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Selected Abstracts

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Implications of the spread of pandemic (H1N1) 2009 virus to pigs: field and experimental studies

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The epidemiology of influenza virus in pig populations is unique, with different lineages of viruses identified based on spatio-temporal characteristics. Co-circulation of viruses leads to the generation of new strains through genetic reassortment and the consequences of independent evolution of influenza viruses in pigs gives rise to considerable genetic diversity at continental level. Whilst the pig has been postulated as a mixing vessel for the generation of new influenza viruses, more recent work would indicate that this is a complex dynamic. However, the emergence of pandemic (H1N1) 2009 virus (pH1N1) in humans is postulated to have derived from pigs. Limited surveillance studies in pigs have revealed changes in virus diversity through the occurrence of novel reassortant viruses containing genes from both avian, human and swine sources. The correlates for successful cross-species transmission are multi-factoral and include host, virus and the impact of prior immunity to endemic swine influenza viruses. The pH1N1 virus has spread from humans to pigs in numerous countries. The future dynamics of infection with this virus in pig populations will be complex and impacted by the immune status and characteristics of viruses circulating in pig populations in different regions. Detailed studies of the transmission, infection dynamics and immunopathology of pH1N1 virus in pigs and it's comparability to human infection will be reported. These studies have also been extended to understanding the epidemiological and evolutionary characteristics of pH1N1 virus in pigs and the associated occupational risks. Preliminary data indicates that the virus has a high capability to transmit within and between pigs and has become established in UK pig populations. The impact of prior immunity to endemic swine strains will, we predict, impact the future epidemiology of influenza virus in pig populations around the globe. Furthermore, clusters of infection within farm networks have been detected through detailed epidemiological investigations, which have also revealed potentially higher seroprevalence to pandemic virus amongst pig veterinarians compared to cohorts of 'non-exposed' humans. The implications of these results will be discussed. Events subsequent to the emergence of the pandemic virus have provided further focus and interest in pigs relating to the evolution and ecology of influenza viruses relevant to veterinary public health.

Slomka et al. 2010. J Mol Genet Med, 4, 262.

Evaluation of two commercial lateral flow devices (LFDs) used for penside testing of H5N1 highly pathogenic avian influenza infections in backyard gallinaceous poultry in Egypt

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Two commercial lateral flow devices (LFDs) from Quickvue and Anigen were evaluated for the detection of H5N1 highly pathogenic avian influenza (HPAI) infections in Egyptian poultry. Sixty-seven birds (65 chickens and two turkeys) from eight flocks in which clinical signs were observed, were sampled prospectively and H5N1 HPAI infection was confirmed in seven flocks. Swabs (tracheal and cloacal) and feathers were collected from each bird for penside testing by the two LFDs. The same clinical specimens were returned to the laboratory at Dokki, Egypt for testing by M gene RRT PCR. This served as the "gold standard" for AI detection. Infection was detected in 57 birds on the basis of at least one swab being positive by M gene RRT PCR, and included 15 chickens that were fresh-dead. The 57 infected birds included 29 that were also positive by the Anigen and 28 by the Quickvue LFDs, *ie* at least one swab was LFD positive. There were nine birds that were AI negative by M gene RRT PCR and both LFDs, while one bird was M gene RRT PCR negative but positive by both LFDs, which suggested a false positive LFD result. Sensitivity of the LFDs relative to M gene RRT PCR was 77.2% for the Anigen and 75.4% for the Quickvue tests, with 90.0% specificity for both LFDs. By including feathers for LFD testing together with swabs, the number of LFD positives among the 57 infected birds increased by four to 33 by Anigen and 32 by Quickvue tests. There were no birds that were AI positive by feathers but negative by both swabs. This increased the sensitivity of the LFDs relative to M gene RRT PCR to 84.2% and 82.5% for the Anigen and Quickvue tests respectively, with specificity for both LFDs remaining at 90.0%. Although the most sensitive commercial LFDs cannot compare to the high sensitivity displayed by optimised, validated and robust AI RRT PCRs, they may be of use for penside testing of galliformes infected with HPAI at the peak titre of viral shedding, *ie* when birds are displaying advanced clinical signs or when sampled as fresh-dead carcasses. Swabs are the classic field specimens collected from poultry outbreaks, but inclusion of feathers from galliforme birds systemically infected with H5N1 HPAI increased the sensitivity of the LFDs. However, the detection of LFD false positives emphasises the importance of returning samples for confirmatory laboratory testing.

Keywords: Lateral flow device (LFD), H5N1 HPAI, penside