



What awaits US in the next bird migration in South America: Prospects for the detection and incidence of HPAIV H5N1 in commercial poultry and wild birds

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Abstract

Highly pathogenic avian influenza virus (HPAIV) H5N1 poses a significant threat to both commercial poultry operations and wild bird populations worldwide. South America, with its rich avian biodiversity and extensive poultry industry, is susceptible to the introduction and spread of this devastating virus. This study explores the imminent challenges and potential outcomes associated with the upcoming bird migration season in South America, focusing on the detection and incidence of HPAIV H5N1. Employing a multidisciplinary approach is necessary to integrate spatial modeling, genomic surveillance, and epidemiological analyses to forecast the dynamics of HPAIV H5N1 in the region. By examining historical migration patterns, host susceptibility, and environmental factors, it will be possible to elucidate potential pathways for virus dissemination among wild bird populations and spillover into commercial poultry farms. Furthermore, this study evaluates the efficacy of current surveillance and monitoring strategies in detecting HPAIV H5N1, identifying potential gaps, and offering recommendations for enhanced surveillance protocols. Leveraging advanced molecular techniques is necessary to analyze viral genomes to track potential mutations associated with increased virulence or altered host range, thereby providing crucial insights for targeted intervention measures. The outcomes of this research will advance our understanding of the ecological and epidemiological factors influencing the spread of HPAIV H5N1 in South America and inform proactive strategies for early detection, containment, and mitigation of future outbreaks. This comprehensive assessment is a pivotal step towards safeguarding poultry industries and avian biodiversity in the face of emerging infectious diseases.

Keywords: HPAI, wild birds, H5N1, Molecular diagnosis, Epidemiology

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