

Exploring the Genetic Architecture of Chicken Resistance to Avian Influenza Virus

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Abstract : Avian influenza, commonly known as bird flu, is a highly contagious viral disease primarily affecting poultry and wild birds, with significant implications for both animal health and public safety. The influenza virus (IV) is notorious for its ability to mutate and infect multiple species, including humans, leading to severe consequences. Avian influenza poses considerable pandemic risks due to the potential evolution of low pathogenic avian influenza (LPAI) into highly pathogenic avian influenza (HPAI), which can cause rapid outbreaks in domestic flocks. While AVI viruses typically do not replicate well in humans, strains such as H5N1 and H7N9 have crossed the species barrier, raising alarm over human infections. The recent documentation of human transmission of the H5N8 strain from birds underscores the ongoing threat posed by avian influenza. This review necessitates a thorough discussion about the genetic foundation of viral pathogens, identifying key candidate genes linked to disease resilience, and discussing powerful tools. This review can help researchers to comprehensively overview the disease severity and combat related to AIV, which causes significant economic impact and set effective control strategies to mitigate the risks associated with avian influenza outbreaks.

Keywords : Avian, candidate genes, chicken, molecular, pathogen, virus

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