

Immunopathology of H5N1 highly pathogenic avian influenza viruses in layer chickens.

Inhalt

Since 2021, clade 2.3.4.4b H5N1 highly pathogenic avian influenza viruses (HPAIVs) have become predominant worldwide, displaying increased virulence and dissemination in poultry and waterfowl. Within the framework of the WiLiMan-ID project, our goal is to gain insight into the mechanisms shaping host-pathogen interactions and contributing to the enhanced virulence of recent HPAIVs. To this end, we demonstrated that three strains, a clade 2.3.2.1c virus from 2013 and two clade 2.3.4.4b isolates (genotypes AB and BB), displayed different immunopathological and transmission profiles in layer chickens. To identify the viral and host factors involved in the virulence and spread of these viruses, an *ex vivo* infection model based on chicken monocyte-derived dendritic cells was developed. As key antigen-presenting cells, dendritic cells bridge innate and adaptive immunity, contributing to inflammatory responses through pathogen sensing and cytokine production. The clade 2.3.4.4b viruses showed significantly increased replication in this model when compared to clade 2.3.2.1c, historically of lower virulence in waterfowl. Additionally, RT-qPCR analysis revealed distinct immune gene expression profiles induced by these three HPAIV strains, including strong differences in key antiviral interferon-stimulated genes. These findings represent an important first step towards identifying new molecular determinants that may contribute to the increased virulence of recent H5N1 HPAIVs.

Keywords

H5N1, HPAIV, dendritic cells, innate immune response, interferon, chicken

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Yes, I am a junior scientist.

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