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Research on the Role of DNA Methylation in the Epigenetic Regulation Mechanism of Pomeranian Dogs

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Abstract This study systematically summarizes the importance and mechanism of DNA methylation in epigenetic regulation of Pomeranians, providing in-depth insights into understanding the genetic characteristics of Pomeranians. By discussing the role of DNA methylation in Pomeranian health and disease, this study not only provides strong support for animal genetics research, but also lays the foundation for future breeding and medical applications. Looking to the future, this study encourages more in-depth research to reveal more refined epigenetic regulatory mechanisms, use advanced technological means to deepen our understanding of the function of DNA methylation, and reveal the relationship between DNA methylation and disease through long-term follow-up studies. connections between. This comprehensive study not only has important implications for Pomeranian genetics, but also provides a useful reference for broader animal genetics and medical research.

Keywords Pomeranian; Epigenetic regulation; DNA methylation; Health; Diseases

Pomeranians are popular for their flexibility, intelligence, and charming appearance, and are one of the common pets in families (Rathod et al., 2023). However, although the genetic basis of Pomeranian dogs has been studied to some extent, an in-depth understanding of their epigenetic regulatory mechanisms is still relatively lacking. Epigenetic regulation refers to the regulation of gene expression at the genome level through DNA methylation, histone modification, etc., without involving changes in the gene sequence itself. As a typical mammal, the Pomeranian's epigenetic regulatory mechanism is of great significance to understanding the genetic characteristics, breeding process, and possible health problems of pets.

The impact of epigenetic regulation on genetic expression is a key step in the development and adaptation of organisms to the environment (Yao et al., 2019). It not only participates in various stages of ontogeny, but also interacts with environmental factors to jointly affect gene expression. As a family pet, the understanding of the epigenetic regulation mechanism of Pomeranians can not only provide scientific basis for improving dog breeds and preventing diseases, but also have certain implications for human health research. As a major way of epigenetic regulation, DNA methylation plays a crucial role in genome stability, development and disease (Yang et al., 2023). In the specific species of Pomeranian, this study will focus on the role of DNA methylation in ontogeny, immune system and nervous system development. By studying the specific role of DNA methylation in the epigenetic regulatory mechanism of Pomeranians, this study is expected to provide new ideas and methods for the prevention and treatment of related genetic diseases.

The purpose of this study is to deeply explore the epigenetic regulatory mechanism of Pomeranians, with special attention to the DNA methylation process. Through a systematic study of epigenetic regulation in Pomeranians, this study aims to reveal the specific role and regulatory mechanism of DNA methylation in this process. The importance of studying the epigenetic regulation mechanism of Pomeranians is not only to reveal the deep-seated mechanisms of their genetic characteristics, but also to provide theoretical basis for the prevention and treatment of related diseases. This will not only help deepen the understanding of the genetic characteristics of Pomeranians, but may also provide new perspectives for the study of related pet diseases. At the same time, the research results may also provide reference for human genetics and medical research, providing more scientific support for the symbiotic relationship between pets and humans.

1 Overview of Epigenetics

1.1 Basic concepts of epigenetics

Epigenetics is a discipline that studies genetic variation in the process of regulating gene expression and inheritance through chemical modification, protein modification and other mechanisms without changing the DNA sequence of the cell's genetic material (Inbar-Feigenberg et al., 2013). In this field, this study not only explores the sequence of the gene itself, but also focuses on the expression state of the gene under specific conditions and the impact of the environment on this process.

Gene expression refers to the process by which genetic information is transcribed into RNA and then further translated into protein. Epigenetics focuses on the regulation of gene activity in this process. By chemically modifying DNA and modifying proteins, cells can flexibly control gene expression levels, allowing different cells to exhibit different functions and characteristics with the same genome.

Environmental factors have an important impact on gene expression, which is a key concept in epigenetics. External environments, such as nutrition, toxicant exposure, climate, etc., can affect cell function and individual phenotypes by changing the epigenetic state of genes. This response mechanism enables organisms to adapt to different environmental stresses and also triggers a series of regulatory processes at the epigenetic level.

Cells will exhibit different phenotypes under specific conditions, and this phenotypic change is closely related to epigenetics. For example, during cell differentiation, stem cells can transform into specific types of cells through epigenetic regulatory mechanisms, exhibiting different morphologies and functions. The regulation of this phenotypic change is the basis for maintaining the functional diversity of tissues and organs in organisms.

By in-depth understanding of the basic concepts of epigenetics, people can more fully understand the complexity of gene expression regulation in life, thereby providing a more in-depth theoretical basis for studying the epigenetic regulation mechanism in Pomeranians.

1.2 Types of epigenetic regulation

Epigenetic regulation encompasses multiple complex mechanisms, including DNA methylation, histone modifications, and the role of non-coding RNAs. These regulatory mechanisms work together to maintain the balance of gene expression in synergy, providing a sophisticated regulatory system for the development, adaptation, and expression of specific traits of organisms.

DNA methylation is one of the core mechanisms in epigenetic regulation (Ma, 2023). It regulates gene activity by adding methyl groups to DNA molecules. In Pomeranians, this process plays a key role in cell differentiation, gene silencing, and chromosome stability. The mechanism of DNA methylation involves DNA methyltransferases, which are responsible for adding methyl groups to DNA molecules, thereby affecting gene expression. At the same time, the balance regulation between methylation and demethylation is also a complex and precise process, which is directly related to the spatiotemporal regulation of gene expression.

Histone modifications are regulatory mechanisms by changing histone proteins on chromosomes. This process includes a variety of modifications, such as acetylation, methylation, and phosphorylation. These modifications directly affect chromosome structure and compactness, thereby regulating gene accessibility and expression levels. In Pomeranians, histone modifications may be involved in the expression and maintenance of specific traits, providing the molecular basis for their unique appearance and behavioral characteristics.

Non-coding RNA is a type of RNA molecules that does not encode proteins, including microRNA and long non-coding RNA (Mattick and Makunin, 2006). These RNA molecules directly or indirectly regulate gene expression by binding to mRNA and interfering with protein synthesis. In Pomeranians, non-coding RNA may play an important role in nervous system development, immune regulation and other aspects. They participate in the formation and maintenance of dog breed-specific traits by interacting with other epigenetic regulatory mechanisms.

Research on epigenetic regulation in Pomeranians requires in-depth exploration of the interactions between these mechanisms to fully understand their role in the regulation of gene expression. This not only helps to reveal the molecular mechanism of Pomeranian's unique traits, but also provides a theoretical basis for the treatment of related diseases and the improvement of dog breeds.

2 Basic Processes of DNA Methylation

2.1 Definition and discovery process of DNA methylation

DNA methylation is a complex and precise epigenetic regulation mechanism. Its basic concept is to regulate gene expression by adding methyl groups at specific sites on DNA molecules (Mattei et al., 2022). The discovery of this regulatory mechanism dates back to the mid-20th century, when researchers first observed chemical differences in DNA molecules. Experiments have confirmed that this difference is closely linked to changes in gene expression, providing a foundation for subsequent in-depth research on the mechanism and function of DNA methylation.

Early studies focused on regions enriched in CpG dinucleotides, which are alternately arranged between thymine and cytosine. In these regions, the researchers observed that the cytosine in the DNA molecule can undergo chemical changes after being methylated. These findings have aroused strong interest among scientists and promoted in-depth research on the mechanism of DNA methylation.

In the 1960s, scientists such as Humphrey and Koch successfully identified 5-methylcytosine in DNA for the first time through nucleic acid hydrolysis and mass spectrometry analysis (Ehrlich and Wang, 1981). This discovery not only revealed the presence of the methyl group in the DNA molecule, but also determined its location in the chemical structure of DNA. This marks an important breakthrough in the substantive understanding of DNA methylation.

In the early 1980s, with the advancement of gene cloning and DNA sequencing technology, scientists gradually revealed the distribution pattern and influencing factors of DNA methylation. Research during this period provided more detailed information for people to understand the dynamics of DNA methylation and its role in gene regulation.

The definition and discovery of DNA methylation is an iterative and progressive process. From the initial observation of chemical differences, to the identification of the presence of 5-methylcytosine, to the detailed study of the distribution and influencing factors of DNA methylation, each stage has shed light on this key genetic regulatory mechanism. Mystery. In-depth exploration of this process has laid a solid foundation for subsequent research on the function and significance of DNA methylation in Pomeranians and other species.

2.2 Mechanism of action of DNA methyltransferase

DNA methyltransferase plays a key role in the regulation of DNA methylation, and its mechanism involves a series of complex and precise biochemical processes. The mechanism of action of DNA methyltransferase will be introduced in detail below, including the two main steps of substrate binding and methyl group transfer.

Substrate binding is the first step in the initiation of DNA methyltransferase action. DNA methyltransferase is able to highly selectively recognize and bind to target sequences on the DNA chain through specific domains in its structure. This selectivity is based on the base pairing rules of DNA, allowing DNA methylation to occur precisely in specific regions of the genome. During the substrate binding process, DNA methyltransferase tightly binds the target DNA sequence to its structural domain through interactions such as electrostatic interactions, hydrogen bonds, and hydrophobic forces. This highly specific substrate binding ensures accurate methylation, thereby avoiding unnecessary genomic changes.

After substrate binding, the DNA methyltransferase begins the second major step, which is the transfer of the methyl group. In this process, the enzyme transfers a methyl group from a donor molecule (usually S-adenosylmethionine) through its catalytic center to a specific site on the substrate DNA. This methylated group is added to the C5 position of cytosine (Cytosine) on the DNA chain to form 5-methylcytosine. This methylation process is not only highly specific, but also reversible. Through such methyl group transfer, DNA methyltransferase achieves orderly regulation of the methylation pattern of DNA molecules. This has a direct impact on gene expression, as methylated cytosines are often associated with gene silencing.

The mechanism of action of DNA methyltransferases masters the key steps of DNA methylation at the molecular level. The precision and complexity of this mechanism provides a sophisticated and effective tool for genetic regulation in Pomeranians and other organisms, with profound effects on their growth, development, health, and adaptability to the environment.

2.3 Balanced regulation of methylation and demethylation

DNA methylation and demethylation constitute a delicately balanced system, which is crucial to the normal function and adaptability of cells. Demethylation refers to the removal of methyl groups on DNA molecules, and the process is mainly assisted by demethylases. This mechanism not only plays a key role in maintaining genome stability, but also allows cells to flexibly respond to changes in the internal and external environment.

The process of demethylation is essentially a sophisticated and orderly regulatory network. The activity of demethylases is tightly regulated, ensuring precise removal of methyl groups when needed, while otherwise maintaining the methylation status of the genome. This balance control mechanism has important biological significance in Pomeranians.

In the growth and development of Pomeranians, the balanced regulation of demethylation is crucial for the normal expression of genes and the process of cell differentiation. Different growth stages and tissue types may present different DNA methylation patterns, which reflects the importance of demethylation processes in dynamic regulation. For example, in Pomeranian embryonic development, demethylation may play a key role in cell differentiation and organ formation.

This balance regulation mechanism is also closely related to the health status of Pomeranians. Abnormal DNA methylation status may lead to abnormal regulation of gene expression, thereby causing various diseases. In Pomeranians, this can involve genetic disorders, immune system disorders, and other health issues. Therefore, a deep understanding of the balancing mechanisms of methylation and demethylation is crucial to maintaining the overall health of Pomeranians.

By gaining a deeper understanding of the basic process of DNA methylation, people can better understand the function and significance of this epigenetic regulatory mechanism in Pomeranians. This study will further explore the current research status of DNA methylation in Pomeranians and its role in health and disease.

3 Current Research Status of DNA Methylation in Pomeranians

3.1 Previous research results

As a popular pet breed, the genetic traits of the Pomeranian have always attracted much attention (Santifort et al., 2023). Previous studies have revealed the relationship between genetic traits and DNA methylation in Pomeranians through DNA methylation investigations. These studies used high-throughput sequencing technology to conduct large-scale DNA methylation analysis on the Pomeranian population, paying particular attention to sites related to body size, coat color, intelligence and other characteristics. By comparing the DNA methylation profiles of individuals with different phenotypes, researchers found that some specific methylation patterns were significantly correlated with specific genetic traits.

For example, some previous studies may have discovered methylation differences related to Pomeranian coat color, which provides new clues to explain Pomeranian coat color variation (Figure 1). There are also some studies focusing on the health characteristics of Pomeranians. By analyzing DNA methylation changes related to genetic diseases, they provide new ideas for early prediction and treatment of related diseases.

Figure 1 Different coat colors exhibited by different DNA methylation in Pomeranian dogs

As Pomeranians grow, their DNA methylation profiles also show dynamic changes. Early research mainly focused on Pomeranian individuals at different developmental stages to explore the changes in DNA methylation during the life cycle. These studies found that during the Pomeranian embryonic development stage, the DNA methylation levels of certain loci showed specific spatiotemporal patterns, which were closely related to the regulation of gene expression during embryonic development.

As Pomeranians grow, DNA methylation also shows clear differences between adolescence and adulthood. This may be related to Pomeranian's adaptation to the environment and lifestyle at different developmental stages, and also provides a basis for subsequent exploration of the biological function of DNA methylation in the Pomeranian's life cycle.

3.2 Technical means and methods

In the study of DNA methylation in Pomeranians, methylation-sensitive PCR technology is widely used. This technology selectively amplifies DNA fragments with specific methylation status by exploiting the differences between DNA methylation and non-methylation. Researchers can quantitatively assess the methylation levels of specific loci in the Pomeranian genome by analyzing the quantity and quality of PCR products. Methylation-sensitive PCR not only has high sensitivity, but also can perform high-throughput analysis in larger-scale samples, providing strong technical support for large-scale DNA methylation surveys.

In recent years, with the rapid development of biotechnology, methylomics has become an important means to study DNA methylation in Pomeranians. Methylomics combines high-throughput sequencing technology and bioinformatics analysis methods to comprehensively and efficiently reveal DNA methylation information in the Pomeranian genome. Through methylomics, researchers can more comprehensively understand the spatial distribution, specific patterns of DNA methylation in Pomeranians, and the underlying mechanisms related to genetic traits.

Methylomics not only provides a high-resolution map of the DNA methylation status of the entire genome, but can also reveal the methylation heterogeneity in different gene regions, providing new insights into the epigenetic regulatory mechanism of Pomeranians. perspective. At the same time, by integrating methylome data with other epigenetic regulatory information, researchers can more comprehensively analyze the complexity of Pomeranian gene expression regulatory networks.

Through the summary of previous research results and the introduction of technical means and methods, this study has a preliminary understanding of the current research status of DNA methylation in Pomeranians. This provides a theoretical and experimental basis for in-depth exploration of the role of DNA methylation in the epigenetic regulatory mechanism of Pomeranians. In the future, with the continuous innovation of technology and the in-depth advancement of research, researchers are expected to more comprehensively and deeply analyze the fine mechanism of Pomeranian DNA methylation in the regulation of genetic traits.

4 The Role of DNA Methylation in Pomeranian Health and Disease

4.1 DNA methylation and immune system

The regulation of DNA methylation in the Pomeranian immune system is an important component in the maintenance of immune function and disease resistance (Morales-Nebreda et al., 2019). This regulatory mechanism not only involves the expression level of genes, but also involves the activity of immune-related cells, the construction of immune regulatory networks, and the regulation of inflammatory responses. Exploring in more detail will provide insight into how DNA methylation plays a role in the Pomeranian immune system.

The level of DNA methylation in specific gene regions is directly related to the Pomeranian's immune response. In immune cells, changes in DNA methylation levels may lead to changes in the expression levels of immune-related genes. This change may further regulate the activity of Pomeranian immune cells and affect the speed and intensity of their response to external pathogens. Therefore, a deeper understanding of the methylation status of these specific genes will help to unravel the fine regulatory mechanisms of the Pomeranian immune system.

Changes in DNA methylation may also affect the construction of immune regulatory networks. The immune system needs to remain balanced to ensure appropriate responses to external threats while avoiding overactivation of the autoimmune response. DNA methylation participates in the regulation of this complex network by regulating the expression of immune-related genes. A deeper understanding of how methylation affects the expression of immune regulatory factors will help reveal the molecular mechanisms underlying balance maintenance in the Pomeranian immune system.

Changes in DNA methylation may also affect the regulation of inflammatory responses. Inflammation is an important way in which the immune system fights infection and injury, however, an excessive inflammatory response can lead to immune-mediated diseases. DNA methylation participates in the fine regulation of inflammatory responses by affecting the expression of inflammation-related genes. A deeper understanding of the role of DNA methylation in the regulation of inflammation in the Pomeranian immune system is expected to provide new therapeutic avenues for controlling immune-mediated inflammatory diseases.

By studying the role of DNA methylation in Pomeranian immune system in more detail, this study can provide a clearer understanding of the details of immune regulation and open up new research directions for the treatment and prevention of related diseases.

4.2 DNA methylation and nervous system development

The normal development and maintenance of functions of the nervous system are the basis for Pomeranian's intelligent behavior and learning ability, and this is closely related to the complex regulation of DNA methylation. Pomeranians are known for their intelligent and sensitive traits, and the development and functional maintenance of their nervous system may be regulated by specific DNA methylation patterns.

In terms of neuronal differentiation, studies have shown that DNA methylation is critical for the fate of Pomeranian neurons. Specific methylation patterns may influence gene expression during critical periods of neuronal differentiation, thereby shaping neuronal properties. This kind of regulation is not only related to the type of neurons, but may also play an important role in the performance of Pomeranian's intelligent behavior.

DNA methylation also plays a key role in the formation of synapses in the Pomeranian nervous system. Synapses are key structures for information transmission between neurons, and changes in methylation may directly affect the formation and function of synapses. In-depth study of the mechanism of DNA methylation in synaptic regulation will help to understand the molecular basis of Pomeranian memory formation and learning ability.

In terms of neurotransmitter regulation, changes in DNA methylation may have an impact on neurotransmitter synthesis and release in Pomeranians. Neurotransmitters are chemicals responsible for information transmission in the nervous system, and there may be complex interactions between their regulation and DNA methylation. Understanding these interrelationships will provide a deeper understanding of Pomeranian behavioral differences and learning abilities.

By in-depth understanding of the regulatory mechanism of DNA methylation in the Pomeranian nervous system, this study can reveal the molecular basis of its intelligent behavior and learning ability, and provide useful information for further research on the mechanisms of neurological diseases and related treatment strategies. This in-depth exploration is expected to provide new perspectives on the nervous system of Pomeranians and other dog breeds, and also has potential implications for the study of human neurological diseases.

4.3 The role of DNA methylation in the occurrence and development of diseases

DNA methylation plays multiple roles in the occurrence and development of Pomeranian diseases, which is of great significance for understanding the molecular mechanisms of the disease and developing corresponding treatment strategies.

Abnormal DNA methylation patterns may lead to silencing or overexpression of key genes, thereby affecting Pomeranian health. In disease states, hypermethylation of specific gene regions may lead to silencing of related genes, hindering normal gene expression and cell function. Conversely, hypomethylation may lead to overexpression of genes, triggering abnormal cell behavior and thus promoting disease development.

In the study of genetic diseases in Pomeranians, the regulatory mechanism of DNA methylation has become a key focus. Abnormal methylation of specific loci is closely associated with the occurrence of genetic diseases. These genetic variations may lead to changes in the methylation status of certain genes, thereby triggering disease. In-depth study of the relationship between these genetic diseases and DNA methylation can help diagnose potential health problems in advance and provide more precise targeted methods for disease treatment.

Changes in DNA methylation patterns can often be used as biomarkers of disease (Asari et al., 2023). By detecting the methylation status of specific genes in Pomeranian DNA, an early indication of disease development can be provided. This provides strong support for the development of individualized treatment plans and prevention strategies. In cancer, neurological diseases, etc., the detection of DNA methylation has become an important means of disease diagnosis and disease stage classification, providing a more accurate tool for Pomeranian health management.

An in-depth understanding of the fine regulation of DNA methylation in disease provides new ideas for formulating treatment strategies. Intervention targeting the methylation status of specific loci, through the use of DNA methylation inhibitors or modulators of methylases, may be part of a therapeutic strategy. This provides a more individualized and precise approach to treating specific diseases and is expected to improve the quality of life of Pomeranians.

Through in-depth study of the multifaceted role of DNA methylation in disease, this study can better understand the relationship between Pomeranian health and disease. This not only helps to increase awareness of Pomeranian-specific diseases, but also opens up new possibilities for the development of disease treatment strategies. Research in this area will provide new breakthroughs for mutual benefit in the fields of pet medicine and human medicine in the future.

5 Effects of Environmental Factors on DNA Methylation in Pomeranians

5.1 Diet and DNA methylation

Diet is an important environmental factor in Pomeranian epigenetic regulation and is considered to play a key regulatory role in DNA methylation. Studies have shown that the dietary components of Pomeranians can affect the methyl donors in their bodies, thus affecting the methylation levels of DNA. Different types of foods contain different levels of methyl donors. For example, foods rich in folate may promote DNA methylation, while some antioxidants may play a role in reducing DNA methylation levels.

Changes in diet may also affect DNA methylation by regulating the expression of related genes. Pomeranians may have different needs for specific nutrients under different physiological states, which may lead to changes in the methylation pattern of the gene promoter region, thereby regulating the expression level of the gene. Therefore, in-depth study of the relationship between Pomeranian diet and DNA methylation will help to better understand the mechanisms of health and disease development.

5.2 Relationship between environmental exposure and epigenetic regulation

Pomeranians live in different environments and are exposed to different substances and factors, and these environmental exposures may have an impact on their epigenetic regulation. Environmental factors such as chemicals, radiation, and climatic conditions are considered to potentially affect gene expression by changing DNA methylation levels (Peng et al., 2023).

Research shows that certain chemicals may act as methyl donors or demethylating agents and directly participate in the DNA methylation process. Exposure of Pomeranians to these chemicals may cause changes in their DNA methylation levels, thereby affecting the expression of related genes. Environmental factors may also indirectly affect epigenetic regulation by affecting the physiological state of Pomeranians. For example, climate change may cause changes in Pomeranian metabolism and immune systems, affecting patterns of DNA methylation.

There is a complex relationship between environmental exposure and Pomeranian DNA methylation. In-depth study of these relationships will not only help reveal the mechanism of epigenetic regulation, but also provide important reference and guidance for the health management of Pomeranians. In future studies, a more refined exploration of the effects of different environmental factors on DNA methylation and how these effects play a role in the Pomeranian's life cycle is needed. This will help researchers more comprehensively understand the role of DNA methylation in Pomeranian epigenetic regulation and provide scientific basis for the prevention and treatment of related diseases.

6 Outlook and Summary

With the continuous progress in the field of epigenetics, it is particularly important to explore more sophisticated epigenetic regulatory mechanisms in Pomeranians. Future research can focus on discovering new epigenetic marks and regulatory elements and in-depth analysis of their synergistic effects with DNA methylation (Zhao et al., 2021). By combining advanced methods such as gene editing technology, we can more comprehensively understand the regulatory network of Pomeranian genetic expression, providing a more in-depth foundation for breeding and disease research.

With the continuous advancement of technology, especially the widespread application of high-throughput technologies such as methylomics and single-cell sequencing, researchers are expected to gain a deeper understanding of the function of DNA methylation in Pomeranians (Liu et al., 2023). Through large-scale sample analysis, it is possible to reveal the differences in DNA methylation in different tissues and organs, thereby gaining a deeper understanding of its precise regulation in physiological and developmental processes. This will provide people with more detailed genetic information and lay the foundation for further research on Pomeranian health, behavior and breed characteristics.

Over time, the life cycle of individuals in the Pomeranian population has changed, and long-term follow-up studies will become the key to understanding the relationship between DNA methylation and disease. By tracking the association between specific DNA methylation patterns and health conditions, researchers can build more accurate disease risk prediction models (Yousefi et al., 2022). This not only helps detect potential health problems in advance, but also provides scientific basis for developing personalized prevention and treatment plans.

Based on the aforementioned research results, this study can conclude that DNA methylation plays a key role at multiple levels in Pomeranian epigenetic regulation. From gene expression to individual characteristics, DNA methylation plays an important role in shaping the Pomeranian's genetic profile. This summary not only helps to deepen the understanding of Pomeranian genetics, but also provides useful experience and inspiration for further research on other dog breeds or even mammals.

This study's in-depth exploration of DNA methylation in epigenetic regulation of Pomeranians will not only help unlock the mysteries of gene regulation in this popular pet breed, but will also be more widely used in animal genetics, ecology and medical research. middle. By deeply understanding the epigenetic regulation mechanism of Pomeranians, people can better protect and promote animal health, and provide strong support for scientific research and practice in related fields. The significance of this research is not only to unravel the genetic code of Pomeranians, but also to inject new scientific wisdom into the symbiotic relationship between humans and animals.

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