

# Unravelling Influenza A (H3N2): From Viral Evolution to Global Impact

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August 30, 2023

## Abstract

Influenza A (H3N2) virus, a prominent member of the Orthomyxoviridae family, continues to pose significant challenges to public health worldwide. This comprehensive review delves into the intricate facets of H3N2, encompassing its virological characteristics, evolutionary trends, global epidemiology, clinical manifestations, immunopathology, vaccination strategies, antiviral interventions, and emerging diagnostic approaches. The evolution and genetic diversity of H3N2 strains are explored in the context of antigenic variation, a phenomenon fueled by genetic drift and shift mechanisms. The implications of such variability on vaccine design and effectiveness are critically analyzed. Moreover, this review examines the broader public health ramifications of H3N2, elucidating its seasonal outbreak patterns, pandemic potential, and the intricacies of global spread. Detailed insights into the clinical presentation and pathogenesis highlight the interplay between viral factors and host immune responses, shedding light on disease severity and susceptibility determinants. The armamentarium of antiviral therapies, encompassing neuraminidase inhibitors and polymerase inhibitors, is evaluated along with the emerging challenge of drug resistance. Notably, this review underscores the evolving landscape of diagnostic techniques, ranging from rapid point-of-care tests to advanced molecular methods, and their pivotal role in timely outbreak detection and surveillance. Looking ahead, the article accentuates the need for multidisciplinary approaches in deciphering viral evolution dynamics, targeting host-pathogen interactions, and refining pandemic preparedness strategies. By synthesizing these diverse dimensions, this review encapsulates a holistic understanding of Influenza A (H3N2) that informs both research endeavors and public health interventions.

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