

Research Report

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Genetic Resolution of Disease Resistance in Poultry: A Genome-Wide Association Study Perspective

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Abstract Poultry diseases pose a serious threat to agricultural production, and resistance is one of the key factors for effective disease response. The aim of this study was to resolve the genetic basis of resistance in poultry through a genome-wide association study (GWAS) approach. A series of poultry populations stomach-selected for reference experimental subjects, including chickens, ducks and geese, were scanned genome-wide. Association analysis of thousands of loci successfully identified multiple genetic variants associated with poultry disease resistance. These variants are involved in key biological processes such as immune-related genes, inflammatory pathways and antiviral responses. Significant differences in resistance genotypes and frequencies were also found among different poultry breeds, which provide important clues for further improvement of poultry disease resistance.

Keywords Poultry diseases; Resistance; Genetic analysis; Genome-wide association studies; Immune genes

In today's society, the poultry industry, as an important part of the global agricultural economy, plays a vital role in human food supply and nutritional security. However, poultry production faces many challenges, one of which is the threat of various poultry diseases. These diseases not only pose a threat to the health and welfare of poultry, but can also lead to significant economic losses and pose indirect risks to human health. Understanding the genetic basis of poultry diseases, especially through genome-wide association study (GWAS) to reveal the mechanisms of disease resistance in poultry, has become one of the important directions of current scientific research.

Poultry diseases cause huge economic losses to agricultural production worldwide. According to statistics, avian influenza alone may cause billions of dollars in economic losses each year. In addition to direct production losses, poultry diseases may cause international trade restrictions, increase the cost of vaccination and treatment, and even threaten human food safety and public health. Poultry disease outbreaks may also lead to price fluctuations in poultry products, affecting consumer choice and nutritional intake (Liu, 2023).

Genetic factors play an important role in the development of disease resistance in poultry. By studying genetic variation in poultry, scientists can identify genes and genetic markers associated with disease resistance. This genetic information is important for improving poultry breeds and enhancing their resistance to specific diseases. For poultry populations that are highly susceptible to avian influenza, genetic selection and breeding strategies can produce poultry breeds that are resistant to avian influenza, thereby reducing the incidence and spread of the disease.

Genome-wide association studies (GWAS) are powerful scientific tools that help scientists identify genes that influence disease resistance in poultry by analyzing associations between genetic variants and specific traits across the genome (Dong et al., 2023). The application of GWAS has greatly advanced the understanding of poultry genetics, particularly in the mechanisms of disease resistance. Through GWAS, researchers have been able to identify key genetic loci associated with resistance in the poultry genome, providing molecular markers for breeding and making selection more precise and efficient. The application of GWAS has also helped to unravel the mechanisms of resistance in poultry to a variety of diseases, which provides a scientific basis for the development of new prevention strategies and vaccines.

In this study, we comprehensively explored the genetic resolution of poultry disease resistance through the perspective of genome-wide association studies (GWAS), covering the economic and social impacts of poultry diseases, the role of genetics in poultry disease resistance, and the importance and application of GWAS. These research results are not only of great significance for the sustainable development of the poultry industry, but also provide a new scientific basis and methodology for the prevention and control of poultry diseases, which is an important contribution to the improvement of global food safety and the protection of public health.

1 Overview of Poultry Diseases

1.1 Classification and characteristics of common poultry diseases

Poultry diseases are diseases that affect various poultry such as chickens, ducks and geese, and they are usually caused by pathogens such as bacteria, viruses, fungi or parasites. Common poultry diseases can be categorized according to the type of pathogen, and each disease has its specific transmission pathway, clinical symptoms and control measures.

Avian influenza (AI) is a highly contagious disease caused by avian influenza viruses and is categorized into highly pathogenic avian influenza (HPAI) and low pathogenic avian influenza (LPAI). Outbreaks caused by highly pathogenic avian influenza viruses are often characterized by acute and high mortality rates, and the main symptoms include respiratory and neurological symptoms, which have caused serious economic losses to the poultry farming industry. Outbreaks caused by low pathogenicity avian influenza viruses are relatively mild, but still affect the performance and immune function of poultry (Mo et al., 2022).

Marek's disease (MD) is an acute infectious disease caused by Marek's virus that mainly infects the respiratory and digestive tracts of poultry. The disease is characterized by rapid spread and high lethality, and clinical symptoms include fever, respiratory distress, and increased mucus secretions. Marek's disease has a serious impact on the performance and immune function of chickens and is one of the important diseases in poultry farming (Abdelsattar et al., 2022).

Infectious bronchitis (IB) is an infectious disease caused by bronchitis virus, which mainly infects the respiratory system of poultry (Rong et al., 2023). The disease is characterized by rapid spread and severe symptoms, such as respiratory distress, coughing, and inflammation of the tracheal mucosa. Infectious bronchitis not only affects poultry performance, but may also lead to complex secondary infections and complications, posing a serious threat to poultry health (Figure 1).

In summary, poultry diseases are categorized according to the type of pathogen causing the disease and the characteristics of clinical manifestations, and each disease has its transmission pathway, clinical symptoms and control measures. Timely and effective preventive measures and control strategies are essential to maintain poultry health and ensure the stable development of the breeding industry.

1.2 Impact of disease on poultry production

The impact of disease on poultry production is multifaceted and it can cause serious economic losses and production disturbances in poultry farming. Diseases can lead to inhibited growth and reduced productivity of poultry. Poultry infected with viral diseases such as avian influenza often suffer from loss of appetite and slow growth, leading to a longer growth cycle for broilers and laying hens and an increase in farming costs.

Diseases can cause increased mortality in poultry. Large-scale mortality often occurs on poultry farms during outbreaks. Especially in the absence of effective preventive and control measures, the mortality rate can be very high, resulting in heavy losses for farmers. Diseases also affect the reproductive ability and reproductive capacity of poultry, resulting in lower hatchability and reduced egg production, which further affects farming efficiency. In addition to direct economic losses, diseases may also raise concerns about the quality and safety of poultry products, affecting market sales and consumer confidence. Effective disease prevention and control are essential to maintain the stability of poultry production and improve economic efficiency (Endersen and Coffey, 2020).



Figure 1 Main manifestations of poultry diseases

Note: A: Specific manifestations of Avian influenza: the diseased chicken crown has necrosis and bleeding, sick chicken with sagging and coronal cyanosis, bleeding in the legs and toes after infection; B: specific manifestations of Malik's disease: sick chicken feet paralyzed, falling to the ground, extending one limb forward, the sick chicken shows a squatting posture, skin lesions with nodular hyperplasia; C: Specific manifestations of Infectious bronchitis: sick chickens open their mouths and stretch their necks to breathe, the kidney of the sick chicken is swollen, pale, and has a betel nut like pattern, sick chickens excrete yolk and egg white like substances

1.3 Genetic nature of poultry diseases

The resistance or susceptibility of poultry to certain diseases is closely related to their genetic background. Recent studies have shown that the resistance of poultry to certain diseases can be significantly improved through genetic selection and breeding techniques. For example, by calibrating and selecting for genetic markers associated with disease resistance, it is possible to breed poultry breeds with higher resistance to diseases such as Marek's disease or avian influenza. This genetically based disease management strategy not only reduces the reliance on vaccines and drugs, but also improves the sustainability of poultry production.

In conclusion, the management and control of poultry diseases is a complex process that requires comprehensive consideration of multiple aspects of pathogenesis, immunology and genetics. Through in-depth understanding of the genetic nature of poultry diseases and the application of modern genetic and breeding techniques, the resistance of poultry to diseases can be effectively improved, providing a solid scientific basis for ensuring the healthy development of the global poultry industry and food safety.

2 Foundations of Genome-Wide Association Studies (GWAS)

2.1 Principles and methods of GWAS

Genome-wide association studies (GWAS) is a widely used method in the field of genetics research that allows scientists to identify genetic variants associated with specific traits or diseases in the genomes of different individuals. This approach has played an important role in unraveling the genetic mechanisms behind disease resistance in poultry.

The core principle of GWAS is based on statistics, which identifies genetic markers associated with disease by comparing genomic differences between individuals with a specific disease (case group) and healthy individuals (control group). This approach does not require prior assumptions about candidate genes and allows for genome-wide exploration (Tan and Zhao, 2023).

Conducting a GWAS usually involves the following steps:

Sample collection: selecting a sufficient number of samples from case and control groups.

Genotyping: Genotype all samples using high-throughput sequencing technology to obtain genome-wide genetic marker information.

Association analysis: Statistical methods are used to analyze the strength of association between each genetic marker and the disease, and identify genetic variants that are significantly associated with the disease.

Validation of results: The results of the association analysis are validated by independent sample sets or further functional studies.

2.2 Genetic markers and mapping of the poultry genome

Genetic markers are specific DNA sequences in the genome that can distinguish between the genetic backgrounds of different individuals, and are often used as "landmarks" for identifying and tracing genetic material. In mapping the poultry genome, genetic markers help scientists to localize genes or gene regions associated with disease resistance.

Mapping the poultry genome involves mapping genetic markers to known genomic locations and constructing genetic linkage maps and physical maps. This process is critical to the success of GWAS because it ensures that genetic variants are correctly associated with specific genes or gene regions.

2.3 How to identify genetic variants associated with disease resistance

GWAS identifies genetic variants associated with disease resistance by comparing differences in genetic markers between case and control groups. These variants may be located within genes that encode important proteins or in non-coding regions that regulate gene expression.

Statistical association: by calculating the difference in the distribution of genetic markers between case and control groups, GWAS can identify genetic markers that are significantly associated with disease resistance. Genes near these markers may be directly involved in disease resistance mechanisms (Pirnay et al., 2021).

Bioinformatics analysis: through bioinformatics tools and databases, researchers can further analyze the functions of genes near these markers to reveal their roles in disease resistance.

Experimental validation: Ultimately, functional genomics experiments (e.g., gene knockout, gene expression analysis, etc.) are used to validate the specific role of these genes or genetic variants in disease resistance.

In summary, GWAS provides a powerful tool for identifying genetic variants associated with disease resistance in poultry on a genome-wide scale. The mapping and association analysis of genetic markers not only enables the discovery of new disease resistance genes, but also provides an in-depth understanding of the function of these genes in the organism, providing a scientific basis for poultry disease prevention, control and breeding. With the advancement of gene sequencing technology and the development of bioinformatics methods, the application prospect of GWAS will be broader and its contribution to the poultry industry will continue to grow.

3 Foundations of Genome-Wide Association Studies (GWAS)

3.1 Specific case studies

In recent years, genome-wide association studies (GWAS) have become an important tool in poultry disease resistance research, helping scientists to understand poultry resistance to diseases at the genetic level.

Avian Influenza is a disease that severely affects the poultry industry and its viruses are highly mutable, making vaccine development and disease control extremely difficult. In an effort to find natural resistance to avian influenza in poultry, a GWAS analysis of chickens was executed with the aim of identifying genetic markers and genes associated with resistance to avian influenza.

By analyzing genomic data from thousands of chickens, the researchers identified several genetic markers significantly associated with avian influenza resistance. Among them, a region located on chicken chromosome 4 was found to be particularly associated with virus resistance. Further studies indicated that a gene named "*MX1*" in this region plays a key role in avian influenza virus infection, and that the level of expression of the *MX1* gene, which is involved in the cellular antiviral response, directly influences the resistance of chickens to avian influenza (Tan et al., 2024).

Domestic researchers further explored the adaptive evolution of the *MX* gene and its association with avian influenza resistance. The results of the study showed that specific variations in the chicken *MX* protein at amino acid position 631 were decisive for its antiviral activity. This implies that certain genetic variants may enhance or attenuate the antiviral capacity of chicken *MX* protein and have a direct impact on avian influenza resistance (Figure 2).

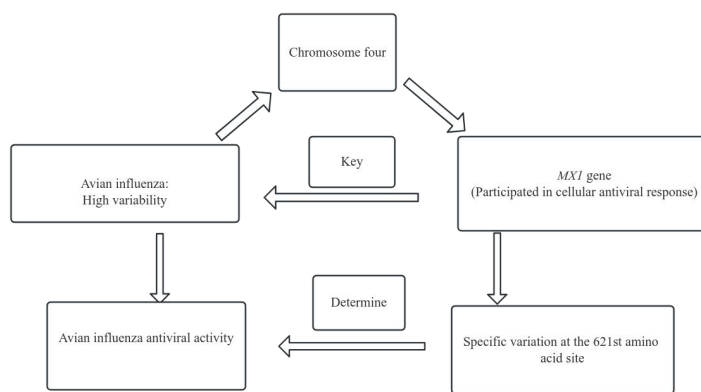


Figure 2 Performance of *MX1* gene in key roles of avian influenza virus infection

Marek's disease is another serious threat to poultry production, mainly affecting chickens. It is a cancer caused by a virus that can lead to extremely high mortality in chickens. Research on resistance to Marek's disease is important to reduce economic losses and improve poultry productivity (Cai et al., 2023).

In a GWAS study on Marek's disease resistance, scientists succeeded in identifying several genetic markers associated with Marek's disease resistance. Among these markers, a specific region on chicken chromosome 1 caught the researchers' special attention. Within this region, a gene called "*MDV1*" is believed to be the key to MHL resistance. This gene is involved in the chicken's immune response, particularly in recognizing and destroying virus-infected cells.

Marek's disease virus is able to multiply on duck embryo fibroblasts, chicken kidney cells and produce typical foci on chick embryo chorioallantoic membrane. Due to the high resistance of the virus, it can survive in feces and bedding for up to 4 months at room temperature, thus increasing the risk of disease transmission. In newly fledged chicks, "*MDV*" has a pronounced pathogenicity that may lead to immunosuppression, neurological signs, retinopathy or tumor formation, especially lymphocytic tumors in various organs such as nerves, muscles, lungs, liver and kidneys (Figure 3).

3.2 Key genetic markers and genes identified

Identifying key genetic markers and genes in genome-wide association studies is a critical step in achieving genetic resolution of disease resistance. Through association analysis of large-scale genotype data, researchers can identify key genetic markers and genes associated with specific disease resistance. These key genetic markers and genes are often the main genetic factors affecting disease resistance in poultry, which is important for understanding the genetic basis of disease resistance and for genetic improvement.

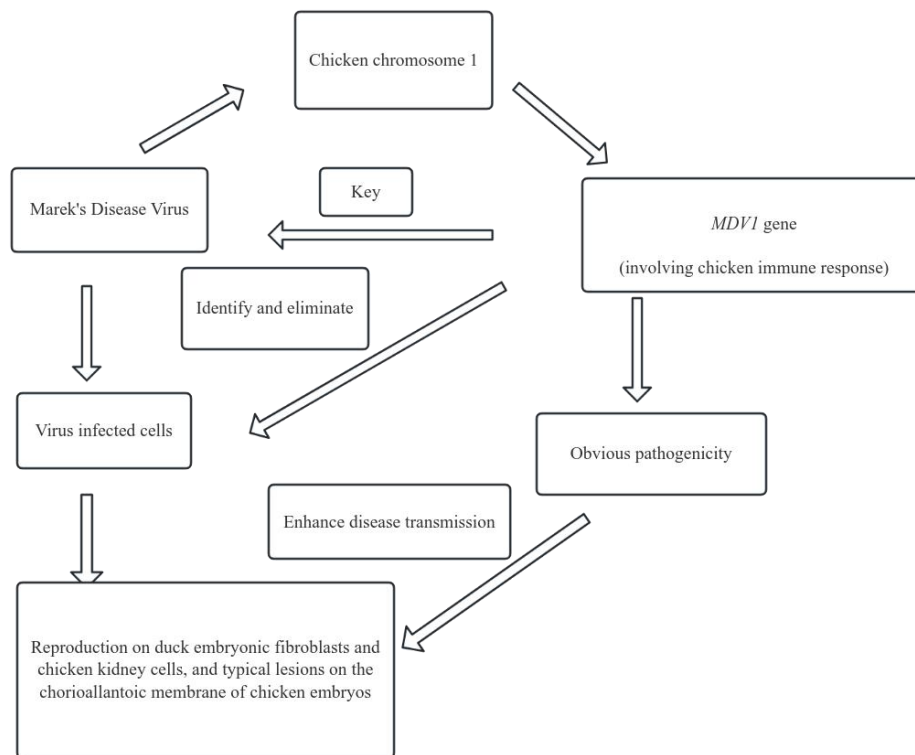


Figure 3 Expression of *MDV1* gene in chicken immune response

Key genetic markers are usually located in genomic regions associated with disease resistance and can be used as candidate markers for further functional validation and genetic improvement. Through in-depth study of these key markers, their mechanism of action in regulating disease resistance can be revealed, providing a theoretical basis for disease prevention and treatment. The identified key genes are also one of the important results of disease resistance research. These key genes may be involved in many aspects of the immune system, cell signaling, pathogen recognition, etc., and are of great significance in resolving the molecular mechanisms of disease resistance.

The in-depth study of key genetic markers and genes can provide important clues and targets for the genetic improvement of poultry disease resistance. The identification of key genetic markers and genes is one of the important achievements of genome-wide association studies in the study of poultry disease resistance, which provides an important theoretical and practical basis for understanding the genetic mechanism of disease resistance, carrying out genetic improvement and improving the production efficiency of the breeding industry.

3.3 Significance and implications of the findings

These two cases demonstrate the potential of GWAS in unraveling the genetic basis of disease resistance in poultry. By identifying genetic markers and genes associated with disease resistance, the research provides valuable information for poultry breeding, enabling breeders to enhance poultry resistance to these diseases through genetic selection. In addition, these findings provide new targets for disease prevention and treatment, helping to develop more effective vaccines and therapeutic strategies.

In the long run, these studies are not only important for improving the production performance and welfare of poultry, but also play a positive role in ensuring global food security and promoting sustainable agricultural development. Through continuous and in-depth genetic and immunological research, it is expected that more key genetic factors will be revealed in the future to further promote the development of the poultry industry.

4 Challenges and Limitations of GWAS

4.1 Limitations of sample size and genetic diversity

Although genome-wide association studies (GWAS) have achieved remarkable results in revealing the genetic basis of disease resistance in poultry, a series of challenges and limitations have been encountered in their application. These challenges involve not only technical and methodological issues, but also the complexity of statistical analysis and bioinformatics.

The effectiveness of GWAS largely depends on a sufficiently large sample size to ensure the strength of statistical analysis and the reliability of results. In the study of disease resistance in poultry, it is often difficult to obtain a large number of samples due to high costs and limitations in experimental conditions. Insufficient sample size may lead to bias in the results, increasing the risk of discovering false positive associations. The genetic diversity within poultry populations also has a significant impact on the outcomes of GWAS. The genetic differences between different poultry breeds may lead to confusion of association signals, making it more difficult to identify genetic variations directly related to disease resistance (Żbikowska et al., 2020).

4.2 Consideration of the interaction between environmental factors and genetics

Poultry disease resistance is not only influenced by genetic factors, but also closely related to environmental factors. Environmental factors such as feeding conditions, nutritional status, and exposure to pathogens can all affect the resistance phenotype of poultry to diseases. In GWAS, it is often difficult to fully control these environmental variables, making it difficult to distinguish the interaction effects between genetics and environment. This complex genetic environmental interaction increases the difficulty of GWAS analysis and also affects the interpretation of the results.

There may be interactive effects between environmental factors and genetic factors. Environmental factors may alter the expression patterns of genetic factors on poultry disease resistance, or affect the phenotypic expression of specific genotypes. Some genotypes may exhibit different levels of disease resistance under different environmental conditions, and this environmental interaction effect may mask or amplify genetic effects, affecting the interpretation of genome-wide association studies. It is necessary to consider the interaction between environmental and genetic factors in research design and data analysis to more accurately evaluate their impact on poultry disease resistance.

There is a complex interaction between environmental factors and genetic factors, which must be considered in the genetic analysis of disease resistance in poultry. By comprehensively considering the influence of environmental and genetic factors, the disease resistance level of poultry can be more accurately evaluated, and more effective strategies and methods can be provided for disease prevention and treatment (Figure 4).

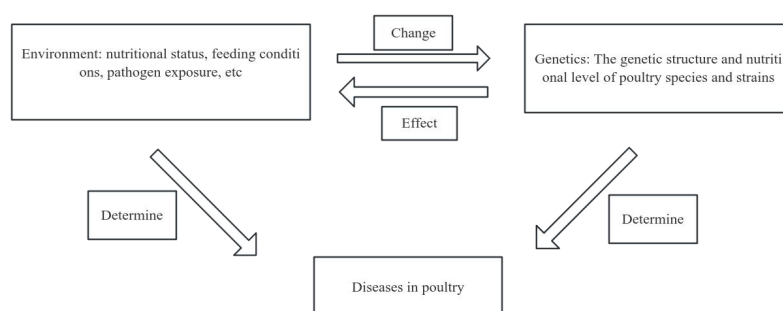


Figure 4 The interaction effect between environmental factors and genetic factors

4.3 The complexity of data interpretation and validation

Even if GWAS successfully identifies genetic markers associated with disease resistance in poultry, interpreting these data correctly remains a challenge. Association discovery is not directly equivalent to causal relationships, and subsequent biological experiments are needed to verify the functions and mechanisms of these genetic

variations. The validation of GWAS results usually requires an independent sample set, which may be difficult to achieve in poultry research (Su et al., 2023). Due to the complexity of the poultry genome, the identified genetic markers are often located in intergenic regions, and their precise biological functions and regulatory mechanisms are unclear, increasing the difficulty of functional verification.

Genome-wide association studies (GWAS) provide a powerful tool for unraveling the genetic basis of disease resistance in poultry, but also face sample size and genetic diversity limitations, complexity of environmental factors and genetic interactions, and challenges in data interpretation and validation. To overcome these limitations, future research will require a multidisciplinary approach that combines high-throughput sequencing technologies, precise phenotypic characterization, and advanced bioinformatics analyses to improve the accuracy and reliability of GWAS. By integrating the reciprocal effects of genetic, environmental and management factors, as well as enhancing functional genomics research, it will contribute to a deeper understanding of the complex mechanisms of poultry disease resistance and facilitate progress in poultry health management and breeding improvement.

5 Conclusion

Genome-wide association studies (GWAS) have made indelible contributions to revealing the genetic basis of poultry disease resistance, providing important scientific support for the sustainable development of the poultry industry. By comprehensively analyzing the application of GWAS in poultry disease resistance research, the challenges it faces, and the outlook for future research directions, we can gain a deeper understanding of the important impact of this research methodology on the long-term development of the poultry industry (Su et al., 2020).

GWAS has successfully identified several key genes and genetic markers associated with poultry disease resistance by analyzing the association between genetic variation and disease resistance in the poultry genome. These findings not only enrich the understanding of poultry genetic diversity, but also provide new strategies for disease prevention and control and breeding for disease resistance. For example, the key genes identified through GWAS for resistance to avian influenza and Marek's disease provide powerful genetic markers for breeding programs, enabling breeders to more precisely select individuals with higher disease resistance, thereby improving the overall health and productivity of poultry populations.

With the continuous development of gene editing technology, future research will focus more on the use of gene editing to validate key genes and genetic variants identified by GWAS. Based on technologies such as CRISPR-Cas9, researchers can precisely edit the poultry genome to validate the function of specific genes in disease resistance and provide more direct evidence for poultry disease resistance breeding. Future research will focus more on the effects of environmental factors and genetic interactions on poultry disease resistance. As the environment continues to change and poultry face multiple pressures from climate, feeding conditions, pathogen exposure, etc., the interaction between environmental factors and genetic variation will become an important direction for research. By integrating environmental and genetic factors, the complex mechanisms underlying the development of resistance phenotypes to diseases in poultry can be better understood. Future research will also enhance the complexity of data interpretation and validation. By combining bioinformatics approaches and functional genomics experiments, the mechanisms by which genetic variants identified by GWAS play a role in disease resistance can be more accurately interpreted and their biological functions can be validated. Researchers need to develop new statistical models and analytical tools to cope with the increasingly large and complex GWAS data and to improve the efficiency of interpretation and validation of results. Future research will also strengthen international collaboration and resource sharing to jointly address challenges and limitations in poultry disease resistance research. The establishment of an international poultry genome database to integrate genetic data and phenotypic information worldwide will help accelerate research progress and promote the development of the poultry industry. At the same time, it will strengthen the protection and utilization of poultry genetic resources and provide reliable data support and resources for future research.

In summary, future research on genetic analysis of poultry disease resistance will focus on gene editing technology, environmental factors and genetic interactions, data interpretation and validation, as well as international cooperation and resource sharing, in order to provide a more reliable scientific basis for the promotion of the healthy development of the poultry industry and precision breeding.

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