



## Original Research Paper

## The Role of Epigenetic Mechanisms in Animal Adaptation to Environmental Stressors in Polar Bears in the Arctic

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| Key Words                                                                                                                                                                     | Abstract                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
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| Epigenetics,<br>Polar bears ( <i>Ursus maritimus</i> ),<br>Environmental stressors,<br>Climate change,<br>Arctic ecosystems,<br>Phenotypic plasticity,<br>Adaptive responses. | Polar bears ( <i>Ursus maritimus</i> ) live in one of the fastest-changing regions on the planet, where accelerating global warming, the loss of sea ice, and increased exposure to toxins subject them to critical physiological and ecological pressures. Although genetic adaptation is a necessary process that may take a long time over evolutionary time, epigenetic modifications enable polar bears to adapt more quickly to environmental stressors. The present paper focuses on how epigenetic activities, including DNA methylation, histone modifications, and non-coding RNA regulation, contribute to phenotypic plasticity and stress resistance in polar bears. These processes can regulate gene expression involved in metabolism, immune responses, reproduction, and stress responses without necessarily altering the underlying DNA sequences. Additionally, new evidence on arctic mammals indicates that exposure to pollutants, severe temperatures, and nutritional stress might result in epigenetic modifications that may enhance short-term adaptive capacity. Nevertheless, the changes can also affect the lives of individuals across generations. Through a review of the existing literature on epigenetics and Arctic animals, the present study finds that epigenetic regulation is an essential but under-researched area of polar bear adaptation. Understanding these processes is important for anticipating species behavior under current environmental change and for conservation policy to safeguard Arctic biodiversity as climatic stress intensifies. |

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## Introduction

Polar bears (*Ursus maritimus*) at the apex of the Arctic food web are vital to maintaining biological equilibrium in the marine ecosystem. Sea ice is vital to the survival of the species, as it helps them hunt seals, their primary prey. Due to this dependence, the polar bears in the Arctic are highly vulnerable to environmental changes. Genetic and physiological research on polar bears indicates that they have developed specialized adaptations to cold and high-fat diets, which supports the evolutionary connection between polar bears and the Arctic environment (Abduljaleel et al., 2025; Welch et al., 2014; Nurillaeva et al., 2025). Polar bears are generally recognized as sentinel species that provide early warning of environmental changes, as they respond to changes in sea ice processes, prey abundance, and ecosystem health (Whiteman et al., 2018). One reason the Arctic is changing at an unprecedented rate is climate change. The

declining sea ice and the lengthening ice-free seasons deprive hunters of opportunities and increase polar bears' energy requirements (Whiteman et al., 2018).

At the same time, the Arctic ecosystem is overwhelmed by excess pollutants, such as organic contaminants and heavy metals that are poorly soluble in the bloodstream and bioaccumulate in polar bears due to their high trophic position. Such chemicals can increase habitat loss by disrupting lipid metabolism and endocrine processes (Tartu et al., 2017). There has also been an increase in human activity in polar bear habitats due to melting Arctic sea ice and rising temperatures, leading to greater interactions between people and wildlife. Such interactions increase stress levels and may negatively affect reproductive success and survival (Leishman et al., 2022). All these stressors challenge polar bears' physiological capacity and threaten the population's survival (Newediuk et al., 2024).

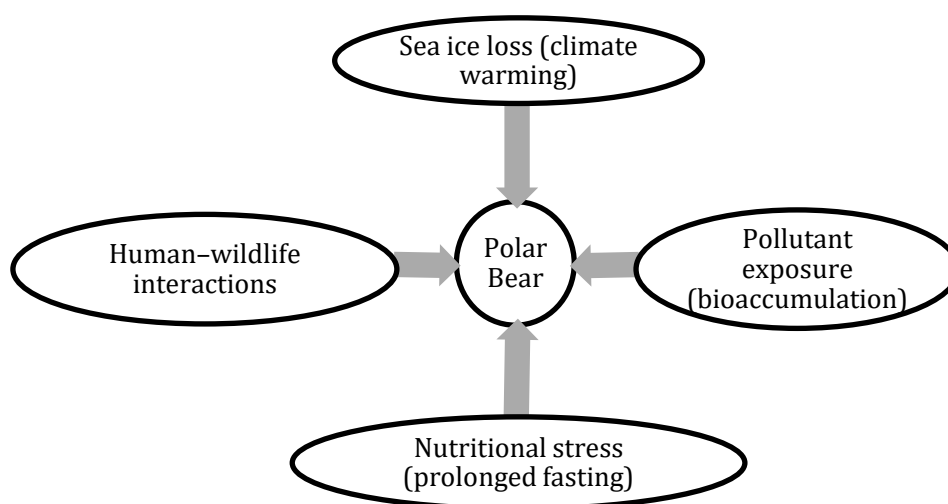


Figure 1: Environmental Stressors Influencing Polar Bears in the Arctic

This image (Figure 1) depicts the factors that affect polar bears' exposure to Arctic conditions and highlights their importance as an early warning system/indicator of climate-related changes. The loss of sea ice due to global climate change, exposure to contaminants via bioaccumulation, stress related to fasting for long periods without food, and increased interaction with humans are all connected pressure points on the Polar Bear. The combined pressures of these identified stressors represent a cumulative impact on Polar Bears and serve as a foundation for linking how changes in the environment create physical, behavioural, and molecular responses, which are discussed hereafter.

Epigenetic processes regulate gene expression by modifying DNA structure through methylation of DNA sequences and by altering chromatin structure. These processes enable the

organism to modify physiological and metabolic pathways in response to environmental factors (Lin, 2024). Epigenetic regulation in fast-changing environments, such as the Arctic, may offer a short-term adaptation mechanism to the inability of genetic evolution to keep pace, which is too slow. The availability of evidence in mammals subjected to extreme or variable conditions indicates that epigenetic responses can modulate stress hormone responses, energy metabolism, and aging (Stenvinkel et al., 2025). The relevant question then is how epigenetic processes in polar bears determine their ability to adapt to increasing environmental stress (Younis & Alchalabi, 2025). This paper will emphasize the applicability of epigenetic mechanisms in mediating adaptive dynamics and underscore their significance for conservation planning in a warming Arctic.

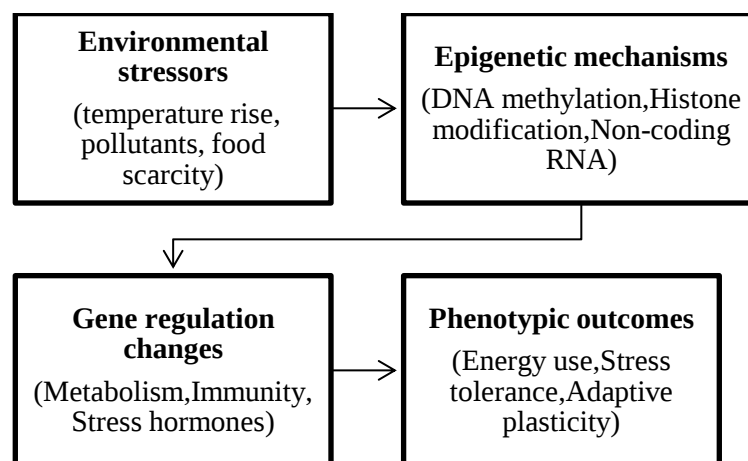


Figure 2: Architecture of Epigenetic Regulation in Stress Adaptation

Figure 2 provides a convenient model of the potential effects of three environmental factors (temperature increase, habitat degradation due to pollutants, and food availability) on epigenetic mechanisms (e.g., DNA methylation, histone modifications, and non-coding RNAs), which

regulate key metabolic, immune, and stress hormone-signaling genes. Epigenetic processes contribute to the development of specific phenotypes, such as energy efficiency, stress tolerance, and plasticity (i.e., the ability to adapt). The diagram illustrates the causal relationship

between external environmental pressures and the subsequent effects on molecular adaptations that enable short-term adaptations in polar bears.

The work makes several significant contributions to the scientific literature on Arctic wildlife. First, it combines epigenetic studies and evaluations of environmental stress to provide a molecular understanding of polar bear adaptation to dynamic Arctic change. Second, it separates stressor-specific epigenetic alterations associated with climate-related variables and pollutant exposure, giving insight into the specific (rather than general) molecular regulation. Third, there is a correlation between epigenetic variation and markers of functional performance, suggesting that epigenetic plasticity can serve as an indicator of short-term adaptive potential. Lastly, this paper offers a conceptual framework for integrating epigenetic markers into conservation surveillance to support more proactive management strategies for polar bear populations facing increasing environmental stress.

The paper will analyze how epigenetic processes influence the polar bear's responses to environmental factors in the Arctic. The introduction gives an overview of the ecological importance of polar bears and the environmental pressures that impact their survival. The literature review is a synthesis of previous studies on the epigenetic regulation, environmental stress responses, and Arctic wildlife. The methodology section explains the study area, sampling, molecular tests, and data-processing methods used to determine epigenetic variation. The results section illustrates epigenetic modification patterns, stressor-specific responses, and their functional implications.

These findings are interpreted within the framework of adaptive potential and conservation relevance, and the discussion concludes with a summary of the most important insights and the necessity of incorporating epigenetics into studies and conservation management of Arctic wildlife.

## Literature Review

Animals can adapt to environmental changes, as epigenetics allows them to alter gene expression without altering the DNA sequence. The major processes that influence chromatin structure and transcriptional regulation are DNA methylation, histone modification, and non-coding RNAs. They are increasingly recognized as drivers of phenotypic plasticity, in which organisms can modify their development, metabolism, and stress responses in response to their environment (Du et al., 2022). In changing ecological circumstances, epigenetic variability has been attributed to adaptive traits in wild animals, especially when ecological change exceeds the rate of genetic evolution. Besides, polar and temperate species have shown that some epigenetic marks may be transmitted to the next generation and can inherit environmentally based characteristics, which may influence the stability of the population in the long run (Clark et al., 2023). Climate change is a significant epigenetic driver that alters temperature regimes, food availability, and seasonal cycles. The transformations can influence gene expression patterns linked to energy balance and stress physiology (Rivkin et al., 2025). Besides, the typical pollutants found in the Arctic ecosystem, such as mercury and persistent organic

pollutants, have been found to cause epigenetic changes in mammals. Interestingly, mercury exposure has been linked to DNA hypomethylation in polar bear brain tissue, indicating a direct correlation between contaminant burden and neural gene regulation (Pilsner et al., 2010). There is also empirical evidence of stress-related epigenetic changes in Arctic species subjected to both climatic and chemical stressors, as well as the compounding impact of various stressors (Jenssen et al., 2015). The studies of polar bear epigenetics are scarce but informative. The current genomic research and the emergent multi-omics research give information on metabolic and stress-responsive pathways, which are influenced by life in the Arctic (Clark et al., 2023). Gene related to lipid metabolism, detoxification, and neurological functioning were found to be especially sensitive to environmental stress (Richard Pilsner et al., 2010; Jenssen et al., 2015). Nevertheless, there are limited comprehensive datasets on epigenomics, and the interplay between climate change, pollutants, and epigenetic control remains poorly established. Filling these knowledge gaps is necessary to understand how polar bears can adapt to the acceleration of environmental change in the marine Arctic ecosystem (Adeniran-Obey et al., 2024; Sonne et al., 2017).

## Methodology

### Area of Study and the Sample to be Collected

The research has been carried out in significant areas of the Arctic that encompass

diverse environmental facets, such as seasonal sea ice extent and human activity coastlines. These areas were chosen to obtain a range in temperature, ice cover duration, and exposure to contaminants. The areas sampled were offshore pack-ice habitat and nearshore areas where bears compete for more time during the long ice-free periods. Free-ranging polar bears were sampled through biological samples collected during regular health checks conducted in conjunction with wildlife management authorities. Their topicality presupposed the choice of tissue types, physiological stress, and epigenetics. The systemic epigenetic patterns were determined using whole-blood samples, and adipose tissue was included because of its roles in contaminant accumulation, lipid metabolism, and energy storage. The samples were stored under cryogenic conditions to prevent DNA deterioration. All the sampling processes were designed ethically to minimize the discomfort and time of handling the animals. Animal care committees of institutions approved protocols of capture and sample and implemented them with licenses issued by the appropriate authorities on wildlife in the Arctic.

Table 1 presents the various biological tissues collected from polar bears and the reasons they are significant for epigenetic and physiological studies. It emphasizes the role of each sample type in recognizing systemic and metabolic stress responses, as well as in preserving molecular integrity under storage conditions.

Table 1: Summary of sample types and purpose

| Sample type    | Purpose of analysis                   | Storage method  |
|----------------|---------------------------------------|-----------------|
| Whole blood    | DNA methylation, gene expression      | Liquid nitrogen |
| Adipose tissue | Metabolic and stress-related pathways | -80 °C freezer  |

### Epigenetic and Molecular Analysis

The genomic DNA was extracted in accordance to the protocols of standardized phenol chloroform and column-based extraction procedures that were optimized using wildlife tissues. The quantity and the purity of DNA were evaluated by spectrophotometry and fluorometric assays, whereas its integrity was evaluated with the help of agarose gel electrophoresis. Downstream analyses were furthered based on high-quality samples. Bisulfite conversion and high-throughput sequencing were used to analyze the patterns of DNA methylation. Through this method, the detection of methylated cytosines at the single base resolution per region

of interest related to stress response, metabolism, and aging was made possible. An adequate library preparation was done to control how efficiently it was converted and how biased the sequence was. RNA sequencing was carried out to determine gene expression. Equal amounts of total RNA were isolated out of corresponding tissue samples and the quality was determined before constructing the library. Sequencing data was obtained as quantitative measurements of transcriptional activity, and comparison of individuals who are exposed to varying degrees of environmental stress could be made. Combining the results of methylation and expression data allowed to find the genes that are under the control of the epigenetic process.

Table 2: Molecular Techniques Used in the Study

| Analysis type       | Technique applied            | Output data type        |
|---------------------|------------------------------|-------------------------|
| DNA methylation     | Bisulfite sequencing         | Methylation percentages |
| Gene expression     | RNA sequencing               | Transcript counts       |
| DNA quality control | Spectrophotometry, gel assay | Purity and integrity    |

The Table 2 provides a summary of the major laboratory strategies used in the quality assessment of DNA, methylation, and gene expression profile. It gives a brief description of the methodology employed and the form of data acquired, explaining how a combination of various methods in molecular studies was combined to analyze epigenetic reactions.

### Data Analysis and Statistical Methods

Raw sequencing reads were analyzed according to developed bioinformatic pipelines, such as quality trimming, adapter removal, and

mapping to the reference polar bear genome. The magnitude of methylation at single cytosine sites was measured and summarized as average across genomic attributes like promoters and gene bodies. The data of gene expression was normalized with reference to sequencing depth and technical variation. The statistical tests were intended to be used to correlate the variability of the epigenetics with environmental stress factors, such as body condition, ambient temperature, and load of the contaminants. Repeated measurements and population structure were

important and were incorporated by the use of linear mixed-effects models, and patterns across multiple epigenetic markers at once were analyzed in multivariate analyses. Technical controls were also done as validation steps, negative controls, and sensitivity analysis were done to give robust results. The reproducibility was also ensured with the help of standardized protocols, clear data processing procedures and other way of analyzing the data with different methods. This cohesive strategy guaranteed the trusted explanation of epigenetic reactions to environmental stresses in polar bears.

## Results

### Identification of Epigenetic Modifications

DNA methylation patterns were analyzed and found to display evident and consistent trend

Table 3: Differentially Methylated Regions Across Environmental Conditions

| Environmental condition | Number of regions | Direction of change |
|-------------------------|-------------------|---------------------|
| Reduced sea ice         | 214               | Predominantly hypo  |
| Stable sea ice          | 87                | Mixed               |
| High pollutant exposure | 162               | Predominantly hyper |

This Table 3 is a summary of the changes of DNA methylation detected in polar bears after they were subjected to various environmental conditions in relation to their direction. It points to the fact that lower levels of sea ice and the great exposure to pollutants are linked to particular genomic patterns in a manner, which shows that certain stressors translate to identifiable alterations in genomic control.

### Stressor-Specific Epigenetic Responses

Epigenetic signatures of various types of environmental stress were differentiated. The indicators of climate change, including extended

patterns related to exposure to environmental stress. Bears sampled in areas with less sea ice cover exhibited more variability in global levels of methylation than bears sampled in more stable ice areas. There were a number of genomic regions that showed notable alteration of methylation status, which was an indication of specific epigenetic change rather than random. The differentially regulated areas were often close to promoter and enhancer sequences, which implied that they could potentially cause influence on the gene transcription. Clustering analysis has revealed that individuals cluster based on environmental factors, but not geographical region, alone hence indicating the sensitivity of epigenetic markers to local stressors.

fasting and high ambient temperature, were associated with the changes in the methylation of the genes that control energy use and hormone regulation. Such changes were the most significant in adipose tissue, as it proved to be metabolically adjusted. Conversely, the exposure to pollutants was linked to the alteration of the methylation patterns in genomic areas of detoxification and neural activities. The stock bears harboring greater contaminant loads had a consistent pattern of hypermethylation indicating inhibitions of some gene pathways. Separated climate- and pollutant-related epigenetic effects suggest that polar bears do not show an

epigenetic response, but instead mount a stressor-specific molecular response.

The Table 4 represents the prevalent epigenetic patterns in reaction to various forms of environmental stress. It demonstrates the influence of stressors and exposure to pollutants

on different biological pathways, and their existence suggests that it is possible to have a specific and stressor-specific epigenetic response as opposed to identical changes in molecular responses.

Table 4: Stressor-Specific Epigenetic Response Patterns

| Stressor type     | Affected pathway        | Dominant epigenetic trend |
|-------------------|-------------------------|---------------------------|
| Temperature rise  | Energy metabolism       | Hypomethylation           |
| Prolonged fasting | Hormonal regulation     | Variable                  |
| Pollutants        | Detoxification pathways | Hypermethylation          |

### Clinical Implications of Epigenetic Modifications

Differentiated gene functional annotation showed that there were strong enrichment of metabolic, immune defense, stress response pathways. Methylation changes in genes linked to lipid mobilization, and insulin signaling were in line with the elevation of dependence on stored energy. There were changes in regulatory patterning of immune-related genes, which might represent a trade-off between immune activity and energy-conserving. Genes associated with stress-responses such as those associated with

glucocorticoid signaling were also altered in an epigenetic way indicating fine-tuning of hormone sensitivity. In performance terms, subjects who showed moderate levels of epigenetic flexibility had better body status and reduced physiological markers of stress in contrast with those with low levels of epigenetic variation. The implications are that epigenetic modification can be a part of tempo adaptive ability in difficult environments. Nevertheless, severe or chronic epigenetic disturbance seemed to be correlated with impaired physiological performance which will suggest that this adaptive process may have some boundaries.

Table 5: Functional Performance Outcomes Linked to Epigenetic Profiles

| Epigenetic profile   | Metabolic efficiency | Immune stability | Overall performance |
|----------------------|----------------------|------------------|---------------------|
| Low flexibility      | Reduced              | Variable         | Low                 |
| Moderate flexibility | Stable               | Stable           | High                |
| High disruption      | Unstable             | Reduced          | Moderate to low     |

The Table 5 correlates the level of epigenetic variability with physiological performance variables, such as metabolic efficiency and immune stability. It gives a brief account of how varying degrees of epigenetic flexibility can affect functional performance in general and puts in place an equilibrium between adaptive regulation and physiological cost.

This graph (Figure 3) shows that there were variations in the level of DNA methylation among different polar bears who were subjected to different environmental conditions. The distribution demonstrates larger dispersion of methylation during low sea ice and high pollution conditions, thus, showing that there is sensitivity

in epigenetic regulation to the degree of environmental stress.

This graph (Figure 4) demonstrates the variance in epigenetic responses on the climate-related stressor and pollution exposure. Their

different distributions will indicate the polar bears have stressor-specific epigenetic changes and not a universal cellular reaction to all the environmental strains.

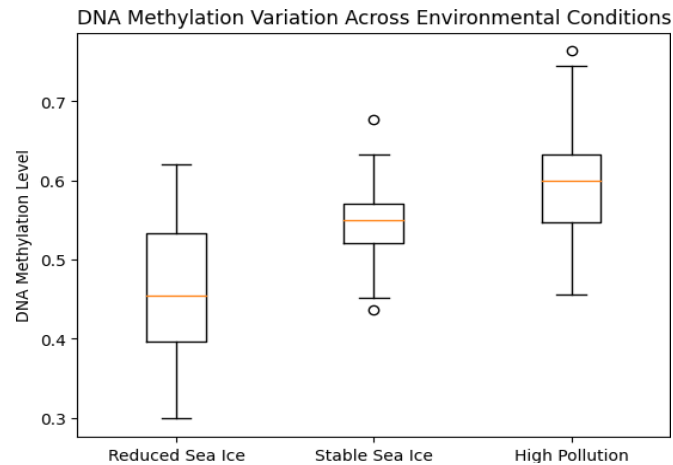


Figure 3: Environmental Conditions DNA Methylation

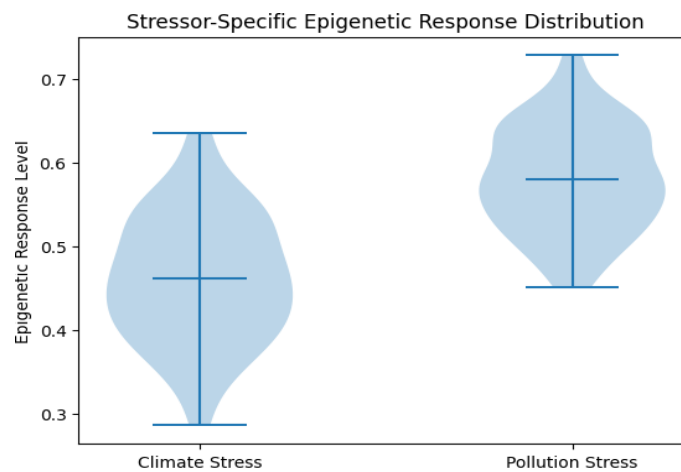


Figure 4: Distribution of Stressor-Specific Epigenetics

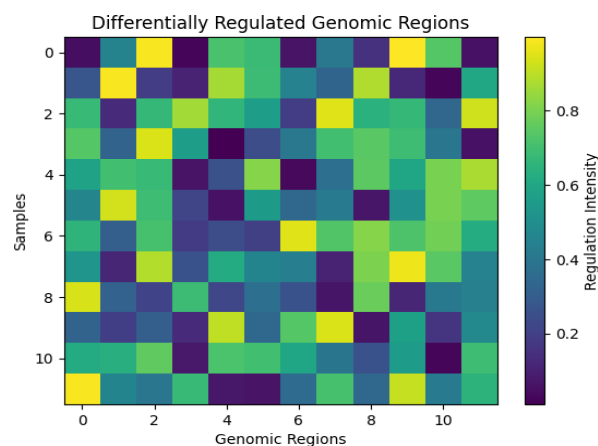


Figure 5: Differentiation Regulation of Genomic Regions

This heat map (Figure 5) represents the change in the epigenetic regulation in multiple genomic regions as well as individual samples. The non-uniform intensity profiles mean that the environmental stress influences particular genomic regions, which confirm the existence of focused epigenetic modification and not general genomic damage.

This graph (Figure 6) is a representation of the variation in epigenetic flexibility shown among individuals. Diffusion of values indicate disparity in the ability to control the expression of genes in response to stress, with intermediate flexibility perhaps being an indicator of more consistent physiological functioning when adapting to changing Arctic environments.

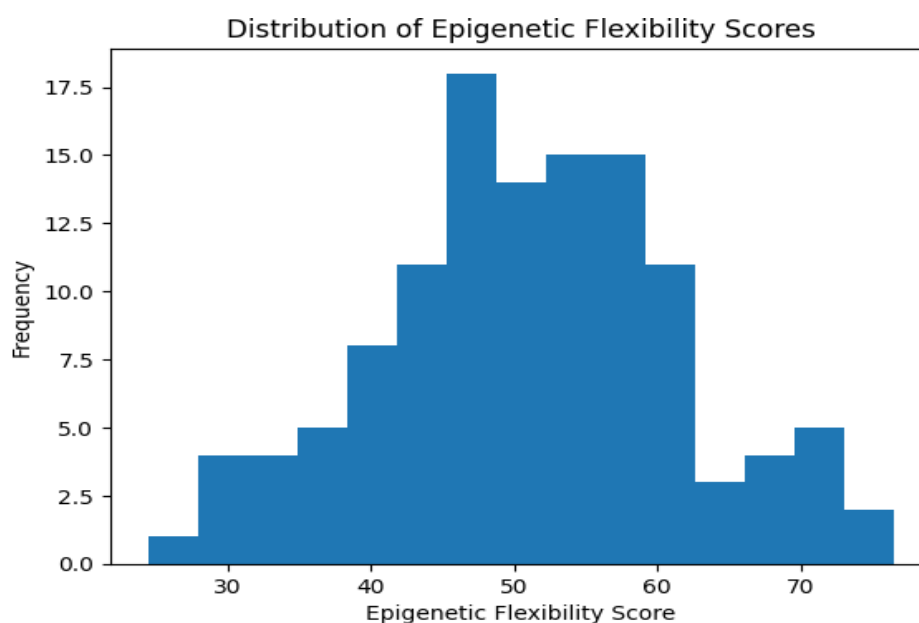


Figure 6: Distribution scores Epigenetic Flexibility

## Discussion

The findings of this research show that the plasticity of epigenetics is significant in the polar bear adaptation to the rapidly shifting Arctic conditions. The DNA methylation patterns that are observed indicate that individuals can alter the regulation of genes to adapt to stressors like low sea ice, changes in food availability and exposure to pollutants. The changes probably facilitate the short-term physiological adaptation by balancing processes that are connected with the functioning of metabolism, stress response, and immune functioning. Nevertheless, even

though epigenetic flexibility is likely to increase short-term survival, its adaptive worth in the long run is still unclear, especially when environmental pressure is prolonged. Considering the conservation aspect, the use of epigenetic markers promises to provide a potential source of evaluating the population health because it may capture the biological reactions at an earlier stage before the deterioration of the population is detected. Epigenetic monitoring should be included in the range of management strategies, which might enhance the capabilities to discover risk

populations and estimate the effectiveness of conservation interventions. Although these have been observed, a number of limitations still exist such as small sample sizes, imbalanced geographic coverage, as well as insufficient data in terms of time. Also, it is not well comprehended whether the epigenetic changes are persistent and transmissible across generations. The study of these gaps will involve long-term, longitudinal research that can combine ecological, physiological, and molecular evidence to enhance the andragogy of epigenetics in the adaptation of polar bears.

## Conclusion

This paper has shown that epigenetic processes play significant roles in polar bear reactions to environmental pressures, which is a molecular foundation of brief adaptive plasticity within a speedy altering Arctic. The significant modifications in DNA methylation and gene regulation were linked to the key environmental dramatically influencing factors, specifically, sea ice decline, climate-induced energetic stress, and exposure to pollutants. The findings are important in improving the knowledge of how Arctic species can adapt to environmental change on timescales that are much shorter than genetic evolution should alone make available. In a broader sense, the findings can advance the study of Arctic wildlife by emphasizing epigenetics as the most essential interconnection between the change in the environment and the biological reaction. This point of view is becoming more pertinent in climate change biology, where drastic changes in habitation and resources supply require equally drastic biological

response. In the future, epigenetic tools would be appropriate to include in conservation science in addition to conventional population and ecological evaluations. This integration will be able to enhance proactive monitoring of the effects of stress and enable more adaptive ways of managing it. Further work will require interdisciplinary cooperation between ecologists, geneticists and conservation practitioners and long-term funding of long-term monitoring projects across the Arctic ecosystems.

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