Special Issue

Genomic Epidemiology and Surveillance of Avian Influenza

Message from the Guest Editors

Avian influenza viruses (AIVs) pose major threats to poultry, wildlife, and public health. Their rapid evolution—through mutation, reassortment, and host adaptation—makes outbreak investigation and risk assessment difficult. Genomic sequencing and bioinformatics have therefore become essential for understanding AIV transmission and evolution.

Genomic surveillance helps track genetic changes, transmission routes, and key amino acid substitutions linked to pathogenicity, host range, and antigenic variation. Combining genomic data with field surveillance provides insights that traditional methods cannot offer.

This Special Issue focuses on the genomic epidemiology of avian influenza. We welcome studies on whole-genome sequencing, phylogenetics, evolutionary analysis, reassortment, mutation profiling, genotype–phenotype links, and bioinformatics tools that improve surveillance and risk evaluation.

Guest Editors

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Message from the Editor-in-Chief

The worldwide impact of infectious disease is incalculable. The consequences for human health in terms of morbidity and mortality are obvious and vast but, when infections of animals and plants are also taken into account, it is hard to imagine any other disease that has such a significant impact on our lives—on healthcare systems, on agriculture and on world economics. *Pathogens* is proud to continue to serve the international community by publishing high quality studies that further our understanding of infection and have meaningful consequences for disease intervention.

Editor-in-Chief

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