AnimalSci Publisher®

International Journal of Molecular Zoology 2024, Vol.14, No.5, 290-296
http://animalscipublisher.com/index.php/ijmz

Review and Progress Open Access

Epigenetics in Pet Breeding: Current Insights and Future Perspectives

Wei Liu, Xinghao Li, Jia Xuan
Institute of Life Science, Jiyang College of Zhejiang A&F University, Zhuji, 311800, Zhejiang, China
Corresponding email: jia.xuan@jicat.org

International Journal of Molecular Zoology, 2024, Vol.14, No.5 doi: 10.5376/ijmz.2024.14.0027
Received: 13 Aug., 2024
Accepted: 25 Sep., 2024
Published: 18 Oct., 2024

Preferred citation for this article:
Liu W., Li X.H., and Xuan J., 2024, Epigenetics in pet breeding: current insights and future perspectives, International Journal of Molecular Zoology, 14(5): 290-296 (doi: 10.5376/ijmz.2024.14.0027)

Abstract Epigenetics, the study of heritable changes in gene expression without alterations to the DNA sequence, has emerged as a critical field in animal breeding. Its relevance to pet breeding lies in its potential to influence breed characteristics, health, and genetic diversity. This study explores current insights into epigenetic mechanisms, such as DNA methylation and histone modification, and how they are shaped by environmental factors. The role of epigenetic regulation in selecting desirable traits and enhancing disease resistance in pets is examined, alongside a case study illustrating its application in a specific breed. Furthermore, this study addresses the challenges of integrating epigenetics into breeding practices, including technical hurdles, ethical considerations, and regulatory concerns. Future perspectives suggest that personalized breeding, informed by epigenetic data, could revolutionize the field. Ultimately, understanding and applying epigenetic knowledge in pet breeding will contribute to healthier, more resilient animals while maintaining genetic diversity.

Keywords Epigenetics; Pet breeding; Genetic diversity; Disease resistance; Personalized breeding

1 Introduction

Epigenetics is the study of heritable changes in gene expression that do not involve alterations to the underlying DNA sequence (Jiang et al., 2004). These changes can be transmitted through cell divisions and can be influenced by various factors such as environmental conditions, developmental stages, and lifestyle choices (Ashe et al., 2021). Key mechanisms of epigenetic regulation include DNA methylation, histone modifications, and non-coding RNA interactions, which collectively contribute to the dynamic regulation of gene activity (Delcuve et al., 2009; Sr, 2022).

In animal breeding, epigenetics plays a crucial role by influencing phenotypic traits that are not solely determined by genetic sequences. Epigenetic modifications can affect traits such as growth rate, disease resistance, and behavior, which are important for the selection and breeding of pets (Iwasaki and Paszkowski, 2014). Understanding these mechanisms allows breeders to make more informed decisions, potentially leading to healthier and more resilient animals. Moreover, epigenetic changes can be induced by environmental factors, making it possible to tailor breeding practices to optimize desirable traits (Abdul et al., 2017; Akhter et al., 2021).

Pet breeding practices have traditionally focused on selecting animals with desirable genetic traits to produce offspring with similar characteristics. This involves careful selection of breeding pairs based on pedigree, physical attributes, and health status. However, modern breeding practices are increasingly incorporating genetic and epigenetic information to enhance the predictability and success of breeding programs. Techniques such as genomic selection and epigenetic profiling are being used to identify and propagate favorable traits while minimizing the risk of hereditary diseases (Portela and Esteller, 2010; Bednarczyk et al., 2021).

This study explores the current status and future prospects of epigenetics in pet breeding, including an understanding of the mechanisms of epigenetic regulation, their impact on phenotypic traits, and how these insights can be applied to improve breeding practices, aiming to identify potential areas for future research and development in the field of epigenetics as it relates to animal breeding.

2 Current Insights in Epigenetics

2.1 Mechanisms of epigenetic regulation

Epigenetic regulation involves modifications that alter gene expression without changing the DNA sequence itself (Figure 1). Two primary mechanisms are DNA methylation and histone modifications (Gagnidze and Pfaff, 2022). DNA methylation typically suppresses gene expression by adding methyl groups to DNA, often at cytosine bases in CpG islands. Histone modifications, such as acetylation and methylation, alter the chromatin structure, making DNA more or less accessible for transcription (Feil and Fraga, 2012). These mechanisms are crucial for cellular differentiation and development, allowing genetically identical cells to perform diverse functions (Lu, 2024).

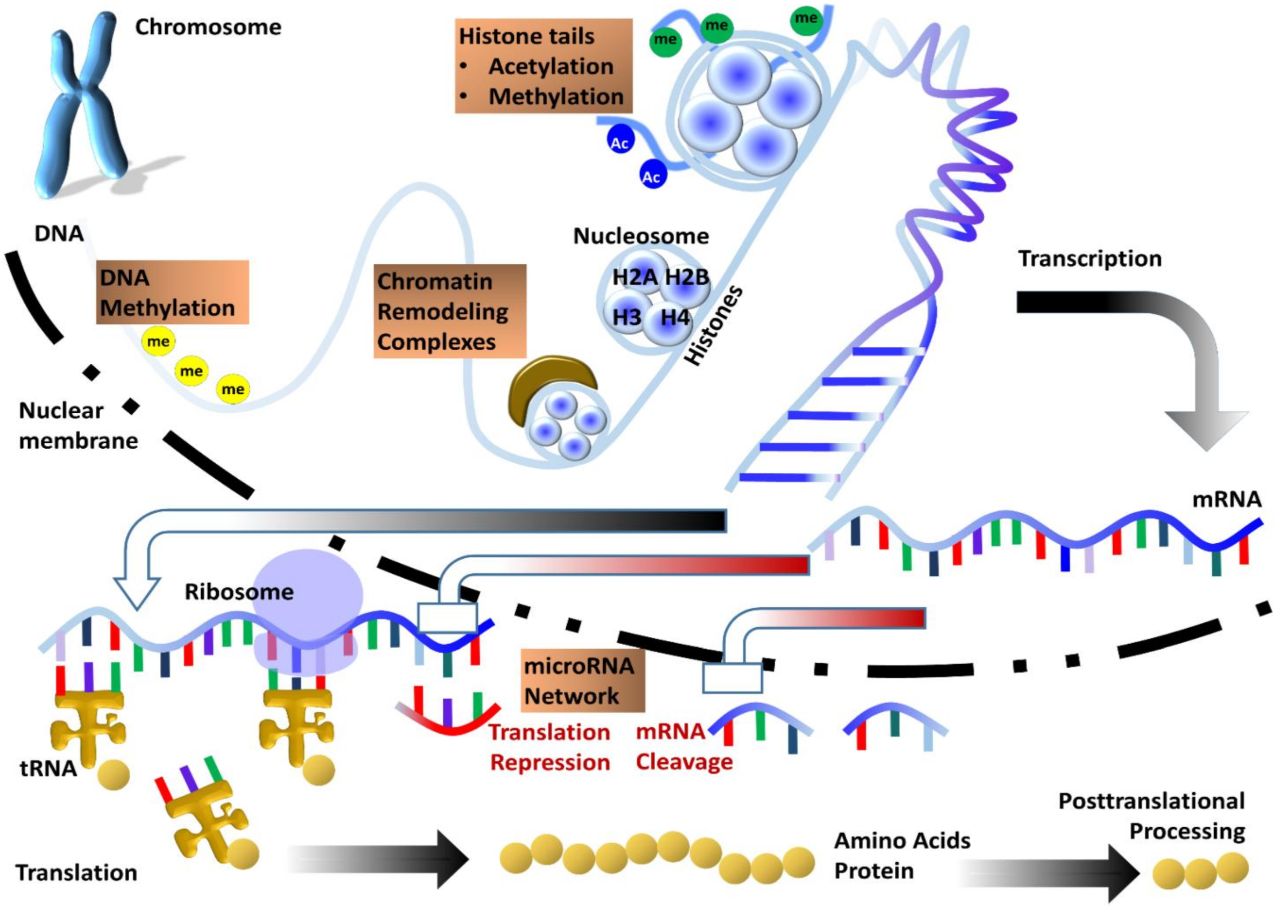


Figure 1 Sketch illustrating the multi-layered control of gene expression by various epigenetic processes. DNA is subject to direct chemical modification by addition or removal of methyl groups at cytosine bases. Epigenetic processes regulating gene expression at a higher level of DNA compaction include histone tail modifications and control of chromatin accessibility by ATP dependent chromatin remodeling complexes. Once transcribed, mRNA can be further regulated by the microRNA network which provides an additional layer of epigenetic control of gene expression. Together, these epigenetic mechanisms function in concert to help fine-tune gene expression within the cell (Adopted from Gopinathan and Diekwisch, 2022)

2.2 Epigenetic changes in response to environmental factors

Environmental factors such as diet, pollutants, temperature, and stress can induce epigenetic changes that affect gene expression and phenotype (McCaw et al., 2020). These changes can be stable and sometimes heritable, influencing not only the individual exposed but also subsequent generations (Wang et al., 2017). For instance, exposure to certain chemicals or nutritional components can lead to DNA methylation changes that persist through cell divisions and potentially across generations, affecting development and health (Vaiserman, 2011). This adaptability highlights the dynamic interplay between an organism's genome and its environment, suggesting that epigenetic mechanisms are a means by which organisms can rapidly respond to environmental changes (Jaenisch and Bird, 2003).

2.3 Implications for breed characteristics and health

Epigenetic modifications have significant implications for breed characteristics and health in pets. These modifications can influence traits such as coat color, behavior, and disease susceptibility (Zhang, 2024). For example, epigenetic changes induced by environmental factors can lead to variations in metabolic processes, potentially predisposing certain breeds to obesity or diabetes (Handel et al., 2010). Understanding these mechanisms opens up possibilities for targeted breeding strategies that consider not only genetic but also epigenetic factors, potentially leading to healthier and more resilient breeds. Moreover, the reversible nature of some epigenetic changes offers potential for interventions that could mitigate adverse health effects, providing a new avenue for disease prevention and treatment in pet breeding.

3 Applications of Epigenetics in Pet Breeding

3.1 Selecting for desirable traits

Epigenetics offers a novel approach to selecting for desirable traits in pet breeding by providing insights into how gene expression can be regulated without altering the DNA sequence. This can be particularly useful for traits that are influenced by environmental factors. For instance, epigenetic modifications such as DNA methylation and histone modifications can lead to stable changes in gene expression that are heritable across generations. These modifications can be targeted to enhance traits such as coat color, temperament, and physical abilities in pets (Meirelles et al., 2014; Roudbar et al., 2015). By understanding and manipulating these epigenetic marks, breeders can achieve more precise and predictable outcomes in their breeding programs.

3.2 Improving genetic diversity

One of the significant challenges in pet breeding is maintaining genetic diversity, which is crucial for the health and vitality of the population. Epigenetics can play a vital role in this aspect by revealing hidden genetic potential that is not apparent through traditional genetic analysis. Epigenetic markers can uncover variations in gene expression that contribute to phenotypic diversity, even among genetically similar individuals. This can help breeders identify and select for a broader range of traits, thereby enhancing genetic diversity within the breeding population (González-Recio et al., 2015). Additionally, understanding the epigenetic landscape can help in managing inbreeding and reducing the risk of genetic disorders.

3.3 Enhancing disease resistance

Epigenetics also holds promise for enhancing disease resistance in pets. Epigenetic modifications can influence the immune response and the expression of genes involved in disease resistance. For example, certain epigenetic changes can activate or silence genes that are crucial for fighting infections or managing stress responses. By identifying these epigenetic markers, breeders can select individuals with a naturally enhanced ability to resist diseases (Feil and Fraga, 2012). This approach not only improves the overall health of the pets but also reduces the reliance on medical interventions and enhances the sustainability of breeding programs.

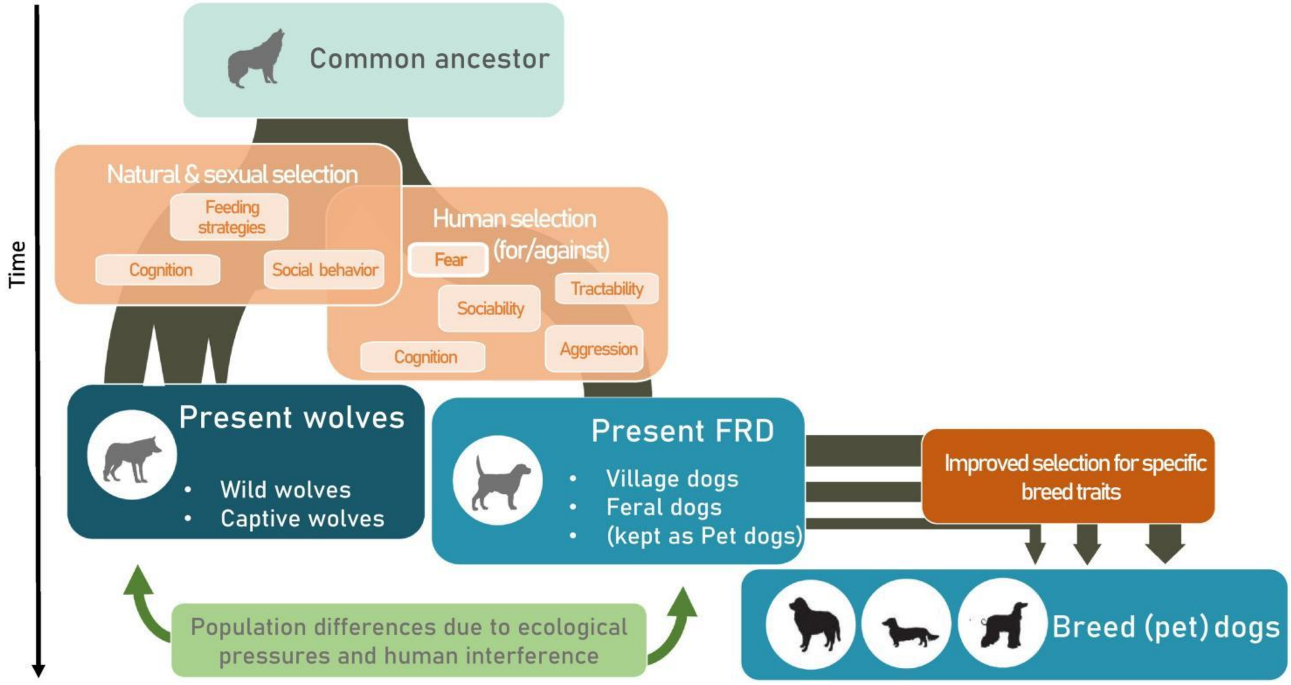
4 Case Study

4.1 Overview of a specific breed or species

In this case study, we focus on the domesticated dog (*Canis lupus familiaris*), specifically examining the epigenetic differences between various dog breeds and their wild ancestor, the wolf (*Canis lupus*). Dogs have undergone significant morphological and behavioral changes through domestication, resulting in a wide variety of breeds with distinct characteristics (Figure 2).

4.2 Epigenetic findings related to the case study

Recent research has highlighted the role of DNA methylation in the brains of dogs and wolves, revealing substantial differences in methylation patterns between the two groups. These differences are not only evident between wolves and dogs but also among different dog breeds. The study utilized a combination of genotype-by-sequencing (GBS) and methylated DNA immunoprecipitation (MeDIP) to analyze the frontal cortex of 38 dogs from 8 breeds and three wolves. The findings suggest that epigenetic factors, particularly DNA methylation, have played a significant role in the speciation from wolf to dog and in the divergence of different dog breeds. Notably, methylation differences were observed in genes related to behavior and morphology, which are crucial for the phenotypic variation seen among dog breeds (Sundman et al., 2020).



Trends in Cognitive Sciences

Figure 2 Key figure. Simplified diagram of the domestication process (Adopted from Range and Marshall-Pescini, 2022)

4.3 Impact on breeding strategies

The insights gained from these epigenetic studies have profound implications for dog breeding strategies. Understanding the epigenetic mechanisms underlying phenotypic traits can help breeders select for desirable characteristics more effectively (Ibeagha-Awemu and Khatibi, 2017). For instance, if certain behavioral traits are linked to specific methylation patterns, breeders could potentially use this information to select for dogs with preferred behaviors. Additionally, recognizing the role of epigenetics in breed formation can lead to more informed decisions in maintaining genetic diversity and health within breeds. This approach could also be extended to other domesticated animals, providing a broader framework for improving breeding practices through epigenetic insights.

5 Challenges in Integrating Epigenetics into Breeding

5.1 Technical and scientific challenges

Integrating epigenetics into pet breeding presents several technical and scientific challenges. One primary issue is the complexity of epigenetic mechanisms, which include DNA methylation, histone modifications, and non-coding RNAs, all of which interact in intricate ways to regulate gene expression without altering the DNA sequence (González-Recio et al., 2015). Additionally, the stability and heritability of epigenetic marks can vary, making it difficult to predict and control phenotypic outcomes across generations (Tonosaki et al., 2022). The lack of comprehensive epigenomic data for many pet species further complicates efforts to apply these insights effectively in breeding programs (Roudbar et al., 2015). Moreover, distinguishing between genetic and epigenetic influences on traits requires sophisticated analytical models and high-throughput sequencing technologies, which are not yet fully developed or widely accessible.

5.2 Ethical considerations and public perception

The ethical implications of using epigenetics in pet breeding are significant. There is a concern that manipulating epigenetic marks could lead to unintended consequences, such as the emergence of new health issues or the exacerbation of existing ones (You and Jones, 2012). Public perception of epigenetic interventions is also mixed, with some viewing it as a natural extension of traditional breeding practices, while others see it as an unnatural and potentially harmful manipulation of animal biology (Bird, 2007). The ambiguity and varying definitions of epigenetics further complicate public understanding and acceptance, necessitating clear communication and education efforts to address misconceptions and ethical concerns (Greally, 2018).

5.3 Regulatory issues

Regulatory frameworks for the use of epigenetics in breeding are still in their infancy. Current regulations primarily focus on genetic modifications and may not adequately address the unique aspects of epigenetic interventions (Henikoff and Greally, 2016). There is a need for new guidelines that consider the reversible and potentially transient nature of epigenetic changes, as well as their long-term impacts on animal health and welfare (Delcuve et al., 2009). Additionally, the lack of standardized methods for detecting and measuring epigenetic modifications poses challenges for regulatory oversight and enforcement. Developing robust regulatory policies will require collaboration between scientists, policymakers, and industry stakeholders to ensure that epigenetic breeding practices are safe, ethical, and transparent.

6 Future Perspectives

6.1 Emerging research areas in epigenetics

Emerging research areas in epigenetics are rapidly expanding, offering new insights and opportunities for pet breeding. One significant area of focus is the understanding of how environmental factors influence epigenetic modifications and, consequently, animal phenotypes. Recent studies have shown that virtually all environmental factors can affect an animal's phenotype through epigenetic mechanisms, which include alterations in chromatin structure and gene expression patterns (Kim and Kim, 2021). Additionally, the identification and characterization of different types of epialleles-permanent, temporary, and intergenerational-are providing new models to explain the complex interactions between genetics, epigenetics, and the environment (Roudbar et al., 2015). These advancements are paving the way for more precise and effective breeding strategies that go beyond traditional genetic approaches.

6.2 Potential applications in personalized breeding

The potential applications of epigenetics in personalized breeding are vast and promising. By incorporating epigenetic information, breeders can achieve a more comprehensive understanding of an animal's phenotype, which is influenced by both genetic and environmental factors. This holistic approach can lead to more accurate estimations of breeding values and reduce biases in selection processes. Furthermore, the integration of epigenetic data can help identify specific epigenetic markers associated with desirable traits, enabling breeders to select animals with optimal genetic and epigenetic profiles (Yakovlev, 2018). This personalized breeding strategy can enhance the overall health, performance, and adaptability of pets, ultimately leading to improved breeding outcomes.

6.3 Recommendations for breeders

For breeders looking to incorporate epigenetic insights into their practices, several recommendations can be made. First, breeders should stay informed about the latest research in epigenetics and its implications for animal breeding (Crisp et al., 2021). Understanding the mechanisms of epigenetic regulation and the impact of environmental factors on gene expression is crucial for making informed breeding decisions. Second, breeders should consider using epigenetic markers in conjunction with traditional genetic markers to select animals with desirable traits. This combined approach can provide a more accurate assessment of an animal's potential and improve breeding outcomes. Finally, breeders should collaborate with researchers and utilize advanced technologies, such as epigenomic profiling, to gain deeper insights into the epigenetic landscape of their breeding populations. By embracing these recommendations, breeders can harness the power of epigenetics to enhance the quality and success of their breeding programs.

Acknowledgments

We are grateful to Miss Wu for critically reading the manuscript and providing valuable feedback that improved the clarity of the text.

Conflict of Interest Disclosure

The authors affirm that this research was conducted without any commercial or financial relationships that could be construed as a potential conflict of interest.

References

Abdul Q., Yu B., Chung H., Jung H., and Choi J., 2017, Epigenetic modifications of gene expression by lifestyle and environment, Archives of Pharmacal Research, 40: 1219-1237.
https://doi.org/10.1007/s12272-017-0973-3

Akhter Z., Bi Z., Ali K., Sun C., Fiaz S., Haider F., and Bai J., 2021, In response to abiotic stress, DNA methylation confers epigenetic changes in plants, Plants, 10(6): 1096.
https://doi.org/10.3390/plants10061096

Ashe A., Colot V., and Oldroyd B., 2021, How does epigenetics influence the course of evolution? Philosophical Transactions of the Royal Society B, 376(1826): 20200111.
https://doi.org/10.1098/rstb.2020.0111

Bednarczyk M., Dunisławska A., Stadnicka K., and Grochowska E., 2021, Chicken embryo as a model in epigenetic research, Poultry Science, 100(7): 101164.
https://doi.org/10.1016/j.psj.2021.101164

Bird A., 2007, Perceptions of epigenetics, Nature, 447: 396-398.
https://doi.org/10.1038/nature05913

Crisp P., Bhatnagar-Mathur P., Hundleby P., Godwin I., Waterhouse P., and Hickey L., 2021, Beyond the gene: epigenetic and cis-regulatory targets offer new breeding potential for the future, Current Opinion in Biotechnology, 73: 88-94.
https://doi.org/10.1016/j.copbio.2021.07.008

Delcuve G., Rastegar M., and Davie J., 2009, Epigenetic control, Journal of Cellular Physiology, 219(2): 243-250.
https://doi.org/10.1002/jcp.21678

Feil R., and Fraga M., 2012, Epigenetics and the environment: emerging patterns and implications, Nature Reviews Genetics, 13(2): 97-109.
https://doi.org/10.1038/nrg3142

Gagnidze K., and Pfaff D.W., 2022, Epigenetic mechanisms: DNA methylation and histone protein modification, In: Neuroscience in the 21st Century: From Basic to Clinical, Cham: Springer International Publishing, pp.2677-2716.
https://doi.org/10.1007/978-3-030-88832-9_69

González-Recio O., Toro M., and Bach A., 2015, Past, present, and future of epigenetics applied to livestock breeding, Frontiers in Genetics, 6: 305.
https://doi.org/10.3389/fgene.2015.00305

Gopinathan G., and Diekwisch T.G., 2022, Epigenetics and early development, Journal of Developmental Biology, 10(2): 26.
https://doi.org/10.3390/jdb10020026

Greally J., 2018, A user's guide to the ambiguous word 'epigenetics', Nature Reviews Molecular Cell Biology, 19(4): 207-208.
https://doi.org/10.1038/nrm.2017.135

Handel A., Ebers G., and Ramagopalan S., 2010, Epigenetics: molecular mechanisms and implications for disease, Trends in Molecular Medicine, 16(1): 7-16.
https://doi.org/10.1016/j.molmed.2009.11.003

Henikoff S., and Greally J., 2016, Epigenetics, cellular memory and gene regulation, Current Biology, 26(14): R644-R648.
https://doi.org/10.1016/j.cub.2016.06.011

Ibeagha-Awemu E., and Khatib H., 2017, Epigenetics of livestock breeding, In: Handbook of epigenetics, Academic Press, pp.441-463.
https://doi.org/10.1016/B978-0-12-805388-1.00029-8

Iwasaki M., and Paszkowski J., 2014, Epigenetic memory in plants, The EMBO Journal, 33(18): 1987-1998.
https://doi.org/10.15252/embj.201488883

Jaenisch R., and Bird A., 2003, Epigenetic regulation of gene expression: how the genome integrates intrinsic and environmental signals, Nature Genetics, 33(3): 245-254.
https://doi.org/10.1038/ng1089

Jiang Y., Bressler J., and Beaudet A., 2004, Epigenetics and human disease, Annual Review of Genomics and Human Genetics, 5(1): 479-510.
https://doi.org/10.1146/ANNUREV.GENOM.5.061903.180014

Kim D., and Kim J., 2021, Multi-omics integration strategies for animal epigenetic studies—a review, Animal Bioscience, 34(8): 1271.
https://doi.org/10.5713/ab.21.0042

Lu Z.N., 2024, Study on the effect of temperature on epigenetic marks in mice, International Journal of Molecular Veterinary Research, 14(1): 32-39.
http://dx.doi.org/10.5376/ijmvr.2024.14.0005

McCaw B., Stevenson T., and Lancaster L., 2020, Epigenetic responses to temperature and climate, Integrative and Comparative Biology, 60(6): 1469-1480.
https://doi.org/10.1093/icb/icaa049

Meirelles F., Bressan F., Smith L., Perecin F., Chiaratti M., and Ferraz J., 2014, Cytoplasmatic inheritance, epigenetics and reprogramming DNA as tools in animal breeding, Livestock Science, 166: 199-205.
https://doi.org/10.1016/J.LIVSCI.2014.05.024

Portela A., and Esteller M., 2010, Epigenetic modifications and human disease, Nature Biotechnology, 28(10): 1057-1068.
https://doi.org/10.1038/nbt.1685

Range F., and Marshall-Pescini S., 2022, Comparing wolves and dogs: current status and implications for human ‘self-domestication’, Trends in Cognitive Sciences, 26(4): 337-349.
https://doi.org/10.1016/j.tics.2022.01.003

Roudbar M., Mohammadabadi M., and Salmani V., 2015, Epigenetics: a new challenge in animal breeding, Genetics in the Third Millennium, 12: 3900-3914.

Sr C., 2022, Epigenetics and its essence in understanding human growth, development and disease, The Journal of Medical Research, 8(5): 165-172.
https://doi.org/10.31254/jmr.2022.8506

Sundman A., Pértille F., Coutinho L., Jazin E., Guerrero-Bosagna C., and Jensen P., 2020, DNA methylation in canine brains is related to domestication and dog-breed formation, PLoS ONE, 15(10): e0240787.
https://doi.org/10.1371/journal.pone.0240787

Tonosaki K., Fujimoto R., Dennis E., Raboy V., and Osabe K., 2022, Will epigenetics be a key player in crop breeding? Frontiers in Plant Science, 13: 958350.
https://doi.org/10.3389/fpls.2022.958350

Vaiserman A., 2011, Hormesis and epigenetics: is there a link? Ageing Research Reviews, 10(4): 413-421.
https://doi.org/10.1016/j.arr.2011.01.004

Wang Y., Liu H., and Sun Z., 2017, Lamarck rises from his grave: parental environment-induced epigenetic inheritance in model organisms and humans, Biological Reviews, 92(4): 2084-2111.
https://doi.org/10.1111/brv.12322

Yakovlev A., 2018, Epigenetic effects in livestock breeding, Russian Journal of Genetics, 54(8): 897-909.
https://doi.org/10.1134/S1022795418080148

You J., and Jones P., 2012, Cancer genetics and epigenetics: two sides of the same coin? Cancer Cell, 22(1): 9-20.
https://doi.org/10.1016/j.ccr.2012.06.008

Zhang A.T., 2024, Research on the role of DNA methylation in the epigenetic regulation mechanism of Pomeranian dogs, Animal Molecular Breeding, 14(1): 72-81.
https://doi.org/10.5376/amb.2024.14.0009