K., Buslyk, T. V., Bankovska, I. B., Korinnyi, S. N., Saienko, A. M., & Pochernyaev, K. F. (2021). Associations of QTL Region Genes of Chromosome 2 with Meat Quality Traits and Productivity of the Ukrainian Large White Pig Breed. *Cytology and Genetics*, 55(1), 53–62. <https://doi.org/10.3103/S0095452721010023>
13. Calderon Martinez, E., Ghattas Hasbun, P. E., Salolin Vargas, V. P., García-González, O. Y., Fermin Madera, M. D., Rueda Capistrán, D. E., Campos Carmona, T., Sanchez Cruz, C., & Teran Hooper, C. (2025). A comprehensive guide to conduct a systematic review and meta-analysis in medical research. *Medicine*, 104(33), e41868. <https://doi.org/10.1097/MD.00000000000041868>

14. Brignardello-Petersen, R., Santesso, N., & Guyatt, G. H. (2025). Systematic reviews of the literature: an introduction to current methods. *American J of Epidemiology*, 194(2), 536–542. <https://doi.org/10.1093/aje/kwae232>
15. Randles, R., & Finnegan, A. (2023). Guidelines for writing a systematic review. *Nurse Education Today*, 125, 105803. <https://doi.org/10.1016/j.nedt.2023.105803>
16. Ibatullin, M., Varchenko, O., Svynous I., Khakhula, B., & Dragan, O. (2019). Organizational and economic bases of pig breeding in Ukraine. *Intern J of Management and Business Research*, 9(1), 59–72.
17. Kramarenko, A. S., Karatieieva, O. I., Liuta, I. M., & Kramarenko, S. S. (2024). Genetic and non-genetic factors influencing piglet stillbirth risk. *Regulatory Mechanisms in Biosystems*, 15(4), 875–881. <https://doi.org/10.15421/0224126>
18. Voloshynov, V., Povod, M., Mykhalko, O., Verbelchuk, T., Verbelchuk, S., Koberniuk, V., Lavryniuk, O., & Shcherbatiuk, N. (2024). The efficiency of pigs from different genetic origins under industrial conditions in Ukraine. *Online J of Animal and Feed Research*, 14(4), 225–233. <https://doi.org/10.51227/ojafr.2024.27>
19. Ostapovets, L., & Starodub, L. (2016). Cytogenetical and biotechnological methods for assessing boar reproductive potential. *Bulgarian J of Agricultural Sci*, 22, 123–126.
20. Balatskiĭ, V. N., & Lisovskiĭ, I. L. (1998). The genetic polymorphism of somatotropin. *TSitologiya i Genetika*, 32(2), 92–104.
21. Burkina, V., Rasmussen, M. K., Oliinychenko, Y., & Zamaratskaia, G. (2019). Porcine cytochrome 2A19 and 2E1. *Basic and Clinical Pharmacology and Toxicology*, 124(1), 32–39. <https://doi.org/10.1111/bcpt.13121>
22. Guo, L., Miao, Z., Ma, H., & Melnychuk, S. (2020). Effects of maternal vitamin D3 during pregnancy on FASN and LIPE mRNA expression in offspring pigs. *J of Agricultural Sci*, 158(1–2), 128–135. <https://doi.org/10.1017/S0021859620000210>
23. Guo, L., Miao, Z., Ma, H., & Melnychuk, S. (2020). Effects of maternal vitamin D3 concentration during pregnancy on adipogenic genes expression and serum biochemical index in offspring piglets. *J of Animal and Feed Sci*, 29(2), 125–131. <https://doi.org/10.22358/jafs/124041/2020>
24. Peka, M., & Balatsky, V. (2024). Bioinformatic approach to identifying causative missense polymorphisms in animal genomes. *BMC Genomics*, 25(1). <https://doi.org/10.1186/s12864-024-11126-z>
25. Peka, M., Balatsky, V., Saienko, A., & Tsereniuk, O. (2023). Bioinformatic analysis of the effect of SNPs in the pig TERT gene on the structural and functional characteristics of the enzyme to develop new genetic markers of productivity traits. *BMC Genomics*, 24(1). <https://doi.org/10.1186/s12864-023-09592-y>
26. Pochernayev, K. K., Kiyuitsa, K. I., Telegeev, G. D., Dybkov, M. V., & Malyuta, S. S. (1996). M13 phage DNA probe informativity rising at studying pig genome. *Biopolymers and Cell*, 12(3), 64–66. <https://doi.org/10.7124/bc.00042F>
27. Kubejko, J., Clop, A., Balatsky, V., Pochernyaev, K., Eghbalsaid, S., & Amills, M. (2017). Mitochondrial DNA variation in Ukrainian wild boars. *Animal Genetics*, 48(6), 725–726. <https://doi.org/10.1111/age.12592>
28. Balatskiĭ V. N. (1992). Multiple forms of pig somatotropin. *TSitologiya i Genetika*, 26(5), 32–36.
29. Balatsky, V. N., Saenko, A. M., & Grishina, L. P. (2012). Polymorphism of the estrogen receptor 1 locus in populations of pigs of different genotypes and its association with reproductive traits of Large White sows. *Cytology and Genetics*, 46(4), 233–237. <https://doi.org/10.3103/S0095452712040020>
30. Matiuk, V. V., Saienko, A. M., Vashchenko, P. A., Slynko, V. H., Fesenko, O. G., Peka, M. Y., & Tsereniuk, O. M. (2025). Association of polymorphisms in estrogen and prolactin receptor genes with reproductive traits in sows of rare breeds. *Regulatory Mechanisms in Biosystems*, 33(1), e25033. <https://doi.org/10.15421/0225033>
31. Syrovnev, G. I. (2014). Genetic polymorphism of FUT1 and MUC4 loci in a local population of Ukrainian meat bread pigs. *Cytology and Genetics*, 48(5), 318–322. <https://doi.org/10.3103/S0095452714050119>
32. 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. <https://doi.org/10.15421/022229>

33. Balatskiĭ, V. N., & Pocherniaev, K. F. (1995). The polymorphic BsuRI restriction site of the swine growth hormone gene. *TSitologiya i Genetika*, 29(1), 45–48.
34. Balatsky, V., Oliinychenko, Y., Sarantseva, N., Getya, A., Saienko, A., Vovk, V., & Doran, O. (2018). Association of single nucleotide polymorphisms in leptin (LEP) and leptin receptor (LEPR) genes with backfat thickness and daily weight gain in Ukrainian Large White pigs. *Livestock Sci*, 217, 157–161. <https://doi.org/10.1016/j.livsci.2018.09.015>
35. Balatsky, V. N., Oliinychenko, Y. K., Saienko, A. M., Buslyk, T. V., Bankovska, I. B., Peka, M. Yu., & Doran, O. (2022). Associations of Polymorphisms in Leptin and Leptin Receptor Genes with Meat Quality in Pigs of the Ukrainian Large White Breed. *Cytology and Genetics*, 56(6), 513–525. <https://doi.org/10.3103/S0095452722060020>
36. Bordun, O., Khalak, V., Skliarenko, Y., Gutyj, B., Stadnytska, O., Ilchenko, M., Shevchenko, O., Kibenko, N., & Kravchenko, N. (2025). Evaluation of the Genotypes of Pigs of Different Origins According to the RYR1 and LEP Genes. *Acta Fytotechnica et Zootechnica*, 28(1), 1–6. <https://doi.org/10.15414/afz.2025.28.01.1-6>
37. Lyadskiy, I. K., Getya, A. A., & Pochernyaev, K. F. (2011). Association of the Asp298Asn polymorphism in the mc4r gene with back fat thickness in pigs of the Large White breed. *Cytology and Genetics*, 45(2), 106–109.
38. Kozyr, V., Khalak, V., & Povod, M. (2019). DNA-type results swine for MS4R-gene and its association with productivity. *AgroLife Scientific J*, 8(1), 128–133.
39. Khalak, V. (2020). Fattening and meat qualities of store pigs of large white breed of different intra-breed differentiation by melanocortin-4 receptor gene (MC4R). *Scientific Horizons*, 23(9), 30–37. [https://doi.org/10.48077/scihor.23\(9\).2020.30-37](https://doi.org/10.48077/scihor.23(9).2020.30-37)
40. Khalak, V., Horchanok, A., Kuzmenko, O., Lytvyschenko, L., Prysiazniuk, N., & Bordun, A. (2021). Interior profile of young pigs of different genotypes and the use of its components for early prediction of quantitative characters. *AgroLife Scientific J*, 10(2), 92–98. <https://doi.org/10.17930/AGL2021211>
41. 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. <https://doi.org/10.46419/vs.54.6.10>
42. Zhukorskyi, O. M., Tsereniuk, O. M., Sukhno, T. V., Saienko, A. M., Polishchuk, A. A., Chereuta, Y. V., Shaferivskyi, B. S., & Vashchenko, P. A. (2023). The influence of genotype and feeding level of gilts on their further reproductive performance. *Regulatory Mechanisms in Biosystems*, 14(2), 312–318. <https://doi.org/10.15421/022346>
43. Tsereniuk, O. M., Vashchenko, P. A., Khokhlov, A. M., Tsybenko, V. H., Shostia, G. M., Saenko, A. M., Peka, M. Y., & Zhukorskyi, O. M. (2023). Comparative characteristics of polymorphisms of melanocortin 4 and ryanodine 1 receptor genes of Myrhorod pigs before and after the African swine fever outbreak. *Regulatory Mechanisms in Biosystems*, 14(4), 601–608. <https://doi.org/10.15421/022387>
44. 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. <https://doi.org/10.15421/022317>
45. Khalak, V., Bordun, O., Skliarenko, Y., Gutyj, B., Zasukha, L., Horchanok, A., Kuzmenko, O., & Priszazhnjuk, N. (2025). Study of Polymorphism of the MC4R Locus in Pigs of the Large White Breed. *Acta Fytotechnica et Zootechnica*, 28(4), 282–287. <https://doi.org/10.15414/afz.2025.28.04.282-287>
46. Balatskiĭ, V. N., & Metlitskaia, E. N. (2001). DNA diagnosis of porcine stress syndrome and RYRI genotype association with viability of young pigs. *TSitologiya i genetika*, 35(3), 43–49.
47. Tsereniuk, O. M., Bobrytska, O. M., Miroshnikova, O. S., & Danchuk, O. V. (2020). DNA-type results of Landrace sows for RYR1-gene and its association with productivity. *Regulatory Mechanisms in Biosystems*, 11(3), 431–437. <https://doi.org/10.15421/022066>
48. 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. <https://doi.org/10.15421/022248>

49. Solé, E., González-Prendes, R., Oliinychenko, Y., Tor, M., Ros-Freixedes, R., Estany, J., & Pena, R. N. (2022). Transcriptome shifts triggered by vitamin A and SCD genotype interaction in Duroc pigs. *BMC Genomics*, 23(1). <https://doi.org/10.1186/s12864-021-08244-3>
50. Vashchenko, P., Saienko, A., Sukhno, V., Tsereniuk, O., Babicz, M., Shkavro, N., Smolucha, G., & Łuszczewska-Sierakowska, I. (2022). Association of NRAMP1 gene polymorphism with the productive traits of the Ukrainian Large White pig. *Medycyna Weterynaryjna*, 78(9). <https://doi.org/10.21521/mw.6698>
51. Saienko, A., Peka, M., Tsereniuk, O., Babicz, M., Kropiwić-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. <https://doi.org/10.15421/012352>
52. Hashim, H. O. & Al-Shuhaib, M. B. (2019). Exploring the Potential and Limitations of PCR-RFLP and PCR-SSCP for SNP Detection: A Review. *Journal of Applied Biotechnology Reports*, 6, 137–144. <https://doi.org/10.29252/JABR.06.04.02>
53. Leite, I. G. C., Benard, G., Cavalcanti, S. C., Bollela, V. R., Del Negro, G. M. B., Martinez, R., Gimenes, V. M. F., & Cocio, T. A. (2024). Comparison between PCR-RFLP and sequencing techniques in the analysis of *Paracoccidioides* spp. biodiversity: limitations and insights into species and variant differentiation. *Mycopathologia*, 189(6), 97. <https://doi.org/10.1007/s11046-024-00902-w>
54. Mekonnen, K. T., Lee, D. H., Beyenssa, B. C., Son, A. Y., Cho, Y. G., & Seo, K. S. (2025). Genome-wide association study identifies genetic variants associated with single-parity reproductive loss in three commercial pig breeds. *BMC Genomics*, 26(1), 1054. <https://doi.org/10.1186/s12864-025-12255-9>
55. Panda, S., Kumar, A., Gaur, G. K., Ahmad, S. F., Chauhan, A., Mehrotra, A., & Dutt, T. (2023). Genome wide copy number variations using Porcine 60K SNP Beadchip in Landilly pigs. *Animal Biotechnology*, 34(6), 1891–1899. <https://doi.org/10.1080/10495398.2022.2056047>
56. Hong, Y., He, X., Wu, D., Ye, J., Zhang, Y., Wu, Z., & Tan, C. (2025). Genome Selection and Genome-Wide Association Analyses for Litter Size Traits in Large White Pigs. *Animals: an open access journal from MDPI*, 15(12), 1724. <https://doi.org/10.3390/ani15121724>
57. Wang, X., Wang, L., Shi, L., Zhang, P., Li, Y., Li, M., Tian, J., Wang, L., & Zhao, F. (2022). GWAS of Reproductive Traits in Large White Pigs on Chip and Imputed Whole-Genome Sequencing Data. *Intern J of Molecular Sci*, 23(21), 13338. <https://doi.org/10.3390/ijms232113338>
58. Du, H., Zhou, L., Liu, Z., Zhuo, Y., Zhang, M., Huang, Q., Lu, S., Xing, K., Jiang, L., & Liu, J. F. (2024). The 1000 Chinese Indigenous Pig Genomes Project provides insights into the genomic architecture of pigs. *Nature Communications*, 15(1), 10137. <https://doi.org/10.1038/s41467-024-54471-z>
59. Boichard, D., Ducrocq, V., Croiseau, P., & Fritz, S. (2016). Genomic selection in domestic animals: Principles, applications and perspectives. *Comptes Rendus Biologies*, 339(7–8), 274–277. <https://doi.org/10.1016/j.crv.2016.04.007>

СПИСОК ВИКОРИСТАНИХ ДЖЕРЕЛ

1. A Comprehensive Review: Molecular and Genealogical Methods for Preserving the Genetic Diversity of Pigs / V. Margeta et al. *Applied Sci*. 2025. Vol. 15. Iss. 6. Article 3394. <https://doi.org/10.3390/app15063394>
2. Advancements in Animal Breeding: From Mendelian Genetics to Machine Learning / M. Panigrahi et al. *Intern J. of Molecular Sci*. 2025. Vol. 26. Iss. 23. Article 11352. <https://doi.org/10.3390/ijms262311352>
3. Assessment of the Genetic Diversity of a Local Pig Breed Using Pedigree and SNP Data / E. Krupa et al. *Genes*. 2021. Vol. 12. Iss. 12. Article 1972. <https://doi.org/10.3390/genes12121972>
4. Genomic selection in a pig population including information from slaughtered full sibs of boars within a sib-testing program / A. B. Samorè et al. *Animal: an Intern. J. of Animal Bioscience*. 2015. Vol. 9. Iss. 5. P. 750–759. <https://doi.org/10.1017/S1751731114002924>
5. Samorè A. B., Fontanesi L. Genomic selection in pigs: state of the art and perspectives. *Italian J. of Animal Sci*. 2016. Vol. 15. Iss. 2. P. 211–232. <https://doi.org/10.1080/1828051X.2016.1172034>

6. Genomic selection in pig breeding: comparative analysis of machine learning algorithms/ R. Su et al. *Genetics, Selection, Evolution : GSE*. 2025. Vol. 57. Iss. 1. Article 13. <https://doi.org/10.1186/s12711-025-00957-3>
7. Challenges and opportunities in genetic improvement of local livestock breeds / F. Biscarini et al. *Frontiers in Genetics*. 2015. Vol. 6. Article 33. <https://doi.org/10.3389/fgene.2015.00033>
8. Emerging issues in genomic selection / I. Misztal et al. *Journal of animal science*. 2021. Vol. 99. Iss. 6. Article skab092. <https://doi.org/10.1093/jas/skab092>
9. Voitenko S. L. Pigs of meat breeds in Ukraine and the need for the revival of pig breeding. *Animal Breeding and Genetics*. 2024. Vol. 67. P. 29–45. <https://doi.org/10.31073/abg.67.04>
10. Genetic diversity of pig breeds on ten production quantitative traits loci / V. N. Balatsky et al. *Cytology and Genetics*. 2015. Vol. 49. Iss. 5. P. 299–307. <https://doi.org/10.3103/S0095452715050023>
11. Polymorphisms of the porcine cathepsins, growth hormone-releasing hormone and leptin receptor genes and their association with meat quality traits in Ukrainian Large White breed / V. Balatsky et al. *Molecular Biology Reports*. 2016. Vol. 43. Iss. 6. P. 517–526. <https://doi.org/10.1007/s11033-016-3977-z>
12. Associations of QTL Region Genes of Chromosome 2 with Meat Quality Traits and Productivity of the Ukrainian Large White Pig Breed / V. N. Balatsky et al. *Cytology and Genetics*. 2021. Vol. 55. Iss. 1. P. 53–62. <https://doi.org/10.3103/S0095452721010023>
13. A comprehensive guide to conduct a systematic review and meta-analysis in medical research / E. Calderon Martinez et al. *Medicine*. 2015. Vol. 104. Iss. 33. Article e41868. <https://doi.org/10.1097/MD.00000000000041868>
14. Brignardello-Petersen R., Santesso N., Guyatt G. H. Systematic reviews of the literature: an introduction to current methods. *American J. of Epidemiology*. 2025. Vol. 194. Iss. 2. P. 536–542. <https://doi.org/10.1093/aje/kwae232>
15. Randles R., Finnegan A. Guidelines for writing a systematic review. *Nurse Education Today*. 2023. Vol. 125. Article 105803. <https://doi.org/10.1016/j.nedt.2023.105803>
16. Organizational and economic bases of pig breeding in Ukraine / M. Ibatullin et al. *Intern. J. of Management and Business Research*. 2019. Vol. 9. Iss. 1. P. 59–72.
17. Genetic and non-genetic factors influencing piglet stillbirth risk / A. S. Kramarenko et al. *Regulatory Mechanisms in Biosystems*. 2024. Vol. 15. No. 4. P. 875–881. <https://doi.org/10.15421/0224126>
18. The efficiency of pigs from different genetic origins under industrial conditions in Ukraine / V. Voloshynov et al. *Online J. of Animal and Feed Research*. 2024. Vol. 14. Iss. 4. P. 225–233. <https://doi.org/10.51227/ojafr.2024.27>
19. Ostapovets L., Starodub L. Cytogenetical and biotechnological methods for assessing boar reproductive potential. *Bulgarian J. of Agricultural Sci*. 2016. Vol. 22. P. 123–126.
20. Balatskiĭ V. N., Lisovskii I. L. The genetic polymorphism of somatotropin. *TSitologiya i Genetika*. 1998. Vol. 32. Iss. 2. P. 92–104.
21. Porcine cytochrome 2A19 and 2E1 / V. Burkina et al. *Basic and Clinical Pharmacology and Toxicology*. 2019. Vol. 124. Iss. 1. P. 32–39. <https://doi.org/10.1111/bcpt.13121>
22. Effects of maternal vitamin D 3 during pregnancy on FASN and LIPE mRNA expression in offspring pigs / L. Guo et al. *J. of Agricultural Sci*. 2020. Vol. 158. Iss. 1–2. P. 128–135. <https://doi.org/10.1017/S0021859620000210>
23. Effects of maternal vitamin D3 concentration during pregnancy on adipogenic genes expression and serum biochemical index in offspring piglets / L. Guo et al. *J. of Animal and Feed Sci*. 2020. Vol. 29. Iss. 2. P. 125–131. <https://doi.org/10.22358/jafs/124041/2020>
24. Peka M., Balatsky V. Bioinformatic approach to identifying causative missense polymorphisms in animal genomes. *BMC Genomics*. 2024. Vol. 25. Iss. 1. <https://doi.org/10.1186/s12864-024-11126-z>
25. Bioinformatic analysis of the effect of SNPs in the pig TERT gene on the structural and functional characteristics of the enzyme to develop new genetic markers of productivity traits / M. Peka et al. *BMC Genomics*. 2023. Vol. 24. Iss. 1. <https://doi.org/10.1186/s12864-023-09592-y>

26. M13 phage DNA probe informativity rising at studying pig genome / K. K. Pochernayev et al. *Biopolymers and Cell*. 1996. Vol. 12. Iss. 3. P. 64–66. <https://doi.org/10.7124/bc.00042F>
27. Mitochondrial DNA variation in Ukrainian wild boars / J. Kubejko et al. *Animal Genetics*. 2017. Vol. 48. Iss. 6. P. 725–726. <https://doi.org/10.1111/age.12592>
28. Balatskiĭ V. N. Multiple forms of pig somatotropin. *Tsitologiya i Genetika*. 1992. Vol. 26. Iss. 5. P. 32–36.
29. Balatsky V. N., Saenko A. M., Grishina L. P. Polymorphism of the estrogen receptor 1 locus in populations of pigs of different genotypes and its association with reproductive traits of Large White sows. *Cytology and Genetics*. 2012. Vol. 46. Iss. 4. P. 233–237. <https://doi.org/10.3103/S0095452712040020>
30. Association of polymorphisms in estrogen and prolactin receptor genes with reproductive traits in sows of rare breeds / V. V. Matiiuk et al. *Regulatory Mechanisms in Biosystems*. 2025. Vol. 33. No. 1. e25033. <https://doi.org/10.15421/0225033>
31. Syrovnev G. I. Genetic polymorphism of FUT1 and MUC4 loci in a local population of Ukrainian meat bread pigs. *Cytology and Genetics*. 2014. Vol. 48. Iss. 5. P. 318–322. <https://doi.org/10.3103/S0095452714050119>
32. Association of Fut1 and Slc11a1 gene polymorphisms with productivity traits of Large White pigs / V. V. Sukhno et al. *Regulatory Mechanisms in Biosystems*. 2022. Vol. 13. No 3. P. 225–230. <https://doi.org/10.15421/022229>
33. Balatskiĭ V. N., Pocherniaev K. F. The polymorphic BsuRI restriction site of the swine growth hormone gene. *TSitologiya i Genetika*. 1995. Vol. 29. Iss. 1. P. 45–48.
34. Association of single nucleotide polymorphisms in leptin (LEP) and leptin receptor (LEPR) genes with backfat thickness and daily weight gain in Ukrainian Large White pigs / V. Balatsky et al. *Livestock Sci.* 2018. Vol. 217. P. 157–161. <https://doi.org/10.1016/j.livsci.2018.09.015>
35. Associations of Polymorphisms in Leptin and Leptin Receptor Genes with Meat Quality in Pigs of the Ukrainian Large White Breed / V. N. Balatsky et al. *Cytology and Genetics*. 2022. Vol. 56. Iss. 6. P. 513–525. <https://doi.org/10.3103/S0095452722060020>
36. Evaluation of the Genotypes of Pigs of Different Origins According to the RYR1 and LEP Genes / O. Bordun et al. *Acta Fytotechnica et Zootechnica*. 2025. Vol. 28. No. 1. P. 1–6. <https://doi.org/10.15414/afz.2025.28.01.1-6>
37. Lyadskiy I. K., Getya A. A., Pochernyaev K. F. Association of the Asp298Asn polymorphism in the mc4r gene with back fat thickness in pigs of the Large White breed. *Cytology and Genetics*. 2011. Vol. 45. Iss. 2. P. 106–109.
38. Kozyr V., Khalak V., Povod M. DNA-type results swine for MS4R-gene and its association with productivity. *AgroLife Scientific J.* 2019. Vol. 8. No. 1. P. 128–133.
39. Khalak V. Fattening and meat qualities of store pigs of large white breed of different intra-breed differentiation by melanocortin-4 receptor gene (MC4R). *Scientific Horizons*. 2020. Vol. 23. No. 9. P. 30–37. [https://doi.org/10.48077/scihor.23\(9\).2020.30-37](https://doi.org/10.48077/scihor.23(9).2020.30-37)
40. Interior profile of young pigs of different genotypes and the use of its components for early prediction of quantitative characters / V. Khalak et al. *AgroLife Scientific J.* 2021. Vol. 10. No. 2. P. 92–98. <https://doi.org/10.17930/AGL2021211>
41. Young pig fattening and meat quality due to varying formation intensities in early ontogenesis and two genotypes of the melanocortin receptor 4 (Mc4r) gene / V. Khalak et al. *Veterinarska Stanica*. 2023. Vol. 54. No. 6. P. 613–624. <https://doi.org/10.46419/vs.54.6.10>
42. The influence of genotype and feeding level of gilts on their further reproductive performance / O. M. Zhukorskyi et al. *Regulatory Mechanisms in Biosystems*. 2023. Vol. 14. No. 2. P. 312–318. <https://doi.org/10.15421/022346>
43. Comparative characteristics of polymorphisms of melanocortin 4 and ryanodine 1 receptor genes of Myrhorod pigs before and after the African swine fever outbreak / O. M. Tsereniuk et al. *Regulatory Mechanisms in Biosystems*. 2023. Vol. 14. No. 4. P. 601–608. <https://doi.org/10.15421/022387>
44. The influence of feeding level on the growth of pigs depending on their genotype / P. A. Vashchenko et al. *Regulatory Mechanisms in Biosystems*. 2023. Vol. 14. No. 1. P. 112–117. <https://doi.org/10.15421/022317>
45. Study of Polymorphism of the MC4R Locus in Pigs of the Large White Breed / V. Khalak et al. *Acta Fytotechnica et Zootechnica*. 2025. Vol. 28. No. 4. P. 282–287. <https://doi.org/10.15414/afz.2025.28.04.282-287>

46. Balatskiĭ V. N., Metlitskaia E. N. DNA diagnosis of porcine stress syndrome and RYR1 genotype association with viability of young pigs. *TSitologija i Genetika*. 2001. Vol. 35. Iss. 3. P. 43–49.
47. DNA-type results of Landrace sows for RYR1-gene and its association with productivity / O. M. Tsereniuk et al. *Regulatory Mechanisms in Biosystems*. 2020. Vol. 11. No. 3. P. 431–437. <https://doi.org/10.15421/022066>
48. The effect of the ryanodine receptor gene on the reproductive traits of Welsh sows / O. M. Zhukorskyi et al. *Regulatory Mechanisms in Biosystems*. 2022. Vol. 13. No. 4. P. 367–372. <https://doi.org/10.15421/022248>
49. Transcriptome shifts triggered by vitamin A and SCD genotype interaction in Duroc pigs / E. Solé et al. *BMC Genomics*. 2022. Vol. 23. Iss. 1. <https://doi.org/10.1186/s12864-021-08244-3>
50. Association of NRAMP1 gene polymorphism with the productive traits of the Ukrainian Large White pig / P. Vashchenko et al. *Medycyna Weterynaryjna*. 2022. Vol. 78. Iss. 9. <https://doi.org/10.21521/mw.6698>
51. Analysis of polymorphism and development of a molecular-genetic system for genotyping by the telomerase reverse transcriptase (TERT) gene / A. Saienko et al. *Biosystems Diversity*. 2023. Vol. 31. No. 4. P. 436–443. <https://doi.org/10.15421/012352>
52. Hashim H. O. Al-Shuhaib M. B. Exploring the Potential and Limitations of PCR-RFLP and PCR-SSCP for SNP Detection: A Review. *J. of Applied Biotechnology Reports*. 2019. Vol. 6. P. 137–144. <https://doi.org/10.29252/JABR.06.04.02>
53. Comparison between PCR-RFLP and sequencing techniques in the analysis of *Paracoccidioides* spp. biodiversity: limitations and insights into species and variant differentiation / I. G. C. Leite et al. *Mycopathologia*. 2024. Vol. 189. Iss. 6. Article 97. <https://doi.org/10.1007/s11046-024-00902-w>
54. Genome-wide association study identifies genetic variants associated with single-parity reproductive loss in three commercial pig breeds / K. T. Mekonnen et al. *BMC Genomics*. 2025. Vol. 26. Iss. 1. Article 1054. <https://doi.org/10.1186/s12864-025-12255-9>
55. Genome wide copy number variations using Porcine 60K SNP Beadchip in Landlly pigs / S. Panda et al. *Animal Biotechnology*. 2023. Vol. 34. Iss. 6. P. 1891–1899. <https://doi.org/10.1080/10495398.2022.2056047>
56. Genome Selection and Genome-Wide Association Analyses for Litter Size Traits in Large White Pigs / Y. Hong et al. *Animals : an open access journal from MDPI*. 2023. Vol. 15. Iss. 12. 1724. <https://doi.org/10.3390/ani15121724>
57. GWAS of Reproductive Traits in Large White Pigs on Chip and Imputed Whole-Genome Sequencing Data / X. Wang et al. *Intern. J. of Molecular Sci.* 2022. Vol. 23. Iss. 21. 13338. <https://doi.org/10.3390/ijms232113338>
58. The 1000 Chinese Indigenous Pig Genomes Project provides insights into the genomic architecture of pigs / H. Du et al. *Nature Communications*. 2024. Vol. 15. Iss. 1. Article 10137. <https://doi.org/10.1038/s41467-024-54471-z>
59. Genomic selection in domestic animals: Principles, applications and perspectives / D. Boichard et al. *Comptes Rendus Biologies*. 2016. Vol. 339. No. 7-8. P. 274–277. <https://doi.org/10.1016/j.crv.2016.04.007>

ГЕНЕТИКА У СВИНАРСТВІ: ОГЛЯД УКРАЇНСЬКИХ ДОСЛІДЖЕНЬ У МІЖНАРОДНИХ НАУКОВИХ ПУБЛІКАЦІЯХ

М. Ю. Пека

Харківський національний університет імені В. Н. Каразіна
пл. Свободи, 4, м. Харків, Україна, 62022

Мета. Метою цього дослідження було систематично проаналізувати публікації з генетики свиней, написані українськими дослідниками та проіндексовані в базі даних Scopus, з акцентом на визначення основних напрямків досліджень, методологічних підходів, часто досліджуваних генетичних поліморфізмів та порід свиней. Додатковою метою було оцінити, як українські дослідження в галузі генетики свиней представлені в міжнародному науковому просторі.

Методи. Було проведено систематичний пошук літератури в базі даних Scopus. Процес відбору включав ідентифікацію, скринінг назв та анотацій, а також оцінку придатності на основі повнотекстового аналізу. Критеріям включення відповідали оригінальні дослідницькі статті та

огляди, присвячені генетиці свиней, принаймні з одним автором, афілійованим в Україні. Критеріям виключення відповідали тези конференцій, дослідження, що не пов'язані безпосередньо з генетикою свиней, та ті, в яких порушені етичні стандарти. Аналіз даних був зосереджений на генетичних маркерах, породах, досліджуваних ознаках та методологічних підходах. **Результати.** Початковий пошук дав 126 записи, з яких 39 публікацій відповідали критеріям включення після скринінгу та оцінки придатності. Набір даних продемонстрував тематичну гетерогенність, причому 29 досліджень безпосередньо стосувалися молекулярно-генетичної мінливості, переважно аналізу однонуклеотидних поліморфізмів. Найбільш досліджуваним геном був MC4R, за ним слідували RYR1, ESR1, PRLR, LEP та LEPR. Дослідження проводилися переважно на свинях української великої білої породи, з обмеженим представленням інших порід. Основними напрямками дослідження були ознаки росту, репродуктивна здатність та характеристики якості м'яса. Методологічно більшість досліджень використовували підходи на основі ПЛР, особливо ПЛР-ПДРФ, тоді як підходи, спрямовані на повногеномний аналіз, такі як секвенування та GWAS, були відсутні. Аналіз також показав відносно невелику кількість публікацій, проіндексованих у Scopus, порівняно з ширшим спектром національних досліджень. **Висновки.** Українські дослідження в галузі генетики свиней, представлені в міжнародно індексованій літературі, мають фокус на поліморфізми кандидатних та каузальних генів, а також на маркер-асоційовану селекцію. Однак їх міжнародна видимість залишається обмеженою, а методологічні підходи відстають від сучасних світових тенденцій. Майбутній розвиток вимагає як впровадження повногеномних технологій, так і посилення інтеграції в міжнародні наукові публікації для підвищення доступності та впливу українських досліджень.

Ключові слова: генетика свиней, свинарство, Україна, поліморфізм, SNP, маркер-асоційована селекція, кандидатні гени, Scopus, ПЛР-ПДРФ.

For citation (APA Style):

Peka, M. Yu. (2026). Genetics in Pig Breeding: a Review of Ukrainian Research in International Scientific Publications. *Svynarstvo i Ahropromyslove Vyrobynytstvo* [Pig Breeding and Agroindustrial Production]. Poltava, 7(85), 42–57 [in Ukrainian]. [https://doi.org/10.37143/2786-7730-2025-7\(85\)4](https://doi.org/10.37143/2786-7730-2025-7(85)4)

The use of artificial intelligence (AI):

The authors of this manuscript confirm that, during the course of their research and the preparation of this manuscript, they did not use any generative AI tools or services listed in the Taxonomy for Delegating Tasks to Generative AI (GAIDeT, 2025) to carry out any tasks. All stages of the work were carried out exclusively by the authors.

Information about the authors:

Mykyta Yuriiovych Peka, PhD Student in Biology, Department of Molecular Biology and Biotechnology, School of Biology, V. N. Karazin Kharkiv National University.