

Review and Progress

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Functional and Interaction Analysis of Key Genes in the Domestic Cat Genome

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Abstract This study provides a systematic analysis of the functional and interactive aspects of key genes in the domestic cat genome, outlining the overall characteristics of the cat genome, including genome size, structure, and variation, with a focus on key genes related to behavior, immune system, hair and skin development in the cat genome. Through molecular-level functional analysis and physiological and behavioral experiments, this study intricately reveals the significant roles these genes play in the physiological functions and behavioral manifestations of domestic cats. At the same time, the interaction networks of these genes, including protein interaction networks and gene regulation networks, were further analyzed, and the relationships and regulatory mechanisms between key genes were deeply explored. The study looks forward to the prospects of cat genome research, explores the application of gene editing technology in cat genome research, and emphasizes the enlightening significance of this research for improving cat quality of life, solving behavioral problems, and in human medicine.

Keywords Domestic cat genome; Key genes; Functional analysis; Interaction networks; Gene editing technology

Cats have been domesticated by humans as early as 7500 BC. As companion animals that have been domesticated for a long time by humans, their companionship and closeness have made them an indispensable part of modern families (Driscoll and Clutton-Brock, 2010). The emergence of cats has not only enriched human daily life and provided companionship and comfort, but also played practical functions in agricultural societies such as catching mice and protecting food (Bradshaw, 2013). Cats also make great mental health companions because of their unique behaviors and personalities, positively impacting their owners' emotional state. However, although cats have been with humans for a long time, the secrets behind their genes still need to be deeply explored. Advances in genomics are providing researchers with new ways to reveal cat biology and behavior. By delving into key genes of the cat genome, humans can more fully understand the nature of this closely related animal to humans.

The rapid development of genomics provides researchers with new tools to unlock the mysteries of life (Yang et al., 2022). Rapid advances in this field are not only transforming our understanding of biology and medicine but also providing opportunities to address many major scientific questions. The new prospects of genomics are driving scientists to delve deeper into the genetic information in organisms, thereby improving people's understanding of health, disease and life.

By digging deeper into the cat genome, this study explores cats' evolution, physiological mechanisms, and the genetic basis of their interactions with humans. Researchers are expected to discover key genes related to behavior, immune system, etc., and better understand cats' nature and behavioral characteristics. Through genome-wide expression profiling analysis, the expression changes of transcription factors and miRNAs in cats under different physiological states and behavioral modes can be identified, revealing the co-expression patterns of these regulatory elements and key genes. Further investigation of the evolutionary conservation and diversity of these regulatory elements will help to understand their origin and evolution in the cat genome. This helps to understand how certain regulatory elements perform specific biological functions in cats and how they adapt to the evolutionary needs of cats in their natural environment and human society. This study provides an in-depth look at key genes in the cat genome and provides a detailed analysis of their functions and interactions. Through the study of the cat genome, this study aims to reveal key genes related to cat behavior, understand the genetic basis of the

cat immune system, analyze genes related to hair and skin development, as well as protective genes related to skin health, and analyze the function of key genes at the molecular level to establish an interaction network of key genes in the cat genome. These research goals provide more comprehensive and in-depth genomic support for cat biology, behavior, and the symbiotic relationship between cats and humans, and have important guiding significance for future cat genetic improvement, disease prevention and control, and understanding of interactions with humans.

1 Overall Characteristics of the Cat Genome

1.1 Genome size and structure

Cat genome are key aspects that provide insight into the nature of its biology. The latest research shows that the size of the cat genome is about 280 million base pairs, which is relatively compact compared to other cats. This sparked a great deal of interest among scientists in the unique adaptations that characterized the evolution of the cat genome. Comparing the genome size differences between cats and other felines (Figure 1) can help reveal the selective pressure and adaptive changes in cats during their evolution.

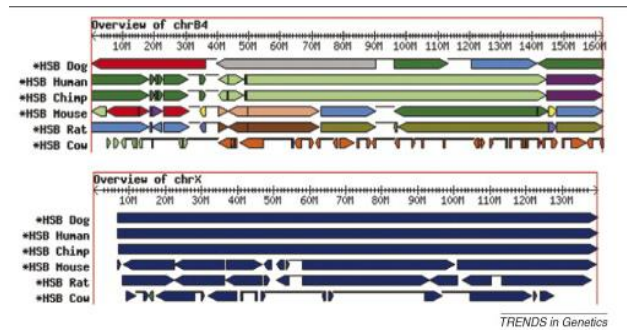


Figure 1 Homologous synteny blocks (HSBs) relative to cat chromosomes B4 and X defined by conserved sequence blocks across six index mammalian species' genome sequences (O'Brien et al., 2008)

In addition to genome size, the structure of the cat genome is also an aspect of great concern. When researchers paid attention to the chromosomal organization of cats, they found that the structure of cat chromosomes may play an important role in their unique physiological and behavioral performance. In addition, the distribution and amount of ribosomal RNA also play an important role in the analysis of the cat genome structure, providing clues to understand the unique architecture of cats at the cellular level.

1.2 Genomic variation and its distribution in cats

Genomic variation is a driving force of natural selection and evolution and is critical to the understanding of cat fitness and diversity. In the cat genome, analysis of single nucleotide polymorphisms (SNPs) and structural variations revealed genetic differences between different cat breeds (Zhao et al., 2022). In-depth study of these patterns of variation helps explain the diversity of cat breeds and also provides clues to the physiological and behavioral differences between individuals. By analyzing the distribution of variants, the researchers were able to identify specific loci associated with cat-specific physiological and behavioral differences, providing a basis for further functional studies.

1.3 Evolution and expansion of gene families

The rich and diverse gene families in the cat genome are key to its adaptation to different environments and lifestyles. Studying the evolutionary path of cat gene families, especially the immune gene family and the sensory gene family, can help reveal how cats respond to external challenges during their evolution. The evolutionary patterns of these gene families provide humans with important clues about cats' evolutionary strategies to fight disease and adapt to the environment. A deeper understanding of the function and evolution of these gene families will provide insights into disease resistance and survival strategies in cats.

2 Key Genes in the Cat Genome

Cats' behavior, immune system, hair and skin development and other characteristics are deeply regulated by the genome.

2.1 Behavior-related genes

Cats' behavioral characteristics are largely regulated by genes, which not only affect their social interactions with humans and other cats, but also involve aspects such as hunting behavior and locomotion.

2.1.1 Cat social behavior and cognitive ability-related genes

Cats are naturally highly social animals, and their social behavior and cognitive abilities have complex regulatory mechanisms at the genetic level. Some genes, such as *OXTR* (*Oxytocin receptor* gene) (Jurek and Neumann, 2018) and *CD38* (*Cyclophosphatase* gene), have been found to be closely related to cat social behavior. The proteins encoded by these genes play key roles in the nervous system, regulating cats' responses to social stimuli and their perception of the environment.

Further research found that a gene related to the establishment of interpersonal relationships, *V1aR* (*Vasopressin 1a receptor*) and *GNB3* (*G protein-coupled receptor* gene), also plays an important role in cats' social behavior. Variations in these genes may cause cats to exhibit different behavioral patterns when faced with unfamiliar environments or new social partners, revealing the diversity in the genetics of social behavior.

In addition, genes related to spatial memory and learning abilities, such as *BDNF* (*Brain-derived neurotrophic factor* gene) and *COMT* (*Catechol O-methyltransferase* gene), also play key roles in cats' cognitive abilities. Through the study of these genes, people can better understand cats' ability to adapt to environmental changes and their individual differences in learning new tasks.

2.1.2 Genes related to hunting behavior and movement ability

A cat's hunting instinct is a natural manifestation of its status as a predator, and this behavior is closely related to specific genes in its genome. The study found that genes related to athletic ability and hunting skills are mainly involved in muscle development, nerve conduction and coordination.

MYOD1 (*Muscle development transcription factor* gene) and *ACTN3* (α -actin genes) are two genes related to muscle development and motor performance that may play an important role in cats' hunting behavior. Variations in these genes may affect the growth and strength of a cat's muscle tissue, affecting its efficiency and speed when catching prey. Genes in the nervous system, such as *TH* (*Tyrosine hydroxylase* gene) and *SLC6A3* (*Dopamine transporter* gene), also affect the cat's movement coordination and reaction speed. By in-depth study of the functions of these genes, people can better understand the synergy of cats' nervous systems during hunting, and provide scientific basis for improving cats' hunting skills.

Research on behavior-related genes not only helps reveal the molecular mechanisms behind cat behavior, but also provides a potential path for optimizing cat behavioral characteristics through gene editing and other means.

2.2 Immune system related genes

The immune system is your cat's body's internal line of defense, protecting it from pathogens. The study of immune system-related genes involves genes related to resistance to disease and infection and immune response regulatory genes, which is crucial for a deep understanding of the immune mechanism of cats.

2.2.1 Genes related to resistance to disease and infection

Cats are exposed to a variety of pathogens such as bacteria, viruses, and parasites in their daily lives (Figure 2). The difference in resistance is mainly affected by gene expression. The expression levels of specific genes may determine a cat's ability to resist infection by different pathogens. For example, some genes may encode receptors on the surface of immune cells that are critical for the recognition and elimination of specific pathogens. By studying these genes in depth, researchers can identify key immune response elements, providing a theoretical basis for improving cats' overall immune levels.

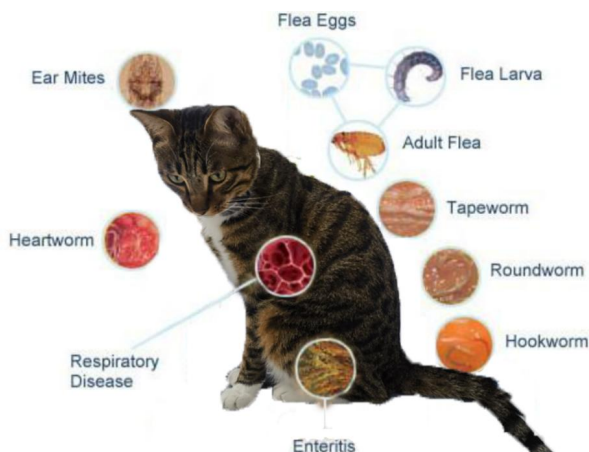


Figure 2 Causes and symptoms of five major cat diseases

In addition, studies have found that some immune-related genes differ among cat breeds, which may lead to differences in the susceptibility of different breeds to specific pathogens. Therefore, the selection and cultivation of disease-resistant germplasm based on genotype is expected to provide an effective means to improve the overall resistance of cats.

2.2.2 Immune response regulatory genes

The balance and regulation of immune responses are critical to maintaining the normal function of the immune system. In this context, some genes encode proteins that act as regulators of immune responses. These genes may be involved in processes such as activation, proliferation, and apoptosis of immune cells to ensure that the immune system can respond quickly and orderly when facing pathogens.

Studies have found that in certain disease states, the abnormal expression of these regulatory genes may lead to excessive activation or suppression of the immune system, thereby triggering the occurrence of autoimmune diseases or infections. Therefore, an in-depth understanding of the functions and regulatory mechanisms of immune response regulatory genes will help reveal the molecular basis of the balance of the cat immune system and provide new strategies for disease treatment and prevention.

Research on immune system-related genes can not only deepen people's understanding of the immune mechanism of cats, but is also expected to provide important scientific basis for disease prevention and genetic improvement of related genes.

2.3 Genes related to hair and skin development

The morphology and characteristics of hair and skin are significant signs of a cat's appearance, and the regulation of their development and characteristics mainly involves a series of complex gene networks.

2.3.1 Genes related to hair color and pattern

Cats display a diverse combination of coat colors and patterns, which originate from a series of key genes in the genome involved in pigment synthesis and distribution. Among them, the genes in the pigment production pathway encode the synthesis of enzymes, which have a direct impact on the depth, brightness and hue of the color. Studies have found that variations in genes such as *TYR* (tyrosinase) (Yu et al., 2019) and *MC1R* (α -MSH receptor) can lead to variations in the production of melanin or red pigment, thereby affecting the color of cat hair. In addition, some genes such as *KIT* and *EDNRB* play key roles in pattern formation and regulate the arrangement and distribution of hair on the body. By in-depth understanding of the functions of these genes, researchers can reveal the mechanisms of hair color and pattern formation, providing a scientific basis for breeding cats with special appearance characteristics.

2.3.2 Skin health and protective genes

A cat's skin is not just part of its appearance, it's a key component of its physiological health. In terms of skin health and protective genes, some genes play an important role in maintaining skin barrier function, resisting external environmental aggression, and regulating skin physiological balance. For example, mutations in the *FLG* (keratin gene), which encodes a keratin protein that is an important component in maintaining the integrity of the skin barrier, may lead to dry and sensitive skin. At the same time, some immune-related genes such as *DEFB4* and *LTF* are expressed in the skin and participate in the antibacterial, anti-inflammatory and healing processes, directly affecting the cat's resistance to external pathogens. By studying these genes in depth, researchers can gain a more comprehensive understanding of the regulatory mechanisms of cat skin health and provide scientific support for preventing skin diseases and improving skin health.

The study of genes related to hair and skin development not only helps to unlock the genetic code that forms the appearance of cats, but also provides people with new ways to improve the overall physiological health of cats. A deep understanding of the functions of these genes will provide scientific guidance for the maintenance and breeding of outstanding cats, so that they can better adapt to changing environments and living conditions.

3 Functional Analysis of 3 Key Genes

3.1 Functional analysis at the molecular level

3.1.1 Gene-encoded proteins and their functions

In the cat genome, the proteins encoded by key genes play diverse and important biological functions. Among them, some genes are closely related to the behavioral and physiological characteristics of cats, providing the molecular basis for cats' unique behaviors. For example, a class of genes closely related to social behavior encodes proteins that may play a key role in signaling between neurons. These proteins may be involved in regulating neuronal excitability and inhibition, thereby affecting cats' social interactions and cognitive abilities.

By in-depth understanding of the structure and function of these encoded proteins, researchers can more accurately understand how they regulate cat behavior at the molecular level. For example, a certain protein may act at a nerve synapse to promote the release of neurotransmitters, thereby affecting the speed and intensity of nerve signal transmission. This in-depth molecular analysis helps reveal the fine regulation mechanism of cat behavior and provides a basis for subsequent physiological and behavioral research.

3.1.2 Gene expression and regulation at the cellular level

The expression and regulatory mechanisms of key genes at the cellular level are critical to understanding their functions. Research has shown that the expression levels of some genes change significantly under specific physiological or behavioral states, suggesting that they may play an important role in specific situations (Schoenfelder and Fraser, 2019). In-depth study of these changes, especially the differences in expression of these genes in different cell types and brain regions, will help to reveal the specificity of genes in the regulation of cat behavior.

This cellular level regulatory mechanism may involve the participation of regulatory factors such as transcription factors and miRNA. By exploring these regulatory networks, researchers can more fully understand the location, timing and extent of regulation of key genes within cells. This not only provides more detailed clues to the molecular basis of cat behavior, but also provides specific targets and directions for future gene editing and intervention research.

3.2 Physiological and behavioral experiments

3.2.1 The relationship between overall behavior and physiological functions and gene expression

In delving deeper into the functions of key genes in the cat genome, through holistic behavioral and physiological experiments, this study was able to more fully reveal the complex roles of these genes at the organismal level. Observing the behavioral changes of cats in different social interaction situations and simultaneously monitoring the expression levels of key genes in the nervous system and other related tissues will allow researchers to establish more refined links between genes and behavior.

A typical application of this experimental approach is to gain insights into genes related to social behavior by recording cats' social behaviors, such as intimate licking and sharing meals. At the same time, by analyzing the dynamic changes in gene expression when these behaviors occur, researchers can discover the spatiotemporal regulation patterns of specific genes in social interactions, providing important clues for analyzing their role in complex social networks.

3.2.2 Effects of genetic mutations on cat physiological processes

In order to simulate the variation in the cat genome, introducing gene mutations has become an effective method (Figure 3). By introducing mutations in specific genes into the cat genome, researchers can observe the direct effects of these variations on physiological processes. For example, by simulating mutations in a certain behavioral-related gene, researchers can observe whether cats' social behavior is inhibited and whether they exhibit abnormal behavior patterns.

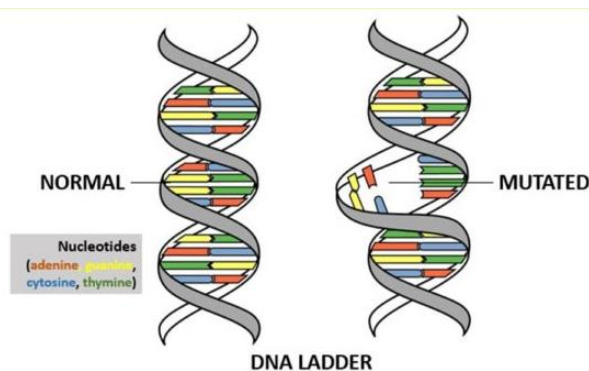


Figure 3 Introduction of mutated genes (Nebert, 1999)

The advantage of this experimental design is that it can precisely control the variation of genes, making it more consistent with the mutation situation in real organisms. By comparing the behavioral and physiological differences between normal cats and genetically mutated cats, this study can provide an in-depth understanding of the precise regulation of key genes on cat physiological processes, and then reveal the exact role of these genes in cat behavior and physiological functions.

This series of experimental methods will provide this study with a more in-depth and comprehensive analysis of key gene functions, and provide rich empirical data for the study of cat behavior and physiological characteristics. This is not only of great value for research in the fields of cat behavior and physiology, but also provides useful insights into the relationship between human genes and behavior.

4 Cat Gene Interaction Networks

4.1 Protein interaction network

Cat genome encode proteins that form an intricate, coordinated network of interactions. Through highly sophisticated protein mass spectrometry technology and bioinformatics analysis, this study successfully revealed the direct or indirect interactions between genes and proteins in this huge network.

In the cat protein interaction network, some genetic proteins were found to play key roles as central nodes. These central nodes connect multiple interconnected genes and proteins, forming a functionally highly integrated network hub. This study will conduct an in-depth study of the functions of these central nodes and explore their specific roles in regulating cat physiology and behavior.

The functions of these central nodes may cover multiple levels, including but not limited to regulating cell signaling, participating in gene expression regulation, and affecting metabolic pathways (Armingol et al., 2021). This study will reveal the molecular mechanisms of these central nodes in the cat genome through further biological experiments and bioinformatics analysis, providing strong support for a deep understanding of the biological functions of cat genes.

This study studies the module structure in the network to understand the interrelationships between different functional modules. This helps people more fully understand the complexity of the cat genome and provides a more detailed theoretical basis for further research on cat behavior and physiological processes. This in-depth analysis will enable researchers to better understand the biological network of the cat genome and provide useful guidance for future genetic research and the regulation of cat behavior.

4.2 Gene regulatory network

Gene regulatory networks play a key role in the physiological and behavioral processes of cats, involving complex regulatory mechanisms of transcription factors and miRNAs. Detailed dissection of this network will be critical to uncovering the details of molecular regulation in cats and the molecular basis of adaptive behavior.

In the cat gene regulatory network, transcription factors and miRNA are the main regulators of gene expression. Transcription factors directly affect the physiological functions and behavioral performance of cats by binding to the promoter region of genes and activating or inhibiting the gene transcription process. By binding to the mRNA of the target gene, miRNA regulates the translation and stability of the gene, thereby indirectly affecting the expression level of key genes.

By deeply exploring the complexity of gene regulatory networks, people will gain a more comprehensive understanding of the physiological and behavioral regulatory mechanisms of cat genes, providing a more profound theoretical basis for cat genetics and gene editing research. This not only helps advance the scientific community in the fields of biodiversity and genomics, but also provides concrete scientific evidence for improving cat breeds, improving quality of life, and deepening interactions with humans.

5 Summary and Outlook

Cat genome research is a promising field, laying the foundation for a deeper understanding of the biology of this close companion of humans. With the continuous advancement of technology, this study can foresee that more genetic data will be available for analysis in the future, thereby deepening the understanding of cat genes. The development of gene editing technology will allow researchers to more precisely study and improve cats' genes, providing the possibility of breeding healthier, smarter and more adaptable cat breeds. As concerns about cat behavior and health increase, genomic research will provide more comprehensive solutions to cat behavioral problems and diseases.

Cat genome research not only helps improve the quality of life of cats, but also provides valuable insights for human medicine and genetic research. Through in-depth research on cat genes, people can better understand the commonalities and differences of genes in mammals (Buckley and Lyons, 2020). This provides a reference for the study of human genetic diseases, helps to gain an in-depth understanding of the pathogenesis of some diseases, and thereby provides new treatment strategies for human medicine. Cats' role in human society also makes genome research socially relevant. By revealing the close relationship between cats and humans, people can better understand the status of cats in human culture and promote harmonious coexistence between humans and animals. This kind of cross-species genetic research will not only help improve the lives of cats, but also help humans better understand and protect their animal companions.

Cat genome research offers vast scope for improvements in cat health and behavior. By gaining a deeper understanding of the genes associated with cat behavior, researchers can develop more targeted training and socialization improvement programs to improve the quality of cat-human interactions. At the same time, for some behavioral problems, such as aggression or excessive intimacy, the application of gene editing technology will also provide new ways to modify behavior. In terms of health, genomic research is expected to reveal the genetic variations that cause common cat diseases, thereby preventing and treating these diseases in advance (Zhang and Schoenebeck, 2020). Through genetic diagnosis, medical staff can develop more personalized medical plans, provide each cat with a customized health management plan, and improve its quality of life.

Cat genome research will provide a more scientific and personalized management method for the overall health and behavior of cats, and also provide new ideas and possibilities for the relationship between humans and animals. As technology and research continue to advance, people's understanding of the cat genome will continue to deepen, paving the way for a shared future for humans and this special companion.

References

- Armingol E., Officer A., Harismendy O., and Lewis N.E., 2021, Deciphering cell–cell interactions and communication from gene expression, *Nature Reviews Genetics*, 22(2) : 71-88.
<https://doi.org/10.1038/s41576-020-00292-x>
PMid:33168968 PMCID:PMC7649713
- Bradshaw J.W., 2013, Evolution and history of the cat, In *The Behaviour of the Domestic Cat*, pp.1-22.
<https://doi.org/10.1079/9781845939922.0001>
- Buckley R.M., and Lyons L.A., 2020, Precision/genomic medicine for domestic cats, *Veterinary Clinics: Small Animal Practice*, 50(5): 983-990.
<https://doi.org/10.1016/j.cvsm.2020.05.005>
PMid:32653264
- Driscoll C.A., and Clutton-Brock J., 2010, The taming of the cat. In *The domestic cat: The biology of its behaviour*, pp.37-52.
- Jurek B., and Neumann I.D., 2018, The oxytocin receptor: from intracellular signaling to behavior, *Physiological reviews*, 98(3): 1805-1908.
<https://doi.org/10.1152/physrev.00031.2017>
PMid:29897293
- Nebert D.W., 1999, Pharmacogenetics and pharmacogenomics: why is this relevant to the clinical geneticist? *Clinical Genetics*, 56(4): 247-258.
<https://doi.org/10.1034/j.1399-0004.1999.560401.x>
PMid:10636440
- O'Brien S.J., Johnson W., Driscoll C., Pontius J., Pecon-Slattery J., and Menotti-Raymond M., 2008, State of cat genomics, *Trends in genetics*, 24(6): 268-279.
<https://doi.org/10.1016/j.tig.2008.03.004>
PMid:18471926 PMCID:PMC7126825
- Schoenfelder S., and Fraser P., 2019, Long-range enhancer–promoter contacts in gene expression control, *Nature Reviews Genetics*, 20(8): 437-455.
<https://doi.org/10.1038/s41576-019-0128-0>
PMid:31086298
- Yang J., Zhong Y.H., Peng P.X., Liu P., Wang P., and Wang L., 2022, Study on lysis spectrum and genomic characteristics of the first *Yersinia pestis* bacteriophage isolated from cats, *Disease Surveillance*, 37(9): 1159 -1164.
- Yu Y., Grahn R.A., and Lyons L.A., 2019, Mocha tyrosinase variant: a new flavour of cat coat coloration, *Animal genetics*, 50(2): 182-186.
<https://doi.org/10.1111/age.12765>
PMid:30716167 PMCID:PMC6590430
- Zhang W., and Schoenebeck J.J., 2020, The ninth life of the cat reference genome, *Felis_catus*, *PLoS Genetics*, 16(10): e1009045.
<https://doi.org/10.1371/journal.pgen.1009045>
PMid:33091014 PMCID:PMC7580993
- Zhao X.P., Pu J., Chong Y., Gao Z.Q., Du S.L., Bai Z.L., Lai P.A., and Wang L., Duplex real-time PCR for accurate identification of tiger-derived materials in animal products, *China Port Science and Technology*, 4(12): 85-91.