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Pathogenesis and epidemiology of swine influenza virus

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Influenza A viruses (IAVs) belongs to the family Orthomyxoviridae and represents major pathogens of both humans and animals. Swine influenza virus is an important pathogen that affects not only the swine industry, but also represents a constant threat to the turkey industry and is of particular concern to public health. The emergence and worldwide spread of the 2009 pandemic H1N1 (pH1N1) containing all eight RNA segments derived from swine viruses provided further evidence of the pivotal role of domestic pigs in the ecology of influenza A virus infections. In this talk, we will discuss the state-of-art knowledge about the pathogenesis and the molecular epidemiology of swine influenza virus, with special focus in South America countries. In this area of the globe, there are several subtypes of IAVs circulating in swine populations, including the 2009 pH1N1, but there are still many research gaps in the epidemiology of the disease. With respect to pathogenesis, the role of PB1-F2 and other virulence markers in the viral genome will be deeply covered.

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Can we identify who might be at risk of death from influenza?

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Respiratory tract viral infections, including influenza, are a major global public health threat. Currently, there is no reliable way to stratify the exposed populations to identify those at high risk of developing complications. Seasonal influenza infections cause substantial morbidity and mortality resulting in estimated 250000-500000 deaths worldwide every year. It affects up to 20% of the population and results in approximately 3-5 million yearly cases of severe illness. There is a need for further research to help predict who will become sick and possibly die, versus those who will not. The goal of this project was to use molecular techniques to identify a marker associated with severe influenza infection and to elucidate its mechanism of action in host immune cells. Microarray results performed in our lab have confirmed that the level of Interferon-alpha inducible gene 27 (IFI27) RNA in blood from severe influenza infected patients was significantly increased compared with that of the healthy controls. IFI27 expression was increased by common strains of influenza virus and correlated significantly with clinical severity. Further data showed that IFI27 expression was unaffected by non-viral conditions such as bacterial infection and SIRS. *In vitro* validation has confirmed that IFI27 expression was produced predominantly by pDCs, a pivotal immune cell subset that links innate immunity with adaptive immunity. This response was mediated via the TLR7-interferon- α pathway, found mainly in pDCs. In conclusion measuring IFI27 gene-expression level may assist risk stratification of infected patients in future influenza pandemics.

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