

Infection Dynamics of Novel Influenza A Viruses Isolated from Australian Pigs

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Background/Objective

H1N1, H3N2 and H1N2 influenza A viruses (IAV) are circulating globally throughout domestic swine populations and are reassorting continuously with human seasonal IAV strains (1). This reassortment process of mixing virulence determinants from human and swine origin IAV can enable the evolution of a human pandemic virus, as demonstrated by the H1N1 pandemic of 2009 (2). In 2012, novel reassortant H1N2 and H3N2 viruses with genetic relationships to older seasonal human IAV were isolated from Australian pigs (3). The genetic constellations and antigenicity of these viruses are unique among global swine and human IAV. This project aims to define the mechanics of host susceptibility, infection and pathogenicity of novel H3 and H1 swine origin IAVs detected in Australia.

Method

These viruses have been characterised in terms of sialic acid containing receptor affinity and infectivity in a range of porcine, human and avian cell lines. The pathogenesis of the novel H1N2 and H3N2 viruses using a ferret model of disease was investigated. Additionally, infection by these IAV in the pig model will be presented including at timepoints of infection through histopathology, immunohistochemistry, virus detection in tissues and expression of immunology markers so as to directly compare to the ferret model.

Result

The H1N2 reassortant viruses with a pandemic H1N1 2009 backbone demonstrated different infectivity of cell lines based on HA and NA gene differences. In-vivo infection model in ferret showed typical pathobiology for season human influenza virus infection. In vivo trials in pigs are ongoing.

Conclusion

The presence of novel swine IAVs in Australian pigs suggests the potential for commercial herds to act as sources of zoonotic transmission of influenza virus as well as the potential for new pandemic strains to be generated.