

New Patterns for Highly Pathogenic Avian Influenza and Adjustment of Prevention, Control and Surveillance Strategies

Padiya Bhalarabidita*

Department of Viroscience, Leiden University, 2300 RA Leiden, Netherlands

Introduction

Highly Pathogenic Avian Influenza (HPAI) continues to pose significant threats to global poultry populations, public health, and economies. Over the years, the virus has displayed evolving patterns, challenging existing prevention, control, and surveillance strategies. In this article, we delve into the emerging patterns of HPAI and discuss the necessary adjustments required in prevention, control, and surveillance efforts to effectively combat this persistent threat.

Description

HPAI viruses demonstrate remarkable genetic diversity, leading to the emergence of novel strains with unpredictable characteristics. Genetic reassortment between avian and other influenza viruses further complicates the landscape, potentially giving rise to strains with increased pathogenicity or altered host range. HPAI strains have shown an increased propensity for global spread through migratory bird populations, poultry trade, and human activities. This globalization of HPAI presents challenges for containment and underscores the importance of coordinated international efforts. HPAI viruses exhibit the ability to infect a wide range of avian species as well as mammals, including humans. Interspecies transmission events raise concerns about the potential for adaptation to new hosts and the emergence of pandemic strains with enhanced human-to-human transmission capabilities. The incidence of HPAI outbreaks often displays seasonal variability, influenced by factors such as environmental conditions, migratory bird movements, and agricultural practices. Understanding these seasonal patterns is crucial for targeted surveillance and control measures [1].

Enhanced biosecurity protocols are essential to prevent the introduction and spread of HPAI within poultry farms. This includes strict control measures for farm access, biocontainment facilities, proper waste management, and hygiene practices. Targeted vaccination programs can help bolster immunity against specific HPAI strains in poultry populations, reducing the likelihood of widespread outbreaks. Continuous monitoring of vaccine efficacy and antigenic drift is necessary to ensure vaccine effectiveness. Implementing early detection systems, including rapid diagnostic tests and sentinel surveillance networks, is crucial for timely identification of HPAI outbreaks. Early detection enables prompt response measures to contain the spread and minimize economic losses. Surveillance efforts should prioritize high-risk areas, such as regions with intensive poultry production, proximity to wild bird habitats, and areas with a history of HPAI outbreaks. Surveillance should encompass both active monitoring of poultry populations and passive surveillance through reporting mechanisms. Developing and implementing rapid response plans is

essential for containing HPAI outbreaks swiftly. These plans should outline procedures for depopulation, disinfection, and disposal of infected poultry, as well as movement restrictions and communication strategies. Developing and implementing rapid response plans is essential for containing HPAI outbreaks swiftly [2,3].

These plans should outline procedures for depopulation, disinfection, and disposal of infected poultry, as well as movement restrictions and communication strategies. Collaborative efforts among neighboring countries and regions are crucial for coordinated response to transboundary HPAI outbreaks. Establishing regional task forces, sharing resources, and harmonizing control measures can facilitate a unified approach to containment. Public awareness campaigns play a critical role in promoting compliance with control measures, enhancing biosecurity practices among poultry producers, and educating the public about the risks associated with HPAI transmission. Adopting a One Health approach that integrates surveillance data from humans, animals, and the environment is essential for early detection of HPAI outbreaks and understanding the dynamics of viral transmission across species boundaries. Leveraging genomic sequencing technologies to monitor the genetic evolution of HPAI viruses can provide valuable insights into virulence, transmissibility, and antigenic variation. Genomic surveillance data can inform vaccine development efforts and guide control strategies. Engaging local communities, farmers, veterinarians, and other stakeholders in participatory surveillance efforts can enhance the timely detection of HPAI outbreaks at the grassroots level. Community-based reporting systems can complement formal surveillance mechanisms and facilitate rapid response [4,5].

Conclusion

The evolving patterns of Highly Pathogenic Avian Influenza present complex challenges for prevention, control, and surveillance efforts. By adjusting strategies to address emerging trends, stakeholders can enhance preparedness and response capabilities to effectively mitigate the risks posed by HPAI outbreaks. A multidisciplinary approach, informed by scientific evidence and international collaboration, is essential for combating this persistent threat to global health and food security.

Acknowledgement

We thank the anonymous reviewers for their constructive criticisms of the manuscript.

Conflict of Interest

The author declares there is no conflict of interest associated with this manuscript.

References

1. Smallman-Raynor, Matthew and Andrew D. Cliff. "The geographical spread of avian influenza A (H5N1): panzootic transmission (December 2003–May 2006), pandemic potential and implications." *Ann Am Assoc* 98 (2008): 553-582.
2. Marchenko, Vasilii Y., Ivan M. Susloparov, Nataliya P. Kolosova and Nataliya I.

*Address for Correspondence: Padiya Bhalarabidita, Department of Viroscience, Leiden University, 2300 RA Leiden, Netherlands; E-mail: badita555@gmail.com

Copyright: © 2024 Bhalarabidita P. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

Received: 01 February, 2024, Manuscript No. Ijbbd-24-134084; Editor assigned: 03 February, 2024, Pre QC No. P-134084; Reviewed: 16 February, 2024, QC No. Q-134084; Revised: 22 February, 2024, Manuscript No. R-134084; Published: 28 February, 2024, DOI: 10.37421/2376-0214.2024.10.81

- Goncharova, et al. "Influenza A (H5N8) virus isolation in Russia, 2014." *Arch Virol* 160 (2015): 2857-2860.
3. Global Consortium for H5N8 and Related Influenza Viruses. "Role for migratory wild birds in the global spread of avian influenza H5N8." *Science* 354 (2016): 213-217.
4. Guinat, Claire, Gaëlle Nicolas, Timothée Vergne and Anne Bronner, et al. "Spatio-temporal patterns of highly pathogenic avian influenza virus subtype H5N8 spread, France, 2016 to 2017." *Eurosurveillance* 23 (2018): 1700791.
5. Napp, S., N. Majó, R. Sánchez-Gonzalez, and J. Vergara-Alert. "Emergence and spread of highly pathogenic avian influenza A (H5N8) in Europe in 2016-2017." *Transbound Emerg Dis* 65 (2018): 1217-1226.

How to cite this article: Bhalarabidita, Padiya. "New Patterns for Highly Pathogenic Avian Influenza and Adjustment of Prevention, Control and Surveillance Strategies." *J Biodivers Biopros Dev* 10 (2024): 81.