

GENETIC AND ANTIGENIC CHARACTERIZATION OF SWINE INFLUENZA VIRUS IN FRANCE: IDENTIFICATION OF NOVEL H1N1 REASSORTANTS

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Swine influenza is a highly contagious viral disease of the respiratory tract in pigs. Three major subtypes of swine influenza viruses (SIV) (H1N1, H3N2, H1N2) co-evolve in pigs. The majority of H1N1 SIV circulating in Europe are of avian origin. H3N2 strains circulating since the mid 1980s in European pigs are reassortants between an H3N2 strain of human origin and an avian-like H1N1 strain. In the early 1980s, H1N2 viruses arose by genetic reassortment of human H1N1 and swine H3N2 strains and possess a haemagglutinin (HA) closely related to that of these human H1N1 strains. Since 2002, no report has been done to characterize circulating SIV strains in France. In this study we aimed to characterize genetically and antigenically SIV strains isolated from 2000 to 2007 in pig farms in Brittany (France). Two subtypes of SIV, H1N1 and H1N2, are currently circulating in Brittany but no H3N2 strain could be isolated. Genetic comparisons showed that there was a relatively low homology between the HA1 gene of H1N1 and H1N2 viruses. Moreover, phylogenetic analysis showed a clear division of the H1N2 viruses into 2 major HA groups. This marked heterogeneity contrasts with the high similarity observed among avian-like H1N1 circulating viruses. Finally, we identified four H1N1 strains with a HA1 gene phylogenetically close to HA1 of H1N2 strains. Sequencing of the neuraminidase gene and the six internal genes showed that these strains are reassortants between avian-like H1N1 and H1N2 strains. Antigenic characterization of our strains is currently undergoing.