International Journal of Molecular Veterinary Research 2024, Vol.14, No.1, 23-31
http://animalscipublisher.com/index.php/ijmvr

Research Report Open Access

Research on the Threat of H5N1 Avian Influenza Virus to Chicken Health and Its Molecular Mechanisms

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International Journal of Molecular Veterinary Research, 2024, Vol.14, No.1 doi: 10.5376/ijmvr.2024.14.0004
Received: 01 Dec., 2023
Accepted: 12 Jan., 2024
Published: 02 Feb., 2024

Preferred citation for this article:
Zhang S.P., and Chen H.Y., 2024, Research on the threat of H5N1 avian influenza virus to chicken health and its molecular mechanisms, International Journal of Molecular Veterinary Research, 14(1): 23-31 (doi: 10.5376/ijmvr.2024.14.0004)

Abstract With the repeated outbreaks of the H5N1 avian influenza virus, in-depth research on its threat to chicken health and its molecular mechanism has become particularly urgent. This study aims to comprehensively analyze the characteristics and transmission routes of H5N1 avian influenza virus, as well as the impact on clinical symptoms and production performance of chickens after infection. Through in-depth research on the interaction between viruses and hosts, the key mechanisms of virus invasion into host cells and the regulatory process of host immune responses have been revealed, providing strong support for understanding the molecular mechanisms of infection. Research results show that infection with the H5N1 avian influenza virus not only causes respiratory symptoms, but also has a significant impact on the production performance of chickens, including reduced egg production and slowed growth. At the molecular level, viruses rely on sophisticated gene expression and regulatory mechanisms to closely interact with host cells to form a complex network of infection. Future research directions include in-depth exploration of the mutation and evolution mechanisms of the H5N1 avian influenza virus, strengthening research on the interaction between the virus and the host immune system, and establishing a more sensitive early warning system. This study provides a scientific basis for formulating more effective prevention and control strategies, and provides an important reference for protecting the poultry industry and human health.
Keywords H5N1 avian influenza virus; Chicken health; Molecular mechanisms; Virus variation; Early warning

H5N1 avian influenza virus, as a highly lethal representative of avian influenza subtypes, not only poses a major threat to the poultry breeding industry, but also poses potential risks to human health. Its high variability and easy transmission allow it to spread rapidly among poultry flocks, causing multiple serious economic losses and food safety issues (Shi and Gao, 2021). Past outbreaks have caused widespread alarm around the world, so it is crucial to have a deep understanding of the transmission and outbreak mechanisms of the H5N1 avian influenza virus and its impact on chicken health. The transmission mechanism of H5N1 avian influenza virus is complex and diverse, and the main routes include airborne transmission, contact transmission, and fecal-oral transmission. Its high variability enables it to rapidly adapt to different host environments, which results in rapid spread among poultry flocks and the formation of explosive epidemics. This transmission mechanism not only makes farms face great challenges, but also provides the possibility for the occurrence of zoonotic diseases (Lewis et al., 2021).

Faced with the threat of H5N1 avian influenza virus to the health of chickens, there is an urgent need to deeply understand the changes in physiological and immune responses caused by it in order to formulate prevention and control measures more effectively. Current research still lacks a comprehensive understanding of the molecular mechanisms of viral infection, which hinders the development of targeted prevention and control methods (Lee et al., 2018). Therefore, it is necessary to comprehensively and deeply explore the impact of H5N1 avian influenza virus on chicken flocks, especially the interaction at the molecular level.

Provide scientific basis for future prevention and control measures. This study will comprehensively understand the potential threat of H5N1 avian influenza virus infection to the overall health of chickens through systematic pathological, clinical and physiological studies. From the early stage of infection to the later stage, this study will track the development of the disease, deeply analyze the changes in the degree of infection, and study the possible physiological changes. In order to respond to the threat of H5N1 avian influenza virus in a more targeted manner, this research will focus on the molecular mechanism between the virus and host cells. By in-depth understanding of these molecular mechanisms, this study hopes to provide a more accurate and innovative scientific basis for vaccine development, design of anti-disease drugs, and the formulation of other prevention and control methods. Through in-depth research on the potential impact and molecular mechanisms of H5N1 avian influenza virus on chicken health, this research aims to provide new understanding and solutions for global avian influenza prevention and control efforts to ensure the healthy and sustainable development of the poultry industry. This research not only has important guiding significance for current epidemic prevention and control, but also provides valuable experience for dealing with similar threats in the future.

1 Basic Knowledge of H5N1 Avian Influenza Virus

Avian influenza is an infectious disease caused by different subtypes of influenza viruses, among which the H5N1 subtype has attracted much attention due to its high pathogenicity and wide spread. Understanding the basic knowledge of the H5N1 avian influenza virus plays an important role in effectively preventing and controlling epidemics.

1.1 Virus characteristics and classification

H5N1 avian influenza virus, as one of the subtypes of influenza A virus, exhibits a complex and sophisticated basic structure, in which two key surface proteins are wrapped on the outside, namely hemagglutinin (H) and neuraminidase (N) (Peiris et al., 2007). These two proteins play key roles in the virus's life cycle.

The hemagglutinin of H5N1 virus is a key factor in infecting host cells. This protein is responsible for binding to specific receptors on the surface of host cells and initiating the key process for viruses to invade host cells. The H hemagglutinin of H5N1 is unique in its structure and forms a specific signature with different subtypes of other avian influenza viruses, which affects the pathogenicity and transmissibility of the virus. Neuraminidase is a key enzyme for viruses to be released from host cells. It facilitates the release of viruses from the surface of infected cells, thus maintaining the life cycle of infection. The structure of the N-neuraminidase of H5N1 also plays a certain role in the immune evasion mechanism of the virus, affecting the spread and adaptability of the virus.

In addition to H5N1, avian influenza viruses also include multiple other subtypes, among which subtypes such as H7N9 and H9N2 have attracted widespread attention. Each subtype exhibits unique biological properties and clinical manifestations, reflecting the diversity of avian influenza viruses.

The H7N9 avian influenza virus causes severe influenza symptoms in humans, and its transmission path among poultry and wild birds has attracted great attention from researchers. The impact of this subtype in humans has made it the focus of clinical and epidemiological research. H9N2 is another avian influenza virus subtype that has caused economic damage to poultry and is considered a potential candidate for a new influenza virus. In-depth research on H9N2 will help understand its transmission dynamics and host adaptability, and provide scientific basis for prevention and control.

In-depth study of the differences between different subtypes will help researchers better understand the evolution and transmission mechanisms of avian influenza viruses, and provide strong support for vaccine development and the formulation of prevention and control measures. This not only helps protect the poultry farming industry, but also has a profound impact on human public health.

1.2 Transmission routes and epidemiology

The transmission mechanism of H5N1 avian influenza virus involves multiple key steps, among which droplet transmission is one of the main ways. The feces and tears of infected birds are rich in virus particles, which are released into the air in the birds' living environment. Virus particles have strong survivability and can be suspended and spread in the air, forming a potential airborne transmission route. This characteristic makes it possible for viruses to spread within poultry flocks and between poultry houses, placing extremely high requirements on the hygienic management of poultry farms and markets.

H5N1 viruses are also spread through direct contact with infected birds or their secretions, making the poultry farming environment a potential source of infection. Dense poultry farms and markets can easily form transmission chains and accelerate the spread of the virus. Therefore, it is particularly urgent to strengthen the monitoring, quarantine and health management of poultry breeding sites.

The development of the H5N1 avian influenza virus epidemic is affected by multiple factors, among which climatic conditions, bird migration patterns and human activities are the three key factors. Meteorological factors such as seasonal changes, temperature and humidity directly affect the survival and spread of H5N1 viruses in the environment. The cold season and humid environment contribute to the stable existence of the virus and increase the risk of transmission (Salaheldin et al., 2018). The migration paths of poultry are closely related to the spread of H5N1 viruses, especially on an international scale. The long-distance migration of birds may serve as a bridge for viruses to cross geographical barriers, triggering regional or global outbreaks. Agriculture, trade and human behavior are important factors in the spread of the epidemic, especially in areas with intensive poultry farming. Man-made transportation and trade activities can spread the virus quickly, and the closer the poultry farms are to each other, the faster the spread.

By in-depth analysis of the transmission patterns of the H5N1 avian influenza virus, researchers can more accurately predict the outbreak and spread trends of the epidemic. This provides an important basis for formulating scientific and targeted prevention and control strategies, and emphasizes the urgency of strengthening international cooperation, information sharing and monitoring systems on a global scale.

2 Threats to Chicken Flock Health

The clinical symptoms and disease development caused by infection with H5N1 avian influenza virus pose a serious threat to the health of chickens. Understanding the mechanisms of these effects has far-reaching implications for effective prevention, control and management.

2.1 Clinical symptoms and disease course

The clinical symptoms caused by H5N1 avian influenza virus infection are very obvious and widespread in chicken flocks. After infection, chickens often show a variety of typical symptoms, including shortness of breath, decreased appetite, and ruffled feathers (Letsholo et al., 2022). These symptoms often develop rapidly in a short period of time and directly affect the overall physiological state of the chicken. Shortness of breath indicates an impact on the respiratory system, while decreased appetite reflects disturbances in their overall metabolic and immune systems. Fluffy feathers may be due to physical discomfort caused by infection and the immune system's response to fight the virus.

In cases of severe infection, high mortality is a common outcome. Even those that survive may suffer long-term effects from reduced productivity. This includes slowed growth, reduced egg production, etc., posing a direct threat to the poultry breeding industry. Therefore, timely identification and understanding of these clinical symptoms can enable effective prevention and control measures to be taken as soon as possible and reduce the losses caused by the epidemic.

The disease development of avian influenza usually includes three stages: incubation period, acute stage and recovery stage. The incubation period refers to the time period during which the virus gradually reproduces in the chicken after infection. At this stage, no obvious clinical symptoms have yet appeared, but the virus has gradually spread in the chickens. This is a critical period, as early detection and isolation of infected chickens can effectively slow the spread of the epidemic. The acute phase is a stage in which viral replication and pathological changes increase dramatically. At this stage, clinical symptoms in the flock become apparent, including shortness of breath and decreased appetite. Due to the rapid replication and spread of the virus, the mortality rate also increases. Early diagnosis and isolation of infected chickens at this stage can help reduce mortality and reduce the economic burden on the breeding industry. The recovery period is the process in which an individual gradually recovers and returns to normal physiological state. During this stage, the flock's immune system gradually overcomes the virus and infected individuals begin to recover. A thorough understanding of the pathological changes and disease course at each stage is crucial for developing early diagnosis and effective treatment strategies. In addition, understanding the recovery period can help to infer the immune response mechanism of chickens to H5N1 avian influenza virus and provide important reference for vaccine development.

2.2 Impact on production performance

After being infected with H5N1, the egg production of chickens decreased significantly, which directly threatened the economic health of the poultry breeding industry (Wang et al., 2023). Reduced egg production not only affects the supply stability of the poultry and egg market, but also poses potential risks to market price fluctuations for consumers. At the same time, the quality of infected eggs may also be seriously affected, including reduced eggshell quality and abnormal internal structure, further weakening the market competitiveness of egg products. This decline in quality poses a challenge for every link in the egg industry chain, with everyone involved, from hatcheries to retailers, threatened with financial losses.

Studying the specific mechanisms of egg production decline plays a decisive role. Possible mechanisms include direct virus damage to the chicken reproductive system, physiological disorders caused by immune responses, and effects on nutrient absorption and metabolism. By in-depth understanding of these mechanisms, humans can formulate more targeted management and health care measures during the epidemic to minimize the adverse impact on the egg industry.

Chicken flocks infected with H5N1 show a tendency to slow down their growth rate, which poses a direct threat to the efficiency and economic benefits of broiler production. The slowed growth rate leads to the extension of the breeding cycle and increases the maintenance and feeding costs of the farm. At the same time, reduced feed efficiency due to infection is also a common problem, causing farmers to face higher investments while maintaining profitability. This not only affects the economic benefits of farmers, but may also lead to a shortage of broiler chickens on the market and affect consumers' food choices.

Understanding the specific mechanisms of slowed growth and factors affecting reduced feed efficiency can enable targeted and effective development of response strategies. Possible mechanisms include the virus directly affecting the metabolic activity of chickens, increased energy consumption due to immune responses, and inhibition of feed nutrient absorption. By in-depth study of these mechanisms, researchers can better optimize the breeding environment and management measures, improve the disease resistance and production performance of chickens, thereby reducing production costs and maintaining the sustainable development of the industry.

3 Molecular Mechanism Research

As the H5N1 avian influenza virus continues to spread and evolve, an in-depth understanding of its interaction with host cells has become an urgent need for scientific research and disease prevention and control. The study of molecular mechanisms is the key to solving the mystery of the life cycle of avian influenza viruses and provides a basis for designing more effective prevention and control strategies.

3.1 Virus-host interaction

In-depth study of the interaction between H5N1 avian influenza virus and host cells is to fully understand how the virus replicates within the host. The mechanism by which viruses invade host cells is a complex and tightly regulated process, in which the specific binding of viral surface proteins to host cell surface receptors is the critical first step (Nuñez and Ross, 2019). This process involves the interaction of the hemagglutinin (HA) protein on the surface of the virus with the glycoprotein on the surface of the host cell, forming a connection between the virus and the cell membrane.

Once the connection is made, the virus enters the host cell and releases its genetic material into the cytoplasm by fusing its envelope with the host cell membrane. In this process, the nucleoprotein (NP) and genomic RNA inside the virus play an important role. After the viral genomic RNA is released into the host cytoplasm, the virus begins to synthesize its own proteins and replicate within the host cell by utilizing the host cell's biological mechanism (Figure 1). During this process, the virus also uses the host cell's organelles and metabolic machinery to complete its life cycle.

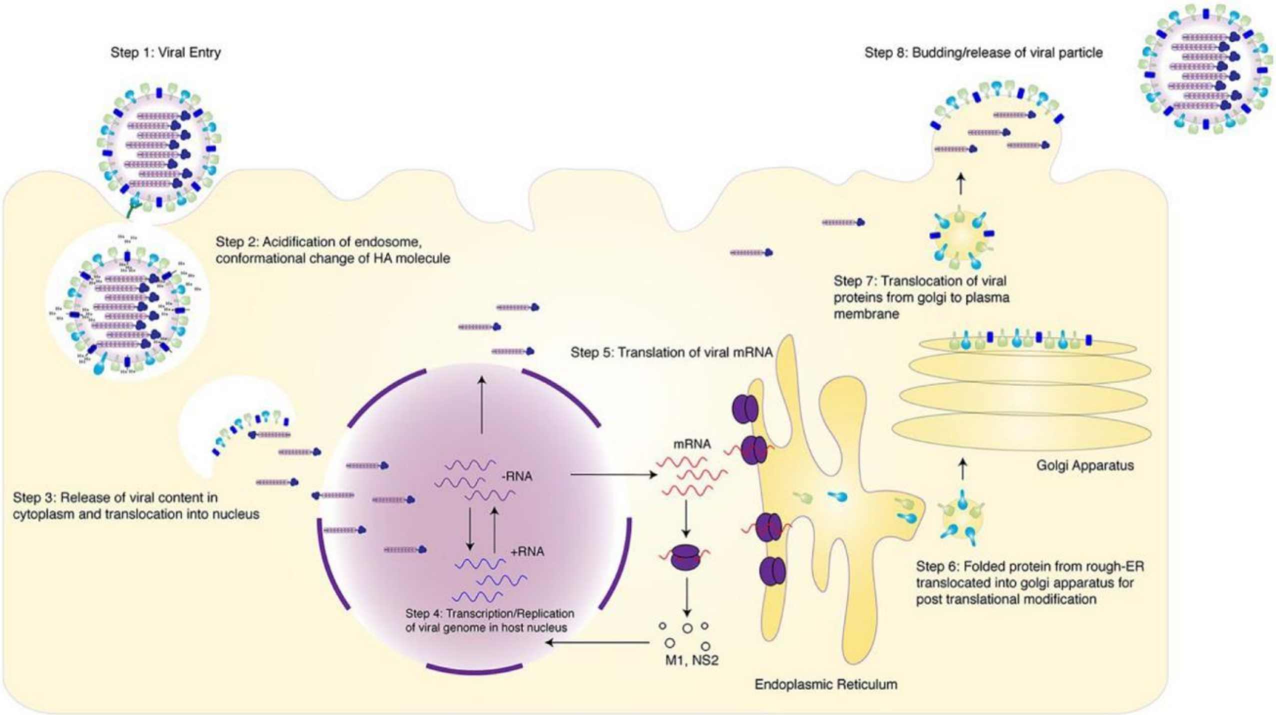

Figure 1 The replication cycle of influenza virus (Nuñez and Ross, 2019)

Understanding the molecular details of this invasion mechanism, including the specific binding of hemagglutinin protein and glycoprotein, the molecular mechanism of membrane fusion, and the replication process of the viral genome in host cells, will help to find key nodes that can be intervened. This not only provides a theoretical basis for the design of new antiviral drugs, but also provides scientific support for the formulation of future prevention and control strategies.

Viral infection triggers a host immune response, and the H5N1 virus evades immune attack through a variety of mechanisms, making the immune response against the virus more complex. Understanding the regulatory mechanisms of the host immune response is to better understand why the H5N1 virus is able to persist in the host.

The host immune response involves the coordinated action of multiple immune cells and molecules, including macrophages, T cells, B cells, and various cytokines. In H5N1 infection, the virus interferes with this complex immune network through multiple mechanisms, such as inhibiting the phagocytosis function of macrophages, interfering with the activity of T cells, and evading antibody recognition. In addition, viruses may also interfere with the regulation of immune responses by affecting host cell signaling pathways.

An in-depth understanding of these mechanisms, including how viruses interfere with the activity of immune cells and inhibit the expression of immune factors, provides key information for formulating more precise treatment strategies (Qin et al., 2023). By intervening at key points where the virus interferes with the immune mechanism, researchers may be able to enhance the host's immune system's effective response to the H5N1 virus, thereby improving treatment effectiveness.

3.2 Gene expression and regulation

During H5N1 infection, viral gene expression and replication are key steps in the virus life cycle. This involves how viruses exploit the host cell's biological machinery for gene expression, replication, and assembly of new viral particles. Understanding these mechanisms not only helps elucidate the molecular aspects of viral infection but also provides strategic directions for intervening in viral replication.

Transcription of viral genes is the primary step in the infection process. During this process, the virus uses the host cell's transcription machinery to synthesize RNA, which becomes the template required for subsequent viral replication. Detailed study of how viral genes interact with host cell transcription factors and regulate the host cell's RNA synthesis mechanism can reveal key points in the regulation of viral gene transcription. Translation of viral genes is a key process in converting synthesized RNA into proteins. Understanding how viral genes utilize the host cell's translation mechanism, including interaction and regulation with the host cell's ribosomes, can help reveal the biosynthetic process of viral proteins and provide important clues for intervention in the viral life cycle. Viral replication involves the replication of the viral genome and the assembly of new viral particles. In-depth study of key nodes in this process, such as the activity regulation of viral replicase and the accuracy of genome replication, will help to find intervention methods for viral replication. This not only provides new targets for treatment, but also provides a theoretical basis for vaccine development.

Host cells respond to viral infection by regulating their own gene expression, forming a complex network of disease resistance mechanisms. In-depth study of this network will help to comprehensively understand the host's disease resistance mechanism and provide guidance for the development of more precise antiviral strategies.

How host cells sense viral invasion is a key starting point for disease resistance mechanisms. Studying the mechanisms of virus recognition receptors and signal transduction pathways can help researchers understand how host cells sense viral invasion and initiate corresponding defense mechanisms.

Host genes play an important role in the process of viral infection. By regulating the expression of host genes, cells can adjust their internal environment to inhibit viral replication. In-depth study of the molecular mechanisms regulating host gene expression can provide a theoretical basis for designing intervention measures.

The immune genes of host cells are activated after infection and participate in the process of resisting viral infection. Understanding the regulatory mechanisms of these immune genes and how they work together to clear the virus is of great significance for the development of new immunotherapeutics (Dai et al., 2023).

Through in-depth research on gene expression and regulation, this study can more comprehensively understand the molecular interaction between the H5N1 avian influenza virus and chickens, and provide in-depth insights for the development of more precise and efficient prevention and control strategies. Not only does this help curb the spread of the virus, it also opens up vast areas for future research to further challenge the understanding and treatment of the disease.

4 Prevention and Control Strategies and Measures

4.1 Vaccine development and application

The threat of the H5N1 avian influenza virus has become increasingly prominent. To effectively prevent and control the spread of the virus, the development and application of vaccines are self-evident. Although some vaccines are currently in use, their effectiveness has certain limitations and requires more in-depth research and innovation.

Existing avian influenza vaccines are mainly based on the hemagglutinin (HA) antigen on the virus surface, which is the key protein for the virus to enter host cells (Dey et al., 2023). However, the H5N1 virus has high variability and is prone to antigenic drift, that is, antigenic differences between virus strains, which challenges the immune effect of existing vaccines in long-term application. Antigenic drift can lead to vaccine ineffectiveness, so vaccines need to be constantly updated to match emerging virus strains.

Secondly, the production cycle of existing vaccines is relatively long and cannot be produced quickly and meet large-scale demand when an epidemic breaks out. This puts a certain amount of time pressure on the effective application of vaccines in the face of sudden epidemics. Therefore, shortening the vaccine production cycle has become one of the urgent problems in the field of vaccine research and development.

In order to overcome the limitations of existing vaccines, researchers are actively exploring the design and development of new vaccines. Among them, an important research direction is multi-antigen vaccines. This kind of vaccine can cover the mutations of multiple virus strains and improve the immunity against different virus strains by containing multiple antigens. The design of multi-antigen vaccines has potential advantages in improving the broad spectrum and long-term effectiveness of the vaccine.

On the other hand, the application of genetic engineering technology has become the key to vaccine development. Through gene editing technology, researchers can design vaccine antigens that are more stable and less susceptible to mutation and improve the long-term immune effect of the vaccine. Research in this area will help address the problem of vaccine ineffectiveness caused by antigenic drift.

In response to the long vaccine production cycle, researchers are also actively exploring rapid response platforms. Among them, mRNA vaccine technology is a technology that has attracted much attention. By using mRNA to transmit vaccine information, vaccines can be produced more quickly and flexibly. The application of this technology is expected to accelerate vaccine production and improve the ability to respond quickly to epidemics.

Generally speaking, the research direction of new vaccines involves many aspects, including improving immune effect, stabilizing vaccine antigens and shortening the production cycle. These innovative studies will provide a more reliable foundation for the future development and application of avian influenza vaccines.

4.2 Epidemic monitoring and early warning

Establishing a sound epidemic surveillance system is the core strategy for rapid response in the early stages of the H5N1 avian influenza outbreak. The multi-level construction of the surveillance system can cover multiple key links to fully understand the spread of the virus.

The monitoring system should cover multiple links such as poultry farms, wild bird migration routes and market sales channels. Poultry farms are potential sources of virus outbreaks. The migration routes of wild birds are involved in the transmission of the virus, and market sales channels are places that may accelerate the spread of the virus. Through systematic monitoring of these links, information on the virus's transmission path and risk areas can be quickly obtained.

The wide application of modern technology provides strong support for the construction of monitoring systems. Satellite remote sensing technology can monitor the range of poultry activities in real time and provide real-time data support in the early stages of the epidemic. Big data analysis helps extract key information about the spread of the virus from huge monitoring data, providing scientific basis for decision-making.

Early identification of infected individuals is the primary task to prevent the spread of the epidemic (Mo et al., 2023). Based on the information provided by the monitoring system, establishing an early warning mechanism is a key step. This mechanism should be combined with modern rapid detection technology to screen poultry in the shortest possible time. For example, highly sensitive detection methods such as PCR technology and immunochromatography can effectively identify infected individuals and improve the ability to detect viruses early.

At the same time, strengthening epidemiological investigations is also a key step in early identification. By gaining a deeper understanding of the source of infection, potential transmission routes, and high-risk areas, the severity of the outbreak and the likely paths of spread can be more accurately assessed. This can help formulate more targeted prevention and control strategies.

Once infection is detected, timely isolation of affected birds is an emergency measure to curb the spread of the virus. In isolation measures, ensure efficient isolation conditions to prevent the spread of viruses within the farm. In addition, tracking and monitoring close contacts, including people and other poultry, can help detect potential transmission chains earlier and improve the targeting of quarantine measures.

In terms of epidemic monitoring and early warning, the comprehensive use of modern technology and traditional epidemiological surveys can build a more sensitive and accurate monitoring system to more effectively respond to the outbreak of H5N1 avian influenza.

5 Conclusion and Outlook

This study deeply explored the threat of H5N1 avian influenza virus to chicken health and its molecular mechanism, conducted systematic experiments and data analysis, and revealed in detail the basic characteristics and transmission routes of H5N1 avian influenza virus. The virus relies on a complex cell infection mechanism and spreads within chicken flocks through airborne transmission and other means, forming an epidemic (Tian et al., 2023); and an in-depth study of the clinical symptoms and course of the disease in chicken flocks after infection found that not only the symptoms Typical respiratory symptoms also have a significant impact on chicken production performance, including reduced egg production and slowed growth rate. At the molecular mechanism level, this study reveals the key aspects of the interaction between the virus and the host, including the mechanism by which the virus invades host cells and the regulation of the host immune response. In addition, studies on gene expression and regulation provide important clues for further understanding of infection mechanisms.

Although researchers have made a series of important discoveries, the problem of avian influenza remains a complex and serious challenge. Future research directions and challenges mainly include: First, it is necessary to conduct in-depth research on the genetic variation and evolutionary trends of avian influenza viruses to better understand the threats of different subtypes of viruses to chickens. This can help provide early warning of the emergence of new viruses and strengthen guidance on vaccine research and development. Secondly, future research should pay more attention to vaccine improvement and the development of new vaccines (Liu et al., 2023). Given the high variability of the virus, vaccine durability and broad spectrum are key issues. The introduction of new technologies and the application of genetic engineering are expected to improve the effectiveness of vaccines and reduce the threat of the epidemic to the health of chickens. In addition, establishing a comprehensive bird flu surveillance system to achieve early warning and rapid response can effectively prevent the spread of the epidemic. At the same time, strengthening the hygienic management of the breeding industry and improving the disease resistance of chickens are also important directions for future research. Challenges include the difficulty of tracing the source of the virus, the long vaccine development cycle, and the cost of building a surveillance system. Therefore, future research requires interdisciplinary collaboration and integration of expertise in biology, medicine, engineering and other fields to jointly address the challenges of avian influenza. Overall, future research will need to focus on understanding the molecular mechanisms of avian influenza at a deeper level and in a wider scope, and explore innovative prevention and control strategies to promote the sustainable development of the breeding industry and maintain the ecological balance of the national poultry and livestock industry.

Based on the research results, there are many ways to deal with the threat of H5N1 avian influenza virus to the health of chickens. Including: strengthening the surveillance system for avian influenza viruses and establishing a complete virus surveillance network, including regular collection of chicken samples and viral gene sequencing, to detect new mutant strains earlier (Blagodatski et al., 2021); optimizing vaccine research and development, Increase investment in the research and development of H5N1 avian influenza virus vaccines to improve vaccine coverage and effectiveness to reduce the risk of outbreaks; strengthen international cooperation to address the global threat of avian influenza viruses, promote international cooperation, and share virus information and vaccine technology and prevention and control experience to jointly maintain global poultry health; strengthen chicken farm hygiene management, improve chicken farm hygiene standards, strictly implement epidemic prevention measures, and reduce the risk of avian influenza virus transmission among chickens.

Taken together, through in-depth research on the impact of H5N1 avian influenza virus on chicken health, this study provides scientific basis and strategic guidance for future prevention and control of avian influenza. However, in the face of constantly mutating viruses and complex host immune systems,, we need to continue to work hard and continuously improve prevention and control strategies to ensure the sustainable development of the poultry industry and the safety of human health.

References

Blagodatski A., Trutneva K., Glazova O., Mityaeva O., Shevkova L., Kegeles E., Onyanov N., Fede K., Maznina A., Khavina E., Yeo S.J., Park H., and Volchkov P., 2021, Avian influenza in wild birds and poultry: dissemination pathways, monitoring methods, and virus ecology, Pathogens, 10(5): 630.
https://doi.org/10.3390/pathogens10050630
PMid:34065291 PMCid:PMC8161317

Dai M.M., Zhu S.F., An Z.H., You B.W., Li Z.W., Yao Y.X., Nair V., and Liao M., 2023, Dissection of key factors correlating with H5N1 avian influenza virus driven inflammatory lung injury of chicken identified by single-cell analysis, Plos Pathogens, 19(10): e1011685.
https://doi.org/10.1371/journal.ppat.1011685
PMid:37819993 PMCid:PMC10593216

Dey P., Ahuja A., Panwar J., Choudhary P., Rani S., Kaur M., Sharma A., Kaur J., Yadav A.K., Sood V., Babu A.R.S., Bhadada S.K., Singh G., and Barnwal R.P., 2023, Immune control of avian influenza virus infection and its vaccine development, Vaccines, 11(3): 593.
https://doi.org/10.3390/vaccines11030593
PMid:36992177 PMCid:PMC10058720

Lee D.H., Torchetti M.K., Hicks J., Killian M.L., Bahl, J., Pantin-Jackwood M., and Swayne D.E., 2018, Transmission dynamics of highly pathogenic avian influenza virus A (H5Nx) clade 2.3. 4.4, North America, 2014–2015, Emerging infectious diseases, 24(10): 1840.
https://doi.org/10.3201/eid2410.171891
PMid:30226167 PMCid:PMC6154162

Letsholo S.L., James J., Meyer S.M., Byrne A.M., Reid S.M., Settypalli T.B.K., Datta S., Oarabile L., Kemolatlhe O., Pebe K.T., Mafonko B.R., Kgotlele T.J., Kumile K., Modise B., Thanda C., Nyange J.F.C., Marobela-Raborokgwe C., Cattoli G., Lamien C.E., Brown I.H., Dundon W.G., and Banyard A.C., 2022, Emergence of high pathogenicity avian influenza virus H5N1 clade 2.3. 4.4 b in wild birds and poultry in Botswana, Viruses, 14(12): 2601.
https://doi.org/10.3390/v14122601
PMid:36560605 PMCid:PMC9788244

Lewis N.S., Banyard A.C., Whittard E., Karibayev T., Al Kafagi T., Chvala I., Byrnea A., Meruyert S., King J., Harder T., Grund C., Essen S., Reid S.M., Brouwer A., Zinyakov N.G., Tegzhanov A., Irza V., Pohlmann A., Beer M., Fouchier R.A.M., Akhmetzhan S., and Brown I.H., 2021, Emergence and spread of novel H5N8, H5N5 and H5N1 clade 2.3. 4.4 highly pathogenic avian influenza in 2020, Emerging Microbes & Infections, 10(1): 148-151.
https://doi.org/10.1080/22221751.2021.1872355
PMid:33400615 PMCid:PMC7832535

Liu B., Zhang Q.M., Qiu R., Li F., Peng F.X., Zhang W.J., Su M.N., Zhang Z.G., Zhang J.Y., Yang X.Y, 2023, Analysis of protein composition of H5N1 influenza virus inactivated vaccine(MDCK cells) bulks, Chinese Journal of Biologicals, 36(4): 385-388, 394.

Mo Y.Q., Wang Y.Q., Lu H., and Liu L., 2023, Research progress on detection methods of avian influenza virus, China Poultry, 45(6): 82-95.

Nuñez I.A., and Ross T.M., 2019, A review of H5Nx avian influenza viruses, Therapeutic advances in vaccines and immunotherapy, 7: 2515135518821625.
https://doi.org/10.1177/2515135518821625
PMid:30834359 PMCid:PMC6391539

Peiris J.M., De Jong M.D., and Guan Y., 2007, Avian influenza virus (H5N1): a threat to human health, Clinical microbiology reviews, 20(2): 243-267.
https://doi.org/10.1128/CMR.00037-06
PMid:17428885 PMCid:PMC1865597

Qin L.D., Sun R.Z., Ma D., Song C.P., and Tian W.X., 2023, Harm of avian influenza virus H5 subtype and research progress on related vaccines, China Animal Health Inspection, 40(5): 55-60.

Salaheldin A.H., Kasbohm E., El-Naggar H., Ulrich R., Scheibner D., Gischke M., Hassan M.K., Arafa A.A., Hassan W.M., El-Hamid H.S.A., Hafez H.M., Veits J., Mettenleiter T.C., and Abdelwhab E.M., 2018, Potential biological and climatic factors that influence the incidence and persistence of highly pathogenic H5N1 avian influenza virus in Egypt, Frontiers in microbiology, 9: 528.
https://doi.org/10.3389/fmicb.2018.00528
PMid:29636730 PMCid:PMC5880882

Shi W., and Gao G.F., 2021, Emerging H5N8 avian influenza viruses, Science, 372(6544): 784-786.
https://doi.org/10.1126/science.abg6302
PMid:34016764

Tian J.M., Bai X.L., Li M.H, Zeng X.Y., Xu J., Li P., Wang M., Song X.D., Zhao Z.G., Tian G.B., Liu L.L., Guan Y.T., Li Y.B., and Chen H.L., 2023, Highly pathogenic avian influenza virus (H5N1) clade 2.3. 4.4 b introduced by wild birds, China, 2021, Emerging Infectious Diseases, 29(7): 1367.
https://doi.org/10.3201/eid2907.221149

Wang X.F., Zhou S.C., Cui G.L., Li J.J., Zhang M.Y., Wang X.M., and Yan W.L., 2023, The effect of inactivated avian influenza vaccines at different doses on laying rate and antibody titer of layer breeders, China Animal Health Inspection, 40(1): 140-143.