ISSN: 2278-5973 (Online) | Vol. 13, No. 4, (July 2025)

Epigenetic Regulation Of Gametogenesis In Non-Model Zoological Species

Rayan Das
Lecturer, Department of Zoology,
Bangabasi Morning College and Bangabasi Evening College

Abstract

Gametogenesis is a fundamental biological process ensuring sexual reproduction and species continuity across the animal kingdom. While genetic determinants of gamete development have been extensively characterized, increasing evidence has demonstrated that epigenetic regulation plays a decisive role in controlling germ cell differentiation, meiosis, and functional maturation. Epigenetic mechanisms, including DNA methylation, histone modifications, chromatin remodelling, and non-coding RNA-mediated regulation, orchestrate precise spatiotemporal gene expression patterns during gametogenesis. Although these mechanisms have been well studied in traditional model organisms such as mice, zebrafish, and *Drosophila*, comparatively little attention has been devoted to non-model zoological species that exhibit diverse reproductive strategies and environmental adaptations.

This review synthesized current knowledge on epigenetic regulation of gametogenesis with a specific emphasis on non-model zoological species, including fishes, amphibians, reptiles, and invertebrates. It examined conserved and divergent epigenetic pathways governing germline development, highlighted species-specific epigenetic plasticity, and discussed the influence of environmental stressors on epigenetic reprogramming of gametes. Furthermore, the article explored emerging evidence of epigenetic inheritance and its evolutionary implications in non-model taxa. Advances in epigenomic technologies and methodological challenges associated with studying epigenetics in non-model organisms were also critically evaluated. Understanding epigenetic regulation of gametogenesis in diverse zoological systems provides valuable insights into reproductive evolution, environmental adaptability, fertility regulation, and conservation biology.

Keywords: Epigenetics, Gametogenesis, Non-Model Species, DNA Methylation, Histone Modification, Reproductive Biology

Introduction

Gametogenesis represents one of the most intricate developmental processes in multicellular organisms, involving the differentiation of primordial germ cells into specialized male and female gametes. This process is fundamental to sexual reproduction, genetic diversity, and evolutionary fitness. Traditionally, studies on gametogenesis have emphasized genetic regulation; however, over the past two decades, epigenetic mechanisms have emerged as crucial regulators of germ cell fate determination and maturation (Cui et al., 2025).

Epigenetics refers to heritable changes in gene expression that occur without alterations in the underlying DNA sequence. These changes are mediated by molecular mechanisms such as DNA methylation, histone modifications, chromatin remodelling complexes, and regulatory non-coding RNAs. During gametogenesis, epigenetic modifications ensure the activation or repression of genes required for mitosis, meiosis, genomic imprinting, and gamete functionality. Epigenetic reprogramming is especially critical in germ cells because it establishes developmental competence for the next generation.

Most foundational insights into epigenetic regulation of gametogenesis have been derived from model organisms, including mammals and insects. While these studies have been invaluable, they do not

Corresponding Author: Rayan Das, rayand1996@gmail.com

capture the full breadth of reproductive diversity observed across the animal kingdom. Non-model zoological species, such as amphibians, reptiles, teleost fishes, mollusks, and echinoderms, exhibit remarkable variation in reproductive modes, including hermaphroditism, environmental sex determination, parthenogenesis, and asynchronous gametogenesis. These systems provide unique opportunities to explore how epigenetic regulation adapts to ecological and evolutionary pressures.

Furthermore, non-model species often inhabit environments subject to fluctuating temperatures, pollutants, and nutritional stressors, making them ideal systems for studying environmentally induced epigenetic changes. Recent research has suggested that environmental factors can alter epigenetic marks during gametogenesis, potentially leading to transgenerational effects on offspring fitness (Skinner et al., 2013). Understanding such mechanisms is increasingly relevant in the context of climate change and anthropogenic stress.

Despite their importance, epigenetic studies in non-model species remain limited due to challenges such as incomplete genomic resources, lack of standardized experimental tools, and logistical constraints in sample collection. However, advances in next-generation sequencing, single-cell epigenomics, and comparative genomics are rapidly overcoming these barriers. This review aimed to consolidate existing knowledge, identify research gaps, and propose future directions for understanding epigenetic regulation of gametogenesis in non-model zoological species.

Conceptual Framework of Epigenetic Regulation in Gametogenesis

Gametogenesis involves tightly regulated transitions between pluripotency, differentiation, and meiotic progression. Epigenetic mechanisms act as molecular switches that integrate intrinsic genetic programs with extrinsic environmental cues. In germ cells, epigenetic regulation fulfils three major functions: (i) maintenance of germline identity, (ii) regulation of meiosis and gamete maturation, and (iii) establishment of epigenetic information for the next generation.

Primordial germ cells undergo extensive epigenetic reprogramming, characterized by global DNA demethylation and chromatin remodelling. This resetting process erases somatic epigenetic marks, allowing germ cells to acquire sex-specific epigenetic signatures later during gametogenesis (Hackett & Surani, 2013). In non-model species, the timing and extent of epigenetic reprogramming may vary, reflecting species-specific reproductive strategies.

Epigenetic regulation is not static; rather, it is dynamic and reversible. DNA methylation patterns, histone modifications, and non-coding RNAs interact in complex networks to fine-tune gene expression. These interactions are essential for ensuring genomic stability, particularly through the silencing of transposable elements during meiosis. Failure of epigenetic regulation often results in defective gametogenesis, reduced fertility, or embryonic lethality.

DNA Methylation and Gametogenesis

DNA methylation is one of the most extensively studied epigenetic modifications and plays a central role in regulating gene expression during gametogenesis. It involves the covalent addition of a methyl group to the 5' carbon of cytosine residues, primarily within CpG dinucleotides, resulting in transcriptional repression when located in gene promoter regions. During germ cell development, DNA methylation patterns were dynamically reprogrammed to facilitate germline specification, meiotic progression, and gamete maturation (Hackett & Surani, 2013).

In vertebrates, germ cells underwent two major waves of DNA methylation reprogramming. The first occurred during primordial germ cell migration, characterized by global demethylation that erased somatic epigenetic marks. The second phase involved sex-specific remethylation during spermatogenesis and

oogenesis, which was essential for genomic imprinting and gamete functionality (Cui et al., 2025). Although these processes were well characterized in mammals, emerging studies indicated that non-model zoological species exhibited distinct methylation dynamics that reflected their reproductive strategies.

In teleost fishes, DNA methylation patterns during gametogenesis appeared to be highly plastic. Species exhibiting sequential hermaphroditism demonstrated reversible methylation of sex-determining genes, allowing phenotypic sex transitions without underlying genetic changes. For example, alterations in methylation of genes such as *dmrt1* and *cyp19a1a* were associated with gonadal restructuring during sex reversal in reef fishes (Todd et al., 2016). These findings suggested that DNA methylation served as a molecular mechanism enabling reproductive flexibility in response to environmental cues.

Amphibians and reptiles also exhibited unique methylation landscapes during gametogenesis. In species with environmental sex determination, incubation temperature influenced DNA methylation status of key regulatory genes, thereby affecting gonadal differentiation and subsequent gametogenic pathways. Although comprehensive methylome analyses in these taxa remained limited, preliminary evidence supported the hypothesis that DNA methylation acted as an interface between environmental conditions and reproductive development.

In invertebrates, DNA methylation was historically considered minimal; however, recent genomic studies revealed functional methylation systems in mollusks, annelids, and echinoderms. These taxa demonstrated gene body methylation rather than promoter methylation, suggesting alternative regulatory roles in transcriptional stability and gametogenic gene expression (Sarda et al., 2012). Such variations underscored the evolutionary diversity of methylation-based regulation in gametogenesis across animal phyla.

Histone Modifications and Chromatin Remodelling

Histone modifications constituted another major layer of epigenetic regulation during gametogenesis. Histone proteins formed the structural core of nucleosomes, and post-translational modifications to histone tails—such as methylation, acetylation, phosphorylation, and ubiquitination—altered chromatin accessibility and transcriptional activity. Specific histone marks were associated with either transcriptional activation or repression, enabling precise control of gene expression during germ cell differentiation (Reproduction Journal, 2024).

During spermatogenesis, histone modifications played a critical role in regulating meiotic entry, chromosomal synapsis, and spermiogenesis. In mammals, active histone marks such as H3K4me3 and H3K9ac were enriched at promoters of genes required for meiosis, whereas repressive marks such as H3K27me3 ensured silencing of somatic genes (Cui et al., 2025). Similar patterns were observed in non-model vertebrates, although species-specific variations in histone code complexity were evident.

In reptiles and amphibians, histone modification dynamics during gametogenesis remained underexplored; however, available studies indicated conserved roles in chromatin condensation and germ cell maturation. In species with prolonged spermatogenic cycles, extended retention of histones before protamine replacement suggested adaptive chromatin regulation mechanisms. These differences may have implications for sperm chromatin integrity and fertility under environmental stress.

In invertebrates, histone modifications exhibited remarkable diversity. For example, in mollusks and arthropods, gametogenesis involved unique histone variants that replaced canonical histones during meiosis. These variants altered chromatin architecture and facilitated transcriptional reprogramming required for gamete formation. The presence of lineage-specific histone variants suggested that

epigenetic regulation of gametogenesis evolved independently across taxa to accommodate reproductive specialization.

Chromatin remodelling complexes further contributed to epigenetic regulation by repositioning nucleosomes and modifying higher-order chromatin structure. These complexes interacted with histone modifications to regulate accessibility of transcription factors and meiotic machinery. Disruption of chromatin remodelling pathways in experimental systems resulted in impaired gametogenesis, highlighting their conserved importance across animal groups.

Non-Coding RNAs in Germ Cell Development

Non-coding RNAs (ncRNAs) emerged as key regulators of epigenetic control during gametogenesis. These molecules, which included microRNAs (miRNAs), piwi-interacting RNAs (piRNAs), and long non-coding RNAs (lncRNAs), regulated gene expression at transcriptional and post-transcriptional levels without encoding proteins.

piRNAs were particularly critical in germ cells, where they suppressed transposable elements and preserved genomic stability during meiosis. In model organisms, piRNA pathways were essential for spermatogenesis and oogenesis, and loss of piRNA function led to sterility (Siomi et al., 2011). In non-model species, recent transcriptomic studies identified diverse piRNA populations in fish, mollusks, and insects, suggesting conserved roles in germline protection.

miRNAs regulated gametogenesis by fine-tuning expression of genes involved in cell cycle control, apoptosis, and differentiation. Species-specific miRNA expression profiles were observed during different stages of gamete development, indicating adaptive regulation. In teleost fishes, miRNAs were implicated in oocyte maturation and follicular development, whereas in invertebrates, they regulated germ cell proliferation and differentiation.

lncRNAs represented an emerging class of regulatory molecules with roles in chromatin modification and transcriptional regulation. Although functional characterization of lncRNAs in non-model species remained limited, comparative studies suggested that they contributed to species-specific epigenetic regulation of gametogenesis.

Integration of Epigenetic Mechanisms

Epigenetic regulation of gametogenesis did not rely on isolated mechanisms but rather on coordinated interactions among DNA methylation, histone modifications, chromatin remodeling, and non-coding RNAs. These mechanisms formed integrated regulatory networks that ensured developmental precision and adaptability. In non-model zoological species, such integration appeared to be highly responsive to environmental conditions, enabling reproductive plasticity.

Understanding these interactions was critical for elucidating how epigenetic regulation evolved across animal lineages. The diversity observed in non-model species highlighted that epigenetic control of gametogenesis was both conserved and flexible, allowing species to adapt reproductive strategies to ecological niches.

Epigenetic Regulation of Gametogenesis in Non-Model Vertebrates

Non-model vertebrates, including teleost fishes, amphibians, reptiles, and birds, exhibit remarkable diversity in reproductive strategies and life histories. These taxa provided valuable systems for understanding how epigenetic mechanisms modulated gametogenesis beyond the constraints of classical laboratory models. Comparative analyses revealed both conserved epigenetic pathways and lineage-specific adaptations that reflected ecological and evolutionary pressures.

Teleost Fishes

Teleost fishes represented one of the most diverse vertebrate groups in terms of reproductive biology, displaying gonochorism, hermaphroditism, sex reversal, and parthenogenesis. Epigenetic regulation played a central role in facilitating this plasticity. DNA methylation patterns in fish germ cells were shown to be dynamic and reversible, particularly in species capable of sex change. For example, methylation status of sex-related genes such as *dmrt1*, *foxl2*, and *cyp19a1a* was altered during gonadal transformation, enabling shifts between male and female gametogenesis without permanent genetic modifications (Todd et al., 2016).

Histone modifications also contributed to gametogenic regulation in teleosts. Studies in non-model fish species indicated that meiotic progression during spermatogenesis was associated with stage-specific enrichment of histone acetylation marks, which facilitated transcriptional activation of meiosis-related genes. Conversely, histone methylation marks were involved in repressing somatic gene expression within germ cells, ensuring lineage fidelity.

Non-coding RNAs were increasingly recognized as critical regulators of fish gametogenesis. miRNAs were differentially expressed during oocyte growth and maturation, while piRNAs played conserved roles in transposon silencing. Importantly, environmental stressors such as temperature fluctuations and chemical pollutants were shown to influence ncRNA expression, suggesting an epigenetic basis for environmentally induced reproductive alterations in fish populations.

Amphibians

Amphibians provided unique insights into epigenetic regulation due to their complex life cycles and sensitivity to environmental conditions. Gametogenesis in amphibians occurred over extended periods and was often synchronized with seasonal cues. Epigenetic mechanisms were thought to integrate environmental signals with intrinsic developmental programs.

DNA methylation studies in amphibians revealed that germ cell differentiation was accompanied by gradual methylation changes rather than abrupt reprogramming events observed in mammals. This gradual epigenetic modulation may have allowed amphibian gametogenesis to remain responsive to environmental variability. Histone modifications were also implicated in chromatin remodelling during meiosis, although comprehensive epigenomic profiles remained scarce.

Amphibians were particularly vulnerable to environmental contaminants, many of which acted as endocrine-disrupting chemicals. Exposure to such stressors altered epigenetic marks in germ cells, leading to impaired gametogenesis and reduced fertility. These findings underscored the ecological relevance of epigenetic regulation in amphibian reproduction and highlighted their utility as bioindicators of environmental health.

Reptiles and Environmental Sex Determination

Reptiles exhibited one of the most intriguing examples of epigenetic regulation through temperature-dependent sex determination (TSD). In species with TSD, incubation temperature during embryonic development determined gonadal sex, which subsequently influenced gametogenic pathways. Epigenetic modifications were proposed as molecular mediators translating thermal cues into stable developmental outcomes.

DNA methylation of promoters of sex-determining genes, including *dmrt1* and *sox9*, was influenced by incubation temperature. These methylation changes affected gene expression patterns that guided gonadal differentiation and later gametogenesis. Histone modifications further stabilized these expression states, ensuring consistent reproductive development throughout the organism's lifespan.

Although reptiles remained underrepresented in epigenetic research, emerging evidence suggested that epigenetic plasticity played a crucial role in their reproductive adaptability. Understanding these mechanisms was particularly important in the context of global climate change, which threatened to disrupt sex ratios and reproductive success in reptilian populations.

Epigenetic Regulation of Gametogenesis in Non-Model Invertebrates

Invertebrates comprised the majority of animal biodiversity and exhibited an extraordinary range of reproductive strategies, from sexual reproduction to asexual and mixed modes. Epigenetic regulation of gametogenesis in these taxa was less well characterized but increasingly recognized as fundamental to germline development and evolutionary innovation.

Mollusks

Mollusks, including bivalves and gastropods, exhibited diverse reproductive modes such as protandry, protogyny, and simultaneous hermaphroditism. Epigenetic studies in mollusks revealed functional DNA methylation systems predominantly localized within gene bodies rather than promoters. This pattern suggested a role in transcriptional stability rather than on-off gene regulation (Sarda et al., 2012).

During gametogenesis, changes in methylation and histone modifications were associated with transitions between male and female gamete production. Such epigenetic flexibility was thought to facilitate reproductive plasticity in response to environmental conditions such as population density and resource availability. Additionally, ncRNAs were implicated in regulating germ cell proliferation and differentiation, although functional validation remained limited.

Arthropods

Arthropods, including insects and crustaceans, provided important insights into alternative epigenetic strategies. While DNA methylation levels were generally low in insects, histone modifications and ncRNAs played dominant roles in regulating gametogenesis. In species such as butterflies and beetles, epigenetic regulation contributed to seasonal reproductive cycles and caste-specific fertility.

In crustaceans, environmental factors such as salinity and temperature influenced epigenetic marks in germ cells, affecting gamete quality and reproductive timing. These findings emphasized the role of epigenetics in mediating phenotypic plasticity in invertebrate reproduction.

Echinoderms and Other Marine Invertebrates

Echinoderms and other marine invertebrates exhibited external fertilization and synchronous gamete release, requiring precise regulation of gametogenesis. Epigenetic mechanisms were thought to coordinate gamete maturation with environmental cues such as photoperiod and tidal cycles.

Recent transcriptomic and epigenomic studies identified stage-specific expression of chromatin modifiers and ncRNAs during gametogenesis in sea urchins and starfish. These regulatory elements were conserved across developmental stages, suggesting ancient epigenetic mechanisms underlying germline development.

Evolutionary Significance of Epigenetic Diversity

Comparative analysis across non-model vertebrates and invertebrates revealed that epigenetic regulation of gametogenesis was both evolutionarily conserved and highly adaptable. Core mechanisms such as chromatin remodelling and transposon silencing were maintained across taxa, while specific epigenetic strategies evolved in response to ecological pressures and reproductive demands.

This diversity underscored the importance of studying non-model species to fully understand the evolutionary trajectory of epigenetic regulation in animal reproduction. Such insights were critical for developing integrative theories of reproductive evolution and adaptation.

Environmental Influences on Epigenetic Regulation of Gametogenesis

Environmental factors played a pivotal role in shaping epigenetic regulation of gametogenesis, particularly in non-model zoological species that often-inhabited variable and unpredictable ecosystems. External stressors such as temperature fluctuations, nutritional availability, chemical pollutants, hypoxia, and photoperiod changes influenced epigenetic marks in germ cells, thereby modulating reproductive outcomes. These environmentally induced epigenetic modifications acted as molecular interfaces linking ecological conditions to reproductive physiology.

Temperature was one of the most influential environmental variables affecting epigenetic regulation. In ectothermic animals, temperature directly influenced enzymatic activity involved in DNA methylation and histone modification. In species exhibiting temperature-dependent sex determination, thermal cues altered methylation patterns of sex-determining and gametogenesis-related genes, resulting in long-lasting effects on reproductive development. Such epigenetic plasticity enabled species to synchronize gametogenesis with favorable environmental conditions but also rendered them vulnerable to climate change–induced perturbations.

Chemical pollutants, including pesticides, heavy metals, and endocrine-disrupting compounds, were shown to interfere with epigenetic machinery during gametogenesis. Exposure to these agents altered DNA methylation profiles, disrupted histone modification patterns, and dysregulated non-coding RNA expression in germ cells. In aquatic non-model species, contaminant-induced epigenetic alterations were associated with impaired spermatogenesis, abnormal oocyte development, and reduced fertility. These findings highlighted the sensitivity of germline epigenetics to anthropogenic stressors and underscored the ecological consequences of environmental contamination.

Nutritional stress also influenced epigenetic regulation of gametogenesis. Availability of micronutrients involved in one-carbon metabolism, such as folate and methionine, affected DNA methylation capacity in germ cells. In non-model species experiencing seasonal food scarcity, epigenetic modulation allowed reproductive investment to be adjusted according to energetic constraints. This adaptive mechanism enhanced survival but could also result in trade-offs between reproductive output and offspring quality.

Epigenetic Transgenerational Inheritance

Epigenetic transgenerational inheritance referred to the transmission of epigenetic information across generations independent of changes in DNA sequence. During gametogenesis, epigenetic marks established in germ cells had the potential to influence gene expression patterns in offspring, thereby affecting phenotype and fitness. Although extensive epigenetic reprogramming occurred during early development, some epigenetic modifications escaped erasure and persisted across generations.

Evidence for epigenetic transgenerational inheritance in non-model zoological species was emerging but remained limited. Experimental studies in fish and invertebrates demonstrated that parental exposure to environmental stressors resulted in altered epigenetic states and reproductive traits in subsequent generations. For instance, changes in DNA methylation and ncRNA expression in gametes were linked to altered growth, stress tolerance, and reproductive performance in offspring.

Such transgenerational effects were particularly relevant in species with short generation times and high reproductive output, where rapid epigenetic adaptation could enhance population resilience. However, the stability and evolutionary significance of these epigenetic changes remained topics of active debate.

Distinguishing true epigenetic inheritance from parental or environmental effects required rigorous experimental designs, which were often challenging in non-model systems.

Methodological Advances in Epigenetic Studies of Non-Model Species

Historically, the study of epigenetic regulation in non-model species was constrained by limited genomic resources and technical challenges. However, recent methodological advances have revolutionized epigenetic research across diverse taxa. High-throughput sequencing technologies enabled genome-wide profiling of DNA methylation, histone modifications, and ncRNA expression even in species lacking fully annotated genomes.

Bisulfite sequencing and reduced representation bisulfite sequencing (RRBS) facilitated quantitative analysis of DNA methylation patterns at single-base resolution. Chromatin immunoprecipitation followed by sequencing (ChIP-seq) allowed identification of histone modification landscapes associated with gametogenic stages. RNA sequencing provided insights into ncRNA-mediated regulatory networks during germ cell development.

Single-cell epigenomic approaches further enhanced resolution by capturing cell-to-cell heterogeneity within germ cell populations. These techniques were particularly valuable for studying asynchronous gametogenesis in non-model species, where bulk analyses could obscure stage-specific epigenetic signatures. Comparative epigenomics also enabled cross-species analyses, revealing conserved and divergent regulatory features.

Despite these advances, challenges remained. Limited sample availability, ethical constraints, and lack of species-specific antibodies complicated experimental workflows. Bioinformatic analysis of epigenomic data from non-model species required careful interpretation due to incomplete reference genomes and annotation gaps.

Challenges and Research Gaps

Several critical gaps persisted in understanding epigenetic regulation of gametogenesis in non-model zoological species. First, taxonomic coverage remained uneven, with most studies focused on a limited number of taxa. Expanding research to include underrepresented groups would enhance comparative insights. Second, functional validation of epigenetic mechanisms was often lacking, as most studies relied on correlative data rather than experimental manipulation.

Third, integration of epigenetic data with physiological, ecological, and evolutionary frameworks was limited. Multidisciplinary approaches combining epigenomics with endocrinology, developmental biology, and environmental science were needed to fully elucidate the role of epigenetics in reproduction. Addressing these challenges would advance understanding of how epigenetic regulation shaped reproductive success and adaptation in diverse animal systems.

Future Directions in Epigenetic Research on Gametogenesis

Future research on epigenetic regulation of gametogenesis in non-model zoological species should prioritize integrative and comparative approaches that bridge molecular biology, ecology, and evolutionary theory. Expanding taxonomic coverage remains essential, particularly among understudied invertebrate phyla, amphibians, and reptiles that exhibit unique reproductive modes. Such efforts would enhance understanding of how epigenetic mechanisms diversified across evolutionary lineages.

Functional validation of epigenetic mechanisms represented another critical research direction. While descriptive epigenomic studies provided valuable correlations, experimental manipulation of epigenetic regulators—through pharmacological inhibitors, gene knockdown approaches, or controlled

environmental exposures—would strengthen causal inferences. Advances in genome editing technologies, including CRISPR-based epigenome editing, held promise for overcoming experimental limitations in non-model species.

Longitudinal and multigenerational studies were also required to elucidate the stability and adaptive significance of epigenetic modifications established during gametogenesis. Investigating how epigenetic marks responded to long-term environmental change would be particularly relevant in the context of climate change, habitat degradation, and pollution. Such studies could inform conservation strategies by identifying epigenetic biomarkers of reproductive health and population resilience.

Finally, integration of single-cell epigenomics with developmental and physiological data would provide unprecedented resolution of germ cell differentiation processes. These approaches would help disentangle cell-type–specific regulatory networks and reveal how epigenetic heterogeneity contributed to reproductive success in complex biological systems.

Conclusion

Epigenetic regulation emerged as a fundamental and evolutionarily conserved mechanism governing gametogenesis across the animal kingdom. While model organisms have provided foundational insights into germline epigenetics, non-model zoological species revealed a broader spectrum of regulatory strategies shaped by ecological context, reproductive diversity, and evolutionary history. DNA methylation, histone modifications, chromatin remodeling, and non-coding RNAs collectively orchestrated gene expression programs essential for germ cell differentiation, meiosis, and gamete maturation.

Studies reviewed in this article demonstrated that epigenetic mechanisms in non-model species were highly plastic and responsive to environmental cues, enabling adaptive reproductive strategies such as sex reversal, seasonal gametogenesis, and environmental sex determination. At the same time, this plasticity rendered germline development vulnerable to anthropogenic stressors, with potential consequences for fertility and population sustainability.

Advances in epigenomic technologies have begun to overcome historical barriers to studying non-model organisms, opening new avenues for comparative and integrative research. A comprehensive understanding of epigenetic regulation of gametogenesis in diverse taxa will not only advance reproductive biology but also contribute to evolutionary theory, environmental toxicology, and conservation science. Continued interdisciplinary research in this field is essential for elucidating how epigenetic mechanisms shape reproductive success and biological diversity in a rapidly changing world.

References

Carrell, D. T., & Hammoud, S. S. (2010). The human sperm epigenome and its potential role in embryonic development. Molecular Human Reproduction, 16(1), 37–47. https://doi.org/10.1093/molehr/gap090

Cui, Y., Deng, J., Zhang, Y., Du, L., Jiang, F., Li, C., Liu, Q., Wang, X., & He, Z. (2025). Epigenetic regulation by DNA methylation, histone modifications and chromatin remodeling complexes in controlling spermatogenesis and their dysfunction with male infertility. Cellular and Molecular Life Sciences, 82(1), Article 343. https://doi.org/10.1007/s00018-025-04915-3

Feng, S., Cokus, S. J., Zhang, X., Chen, P. Y., Bostick, M., Goll, M. G., Hetzel, J., Jain, J., Strauss, S. H., Halpern, M. E., Ukomadu, C., Sadler, K. C., Pradhan, S., Pellegrini, M., & Jacobsen, S. E. (2010). Conservation and divergence of methylation patterning in plants and animals. Proceedings of the National Academy of Sciences of the United States of America, 107(19), 8689–8694. https://doi.org/10.1073/pnas.1002720107

Hackett, J. A., & Surani, M. A. (2013). DNA methylation dynamics during the mammalian life cycle. *Philosophical Transactions of the Royal Society B: Biological Sciences, 368*(1609), 20110328. https://doi.org/10.1098/rstb.2011.0328

Lyko, F. (2018). The DNA methyltransferase family: A versatile toolkit for epigenetic regulation. Nature Reviews Genetics, 19(2), 81–92. https://doi.org/10.1038/nrg.2017.80

Marshall Graves, J. A., & Peichel, C. L. (2010). Are homologies in vertebrate sex determination due to shared ancestry or to limited options? Genome Biology, 11(4), 205. https://doi.org/10.1186/gb-2010-11-4-205

Reik, W., Dean, W., & Walter, J. (2001). Epigenetic reprogramming in mammalian development. Science, 293(5532), 1089–1093. https://doi.org/10.1126/science.1063443

Sarda, S., Zeng, J., Hunt, B. G., & Yi, S. V. (2012). The evolution of invertebrate gene body methylation. Molecular Biology and Evolution, 29(8), 1907–1916. https://doi.org/10.1093/molbev/mss062

Sharpe, R. M., & Irvine, D. S. (2004). How strong is the evidence of a link between environmental chemicals and adverse effects on human reproductive health? BMJ, 328(7437), 447–451. https://doi.org/10.1136/bmj.328.7437.447

Siomi, M. C., Sato, K., Pezic, D., & Aravin, A. A. (2011). PIWI-interacting small RNAs: The vanguard of genome defence. Nature Reviews Molecular Cell Biology, 12(4), 246–258. https://doi.org/10.1038/nrm3089

Skinner, M. K., Guerrero-Bosagna, C., Haque, M. M., & Nilsson, E. E. (2013). Environmentally induced epigenetic transgenerational inheritance of sperm epimutations promotes genetic mutations. Epigenetics, 8(10), 1037–1047. https://doi.org/10.4161/epi.26191

Todd, E. V., Liu, H., Muncaster, S., & Gemmell, N. J. (2016). Bending genders: The biology of natural sex change in fish. Sexual Development, 10(5–6), 223–241. https://doi.org/10.1159/000449297

Vandeputte, M., & Dupont-Nivet, M. (2019). Epigenetics in aquaculture: Applications and perspectives. Aquaculture, 507, 387–397. https://doi.org/10.1016/j.aquaculture.2019.04.034