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GENETIC RESEARCH IN MODERN CYNOLOGY: SELECTION GOALS AND DIRECTIONS FOR SUCCESS

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Modern scientific approaches, challenges and prospects in the field of domestic dog breeding (Canis lupus familiaris), with an emphasis on combining genetic, behavioural, social and ethical aspects of selection, are under constant attention of both individuals and clubs, professional organisations that carry out targeted work in this field. The complexity of making the right choice in breeding is due, on the one hand, to recent changes in social demand for certain breeds and, on the other hand, to the wide variety of dog breeds: toy (companion) and non-sporting (with unique or mixed functions); sporting (for hunting); working (guard, rescue, sled dogs); herding; hounds (search by scent or hunt by sight), terriers (for burrowing hunting). Each of these groups must perform specific tasks, which historically determined the peculiarities of imprinting and habituation of certain breeds. The process of domestication of dogs is analysed as a multiphase phenomenon, with constant accompaniment and development of affiliative behaviour, and as a result, a strong social bond with humans. Contemporary challenges in dog breeding are considered, in particular the problem of uncontrolled crossbreeding, the emergence of new breeds, the impact of inbreeding, standardisation and the reduction of genetic diversity. Particular attention is paid to the possibilities of using genomic technologies (GWAS, DNA sequencing, breeding value estimation, STR markers) to predict the performance, behaviour and health traits of dogs for various purposes. The need for a clear definition of selection goals and the use of genetic-statistical selection criteria that take into account market demands, the social functions of dogs and welfare requirements is justified. Modern approaches to breeding work in dog breeding are considered, taking into account the achievements of genetics, biotechnology and bioinformatics. The material is based on an interdisciplinary analysis of contemporary scientific literature and leading research in biology, genetics, and genomics of dogs, using analytical, synthetic, and comparative approaches. The results of the studies indicate the need to rethink the goals of dog breeding – from narrow-breed aesthetics to preserving the health, adaptability and social significance of dogs in modern society.

Keywords: dogs, cynology, dog breeds, selection programmes, genomics, biotechnology, heredity, genetic diversity

ГЕНЕТИЧНІ ДОСЛІДЖЕННЯ В СУЧАСНІЙ КІНОЛОГІЇ: ЦІЛІ СЕЛЕКЦІЇ ТА НАПРЯМИ УСПІШНОСТІ

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Сучасні наукові підходи, виклики та перспективи у сфері розведення домашніх собак (Canis lupus familiaris), з акцентом на поєднання генетичних, поведінкових, соціальних та етичних аспектів селекції, знаходяться під постійною увагою як окремих людей так і клубів, професійних організацій які проводять цілеспрямовану роботу в цій сфері. Складність правильного вибору в розведенні, з одного боку зумовлено змінами в останні часи соціального попиту на певні породи, а з другого широкою розгалуженістю порід собак на: іграшкові (компаньйони) та неспортивні (з унікальними або змішаними функціями); спортивні (для полювання); робочі (охорона, порятунок, їздові собаки); пастуші; гончаки (пошук за запахом або полювання за візуальним зображенням), тер'єри (для норного полювання). Кожна з цих груп повинна виконувати конкретні завдання, що історично зумовило особливості імпринтингу та габітуації певних порід. Аналізується процес одомашнення собак як багатофазне явище, з постійним супроводженням та розвитком афіліативної поведінки, й як наслідок сильним соціальним зв'язком з людиною. Розглядаються сучасні виклики в собаківництві, зокрема проблема неконтрольованого схрещування, поява нових порід, вплив інбридингу, стандартизації та скорочення генетичного різноманіття. Окрему увагу приділено можливостям використання геномних технологій (GWAS, секвенування ДНК, оцінка племінної цінності, STR-маркери) для прогнозування ознак продуктивності, поведінки і здоров'я собак різного призначення. Обґрунтовано необхідність чіткого визначення цілей селекції та використання генетико-статистичних критеріїв відбору, які враховують ринкові запити, соціальні функції собак і вимоги до їхнього добробуту. Розглянуто сучасні підходи до провадження селекційної роботи у собаківництві з урахуванням досягнень генетики, біотехнології та біоінформатики. Матеріал базується на міждисциплінарному аналізі сучасної наукової літератури, провідних досліджень з біології, генетики та геноміки собак із використанням аналітичного, синтез- та порівняльного підходів. Результати проведених досліджень вказують на необхідність переосмислення цілей собаківництва – від вузькопородної естетики до збереження здоров'я, адаптивності та соціальної значущості собаки в сучасному суспільстві.

Ключові слова: собаки, кінологія, породи собак, програми відбору, геноміка, біотехнологія, спадковість, генетичне різноманіття.

Introduction. *Canis lupus* familiaris, the domestic dog, belongs to the wolf species (*Canis lupus*) and is a subspecies of mammals, one of the first to be domesticated by humans, making this species an integral companion to societies on different continents. In evolutionary biology, this process is considered "multiphase," with the first phase being when different groups of wolves were tamed by a specific anthropogenic niche, and the second phase being characterised by the gradual formation of mutual, multifaceted relationships between wolves and humans. D. Tancredi, I. Cardinali (2023) provided a historical overview of the domestication *of Canis familiaris,* highlighting the ecological differences between dogs and wolves, using the example of molecular mechanisms that influenced affiliative behaviour first observed in foxes, and based on genetic studies of ancient European dogs. Affiliative behaviour refers to actions that promote social bonding and encompasses friendly interactions that promote, maintain, or strengthen them as a whole. Such behaviour is common in many mammalian species, including humans, and is important for achieving social cohesion and shared well-being. Recently, genetic research has played an increasingly important role in breeding programmes for most domestic and farm animal species in order to achieve the desired results quickly. At the same time, H.F. Proschowsky et al. (2024) note certain changes in the goals of purebred dog breeding over the past decades, which have led to the following consequences: 1) a decrease in the influence of traditional kennel clubs, with more dogs being sold without pedigrees due to strict legal restrictions on dog breeding in these clubs; 2) an increase in the popularity of uncontrolled crossbreeding of established breeds (i.e., the creation of designer breeds) and a growing craze for breeding mixed-breed dogs. H.F. Proschowsky et al. (2024) argue that newly invented designer and mixed breeds have health and behavioural problems, are unpredictable in terms of body size and basic behaviour, and require increased care. The authors suggest that breed clubs or their successor organisations open breed registries, remove wording from breed standards that currently promote extreme conformation, support selection against genotypes and phenotypes that contribute to disease, and refocus dog shows and breeding to promote health and appropriate behaviour.

The International Cynological Federation (FCI) attempts to ensure mutual recognition of pedigrees and judges by all FCI member countries, but unlike national cynological clubs, it does not issue pedigrees to individual dogs. Without denying the importance of national clubs, E.D'Agaro et al. (2020) note that the general actions to be taken as part of a dog breed genetic improvement programme should include: 1) genomic identification and characterisation of individuals, highlighting individual potential in terms of contribution to biodiversity, abilities and practical use; 2) monitoring demographic parameters and assessing the risk of genetic variability decline; 3) characterising and assessing intraspecific genetic variability for proper management. Modern molecular methods can be useful for improving management strategies, even for minor breeds and selection based on qualitative traits. The working hypothesis is to add molecular data to classical schemes (auxiliary selection) to improve the accuracy of such assessments. Traditionally, the first step in planning an improvement programme consists of: 1) defining selection goals; 2) identifying the traits to be fixed; 3) assessing the gene effect of the traits to be selected; 4) assessing the influence of the environment (epigenetic effect) on the traits to be selected.

The long-standing partnership between humans and dogs has always involved a desire to meet a wide range of shared needs, with human demand exceeding current capabilities in breeding highly productive and, especially in recent times, healthy dogs. New genetic-statistical approaches and genomic technologies have the potential to accelerate this process by moving from phenotypic selection to methods that can preserve

genetic diversity while increasing the proportion of successful dog breeds. To fully utilise this technology, large data sets on hundreds of thousands of animals will be required. F. L. Chen et al. (2021) reviewed recent advances in breeding and how a new approach to dog breeding will meet the needs of working dog breeders today, as well as provide them with a path to the next generation. Experts have already provided step-by-step guidance for dog breeders to begin implementing selection based on estimated breeding value in their programmes, based on genotyping and DNA sequencing. In this situation, the task is to exchange data between breeding programmes (F. L. Chen et al., 2021; Ruban, 2023) as a way to achieve a future that can be beneficial for all domestic animal species and dog breeds, as well as their human partners. The long-standing partnership between humans and dogs is constantly striving to meet emerging needs, as demand exceeds our ability to safely breed highly productive and healthy dogs. New statistical genetic approaches and genomic technologies have the potential to accelerate breeding by moving away from traditional phenotypic selection to methods that can preserve genetic diversity and increase the proportion of successful dogs. To fully utilise this technology, very large datasets with hundreds of thousands of dogs will be needed. Today, dog breeders are trying to apply the tools available to them, often ignoring the accumulated experience in statistical genetics and genomics.

S. Wang et al. (2018) in their study on dog breeding and management in kennel clubs indicate that national kennel clubs are key players in the management and regulation of dog breeding to improve the health and welfare of breeding dogs. Fifteen kennel clubs from 11 European countries (Austria, Belgium, Denmark, France, Germany, Ireland, Latvia, the Netherlands, Norway, Sweden and the United Kingdom) and four non-European countries (Australia, Mexico, Uruguay and the United States) took part in a survey conducted to study the differences between kennel clubs in breeding policies and the management of pedigree dogs. The most important concerns reported by dog club representatives were exaggerated morphological traits and hereditary diseases. A wide range of information, tools and strategies were used to address these issues, with implementation varying by country and breed. The implementation of advanced breeding tools, such as genetic evaluation and online mating advisory tools, as well as balanced breeding strategies approved by clubs and breeders, remains a challenge and requires further development.

The aim of the study was to analyse recent advances in animal breeding and how these approaches could be implemented in dog breeding, as well as to explore the potential for using breeding value selection in such programmes, using DNA genotyping and sequencing procedures that are becoming more accessible and can be successfully integrated into selection programmes.

Materials and methods. Research methods: analytical, synthesis approach, interdisciplinary and search-comparative. A review of specialised scientific literature in the fields of cynology, genetics and breeding was studied and analysed. The authors used data from the journal Animals, which is indexed in Scopus, Web of Science, PubMed, PMC, Embase, PubAg, and AGRIS. An analysis was conducted of 16 key publications on cynology in various issues of this journal, which most fully and professionally reflect the prospects for the application of genetic research in cynology.

Research results. The breeding of domestic dogs has led to the emergence of a large number of breeds designed to perform various functional tasks. Despite the heritability of behavioural traits typical for each breed, the identification of causal loci has proven difficult due to the complexity of the *Canis familiaris* population structure. D. Tancredi & I. Cardinali (2023) conducted an analysis on three Mediterranean peninsulas (Balkan, Pyrenean, and Italian), which together represent a geographical

region with a diverse demographic composition. This feature of studying the dynamics of domestication is characteristic of other geographical regions, since in the first case, the genetic variability of dog populations was formed due to partial isolation and contact with certain ethnic groups or historically formed communities of people with unique characteristics of culture, language, origin, way of life, and awareness of their unity and differences from others. Determining the genetic structure of dog breeds based on the analysis of uniparental genetic markers (inherited from only one parent, either the mother or the father) and their phylogeny revealed the most contrasting differences between these groups. E.V. Dutrow et al. (2022) proposed a method for identifying genetic factors associated with dog behaviour. This involved using genetic data for more than 4,000 domestic, semi-wild and wild canids, as well as behavioural research data for more than 46,000 dogs. The authors pointed to the influence of non-coding regulatory variations on such behavioural differences when genes in co-expression neurodevelopmental networks identify different manifestations of axon guidance functions (nerve cell processes that conduct nerve impulses). This work provides a basis for the diversification of dogs and positions the domestic dog as a unique system for identifying genetic diversity in the manifestation of its own behaviour. This raises the question of why dogs are bred and what their role is (apart from food) in social relationships with humans. K. Northrope et al. (2024) investigated how people's relationships with dogs are related to mental health and how this compares to their relationships with other people. The unexpected results showed that owners who had a strong attachment to their dogs tended to have poorer mental health outcomes. The link between strong attachment to their pets and poor mental health may be partly due to these owners having an anxious style of relating to other people, suggesting that these owners turn to their dogs for the emotional support they need, which is caused by a lack of reliable connections among people. In addition to this study, C. Sulonen et al. (2024) showed, based on an analysis of cortisol concentrations in dog hair, that animals from shelters had higher levels of long-term stress than those that had been rehomed. A.C. Johnson & C.D.L. Wynne (2024) also demonstrated that owners who had a strong attachment to their dogs tended to have poorer mental health outcomes.

In their study of dog personality traits, J. Ilska et al. (2017) used dog owners' knowledge to create a large dataset on the personality traits of Labrador Retrievers. Taking into account key environmental factors, it was demonstrated that genetic variation can be detected for dog personality traits assessed using questionnaire data. The researchers found genetic variation for several traits, including retrieving propensity and fear of loud noises, while other traits showed little heritability. Genetic correlations were also estimated between traits; however, due to fairly large standard errors (SE), only a few trait pairs yielded statistically significant estimates. Genomic analysis showed that these traits are predominantly polygenic, meaning that individual genomic regions have a small effect, and suggested chromosomal associations for six traits.

K. Vékony et al. (2024) investigated whether social rank could be a factor in individual variability in dogs' tolerance to frustrating situations (the presence of obstacles) when a person cannot achieve their goals or satisfy their needs and experiences irritation, frustration, and negative emotions. The results show that the social rank of dogs influences their resource-related behaviour in such cases. A. Lamontagne et al. (2025) presented the first direct comparison of dogs' ability to synchronise their behaviour with both other dogs and humans, with noticeable differences depending on whether they had interacted with individuals of the same or different species before. The study also highlights the influence of daily experience.

To achieve stable olfactory characteristics and meet usage-oriented needs, Chinese breeders continue to carry out the same artificial selection. Although olfactory behaviour

is a genetic behaviour in dogs, the genotypes of OR genes formed by breeding patterns are largely unknown. In this regard, M. Yang et al. (2022) characterised 26 SNPs, 2 deletions, and 2 insertions of 7 OR genes between search dogs and guide dogs to identify candidate alleles associated with specific working traits. The results showed that there were candidate alleles of functional SNPs at one locus that had statistically significant differences between the two subpopulations. In addition, polymorphism levels were not high at all loci, and linkage disequilibrium occurred only within one OR gene. The scientists concluded that artificial selection for working abilities affected the SNP alleles of OR genes in the dog breed and directed evolution in line with human intentions, although the changes are limited to decades of strategic selection.

H.G. Molinaro et al. (2025) concluded that dogs' emotional states could be assessed using an attention bias test, indicating that such a test is a promising tool for this type of assessment. Using this test could improve our understanding of dogs' emotions and, consequently, improve our ability to provide dogs with quality care. L.P. Case (2023), considering dog breeds, their selection methods and genetic testing programmes, focused on their sporting and social purposes, highlighting the threats posed by specific diseases, infectious and atopic diseases (allergic skin diseases), as well as the importance of effective vaccines and vaccination schedules for R. R. Ha et al. (2024) examined the impact of inbreeding on behavioural problems (anxiety and aggression) and how this potentially affects the future health of the breed. The authors pointed to the dominant significance of breed as an indicator of behaviour and other individual differences.

P. Verbeek et al. (2024) studied how the relationship with a human partner affects a dog's well-being. According to the Five Freedoms of Animals concept contained in the World Declaration of Animal Welfare (https://europaregina.eu/wp-content/uploads/2023/05/udaw-universal-declaration-on-animal-welfare-wspa.pdf), animals have the right to: freedom from hunger and thirst; freedom from discomfort; freedom from pain, injury and disease; freedom to express normal behaviour; freedom from fear and distress. Researchers found 706 publications on the relationship between humans and dogs, 246 of which were devoted to welfare studies, and found that the characteristics and origins of the dog and its owner influence both the nature of their relationship and the welfare of the dog, both positively and negatively. The concept of welfare is based on a certain contradiction between the biological characteristics of the animal on the one hand, and the economics, ethics and psychological satisfaction of the human on the other (Ruban, 2023). In general, dog breeding requires the definition of goals and specific selection criteria (a clear numerical value for the assessment of a particular trait or characteristic for each animal) according to which information is regularly collected (Fig. 1).

In such a situation, it is necessary to focus on market demand, which in dog breeding is often linked to people's preferences. It is relatively easy to establish selection criteria for service dogs, dogs for sports and hunting, although personal "aesthetic" preferences are sometimes also incorporated into certain clear requirements. Australian researchers E.S. Power et al. (2024) conducted a survey of residents about what the ideal dog should be like. The results of these responses included: being medium-sized, with short hair that sheds little or not at all; being affectionate, healthy, non-aggressive, safe with children; house-trained, harmless when left alone, and not running away from the territory. Breeders, potential owners, and policymakers can benefit from this research, which may help reduce animal abandonment and impr ove human-dog relationships.

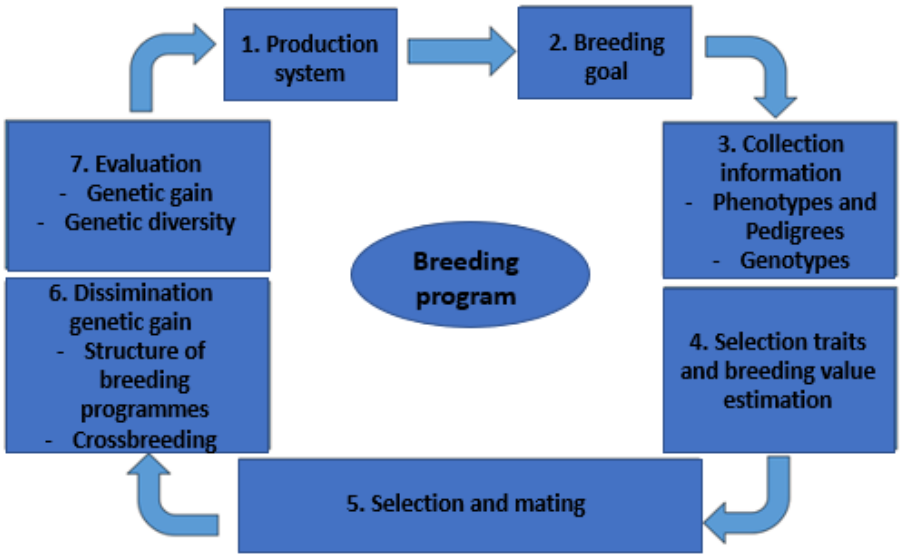

Fig. 1. **Schematic diagram of the organisation of a breeding programme with domestic animals and companion animals**

Source: https://wiki.groenkennisnet.nl/space/TAB

At the same time, it is important to understand that the correct evaluation and selection of animals is based on certain genetic and statistical methods (Table 1), which are widely used in selection programmes for domestic and farm animals.

The very system of selecting traits for breeding depends on the breeding goals and is quite diverse in dog breeding. Thus, L. Peterca et al. (2025) studied how well French bulldogs understand non-verbal communication, in particular, whether a close relationship with the owner helps them interpret training gestures. The authors suggest that future studies should include more dog breeds to better understand how the relationship between the owner and the dog affects social skills over time. P. Dobos and P. Pongrácz (2025) tested companion dogs in a scenario of copying their owner's behaviour or independently solving a specific task, which made it possible to determine the degree of socialisation of the dogs (copying the solution suggested for the dog by the owner). B. McGuire et al. (2025) based their research on the possibility of focusing training efforts on dogs that grab the leash during walks. E.L. Buckland et al. (2025) studied the results of the "Post-Adoption Support" project, launched in 2018 by Dogs Trust in the UK, which aimed to monitor the behaviour and health of dogs after rehoming (rehoming - relocating dogs or placing them with a new owner, which involves finding a new home for an animal that for some reason cannot remain in its previous home)**.** These studies provided insight into the welfare of dogs during the first four months after rehoming. S.B. Sidel et al. (2025) developed and tested methods for protecting dogs during psychological stress tests, based on a scale that measures fear and anxiety through body language. This method made it possible to identify the most effective ways to create comfortable conditions. V. Bakos et al. (2025) proved that rank among dogs can influence each dog's attachment to its owner, mainly under the influence of competition from other dogs living together.

Table 1

List of the main methods used in the system of assessing the genetic (breeding) value of animals

Method	Purpose, brief description of input information
Family selection index	Assessment of the breeding value (BV) of an animal based on its own data and that of its relatives (parents, siblings, half-siblings, offspring)
Best linear unbiased prediction – BLUP	
Father (sire) model	Evaluation of BV, taking into account "father-offspring" family ties. When including the kinship matrix between sires, "father-son" and "father-mother-grandchildren" family ties are also taken into account.
Father-mother's father model	PC evaluation, taking into account the family relationships "father - offspring" and "father of the mother - granddaughter", the breeding value of the father of the mother. When including the kinship matrix between sires, the family relationships "father - son" and "father of the mother - grandson" are also taken into account.
Animal model	PC evaluation takes into account all family relationships between animals.
Animal model with multiple trait measurements	Increased accuracy of PC by reducing residual variance
Animal model with inclusion of maternal effect	PC evaluation, taking into account the influence of the mother on the traits of the offspring
Animal model for multiple traits	Estimation of breeding value, taking into account genetic and environmental correlations between traits, thereby increasing the accuracy of the estimation of the breeding value of animals for each trait and allowing predictions of breeding values for missing traits to be obtained.
Animal model with inclusion of non-additive effects	PC evaluation, taking into account additive and non-additive (epistatic: dominant, additive-additive, additive-dominant, etc.) genetic effects
Animal model for several breeds	PC evaluation, taking into account the influence of breed on the breeding value of an animal, the effect of heterosis, recombination losses and possible heterogeneity of genetic and environmental dispersions and covariances across breed groups.
Animal model with genetic groups	PC evaluation, taking into account genetic differences between groups
Animal model with random regression coefficients	PC estimation, genetic value is expressed by one or more (equations) random regression coefficients
Animal model incorporating the effects of individual markers	PC evaluation, taking into account the effects of individual genetic markers
Genomic BLUP	PC evaluation is based on the use of a large number of genetic markers covering the entire genome

Auxiliary methods	
Restricted maximum likelihood – REML	Calculations of variance and covariance components for the estimation of genetic parameters (heritability, repeatability, genetic and environmental correlations between traits).
Economic selection index	Calculation of the total economic value of an animal by combining breeding value estimates for individual traits, taking into account their economic weights

J. Kim et al. (2018) compared whole genome sequence data between sporting and hunting breeds and terrier breeds and demonstrated that genes controlling cardiovascular, muscle and neural functions are under strong selection in sporting and hunting breeds, including ADRB1, TRPM3, RYR3, UTRN, ASIC3 and ROBO1. The scientists identified the TRPM3 allele, which was significantly associated with increased speed in whippets, accounting for 11.6% of the total variance in racing performance. The researchers also observed a significant association of ROBO1 with breed-specific achievements in obstacle course competitions. These results provide strong evidence that breeds designed for sporting hunting have been adapted to their professions through improved endurance, cardiac function, blood flow, and cognitive abilities, demonstrating how strong behavioural selection alters physiology, creating breeds with different capabilities.

Discussion. The development of dog breeds from wild ancestor populations is a successful model for studying domestication and genetic diversification. The initial domestication processes created genetic bottlenecks, which have since been exacerbated by further selective pressure in the creation of specific breeds (Hsu et al., 2023), and now almost every breed is classified according to a standard that includes morphological criteria, behavioural traits and coat colour. These recommendations were applied during the development of modern purebred dogs, resulting in a significant reduction in phenotypic and genetic heterogeneity within breeds, while maintaining diversity between breeds. Previous studies of genomic diversity have used summary statistics to measure locus-specific divergence in allele frequencies. J.M. Akey et al. (2002) demonstrated that, in combination with high-density SNP markers, statistics were a powerful tool for scanning the dog genome for selection signatures (unique sequences), and developed a modified approach to identify breed-specific loci.

The dog gut microbiome plays a vital role in overall health and well-being by regulating various physiological functions, including digestion, immune responses, energy metabolism, and even behaviour and temperament (Kim et al., 2025). Thus, a comprehensive understanding of the diversity and functional roles of the canine gut microbiome is crucial for maintaining optimal health and well-being. Maintaining eubiosis (eubiosis is a state of healthy microbial balance in a living organism, particularly in the context of the gut microbiome) requires individualised management strategies that take into account both physiological characteristics and environmental influences. H. Kim et al (2025) outline the structure and function of the canine gut microbiome, with a particular focus on its role in health and the key factors that support it.

T. Gong et al. (2024) conducted the largest (n=97552) genome-wide association study (GWAS) of dogs of European origin, which expanded our understanding of the genetic architecture of certain groups. E. Strandberg et al. (2025) assessed the genetic parameters of behavioural heritability based on a new scale, BPH (behaviour and personality assessment dogs), for eight breeds: American Staffordshire Terrier; Golden Retriever; Labrador Retriever; Lagotto Romagnolo; Nova Scotia Duck Tolling Retriever; Perro de Agua Espanol; Rhodesian Ridgeback; Staffordshire Bull Terrier. It was concluded that it is possible to successfully select dogs based on BPH, which will lead to

changes in their behaviour in subsequent generations. I. Zapata et al. (2022) confirmed previous findings that small body size is associated with many problematic behaviour patterns, while large size is associated with increased learning ability. Using threshold models of body weight in Pit Bull Terriers, the possibility of a reduced risk of aggression towards the owner and an increased risk of fear towards other dogs was demonstrated.

A. Halvoník et al. (2025) investigated HRR (Homologous Recombination Repair) genetic regions (a group of genes that encode proteins responsible for repairing DNA damage through homologous recombination), expanding the understanding of their significance, which may help in identifying disease-related genes, thereby improving veterinary care and treatment strategies. J. A. Thorsrud et al. (2025) conducted research to improve the breeding of guide dogs by using genetic information to predict important health and behavioural traits. Genetic analysis data on German Shepherds, Golden Retrievers, Labrador Retrievers, and their crossbreeds can be used for further genetic prediction. T. Sugasawa et al. (2024) developed a method for sequencing mitochondrial DNA (mtDNA) using faecal samples. This method has been proven to be a form of genetic sampling that provides a suitable sample for mtDNA decoding. The results presented will contribute to the future development of veterinary medicine and animal welfare. There is growing concern that excessive breed standardisation contributes to a reduction in effective population size and high levels of inbreeding, leading to a loss of genetic diversity in many breeds. A. Radko and A. Podbielska (2021) examined genetic diversity among eight popular dog breeds in Poland and evaluated the effectiveness of a panel of 21 microsatellites (STRs) recommended by the International Society for Animal Genetics (ISAG) for parentage testing. The breeds characterised were German Shepherd, Maltese, Irish Wolfhound, Yorkshire Terrier, Beaver Yorkshire Terrier, Golden Retriever, Labrador Retriever and French Bulldog.

J. M. Akey et al. (2010) described a genome-wide scan for selection in 275 dogs from 10 phenotypically diverse breeds that were genotyped on more than 21,000 autosomal SNPs. They found 155 genomic regions with strong signatures of recent selection and candidate genes for phenotypes that are most different between breeds, including coat size, colour, and texture, behaviour, skeletal morphology, and physiology. The study also demonstrated a significant association between HAS2 and skin wrinkling in Sharpeis and provided evidence that regulatory evolution played an important role in the phenotypic diversification of modern dog breeds. These results illustrate how genetic maps can rapidly identify the genetic basis of phenotypic variation in dogs and provide a basis for determining the mechanistic basis of how artificial selection contributes to rapid and pronounced phenotypic evolution.

H.S. Kim et al. (2023) investigated conservative and global molecular transitions in transcriptional remodelling (transformation) in dogs of 15 breeds, proving that genes underlying hormone regulation and developmental programmes were differentially regulated during ageing. These results emphasise that the rate of age-related transcriptional remodelling is influenced not only by lifespan but also by the timing of critical physiological stages. N. Bhowmikwe et al. (2024) used data from 615 dogs to assess heritability and conducted a genome-wide associative study of behavioural phenotypes in dogs in a commercial breeding group. An allele and weighted risk scores were identified where fear-related behaviour may be amenable to genetic improvement.

Using next-generation whole-genome sequencing technology combined with unsupervised machine learning for pattern recognition, Z. Li et al. (2023) created and analysed a high-resolution sequence map for 76 breeds. Genomic structures, including new single nucleotide polymorphisms (SNPs), SNP clusters, insertions, deletions (INDELs), and short tandem repeats (STRs) among breeds, can serve as specific markers

for their identification and, most importantly, be used in selection programmes.

Conclusions. In modern cynology, genetic research is beginning to be widely used in selection programmes, gradually creating a dominant environment alongside traditional approaches. Direct and predictive (indirect) traits that characterise dog behaviour are becoming increasingly important. The following conclusions were drawn from the analytical study.

1. The affiliative behaviour of dogs, which refers to actions that promote social bonding, has been proven. Such behaviour is common in many species of mammals, including humans, and is important for achieving social cohesion and shared well-being, which makes companion dogs popular among different ethnic groups.

2. When breeding dogs, genetic testing programmes are used that focus on their athletic and social purpose, while considering the threats posed by breed-specific diseases, infections and atopic diseases.

3. Breed remains an indicator of behaviour and other individual differences, with proven effects of inbreeding on behavioural problems (anxiety and aggression) and how this potentially affects the future health of dogs of this breed.

4. The use of genome-wide association studies (GWAS) reveals the potential for rapidly achieving breeding goals and implementing successful programmes for working with different dog breeds.

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