

VP-416**IDENTIFICATION OF NOVEL REASSORTANTS OF SWINE INFLUENZA H1N1 VIRUS IN FRANCE**

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Swine influenza is a highly contagious viral disease of the respiratory tract in pigs. Three major subtypes (H1N1, H3N2, H1N2) of swine influenza virus (SIV) co-evolve in pigs worldwide. In Europe, H1N1 SIV originated from the transmission of reassortants between an H3N2 strain of human origin and a swine avian-like H1N1 strain that gave its internal genes. In the early 1980s, H1N2 viruses arose by genetic reassortment of human H1N1 and swine H3N2 strains. Thus, they possess a haemagglutinin (HA) closely related to that of these human H1N1 strains. Understanding the genetic and antigenic evolution of SIV is of veterinary and public health interest, but no report has been done to characterize circulating SIV strains in France since 2000. In order to guarantee an effective epidemiological surveillance in this country, we examined genetic and antigenic variation in SIV isolated from 2000 to 2007 in pigs in Brittany, the leading-pig producing region. SIV of H1N1 and H1N2 subtypes are currently circulating in Brittany in equal proportions, but no H3N2 strain could be isolated. Genetic comparisons of HA1 genes showed a marked heterogeneity among H1N2 strains possessing human-like HAH1, which contrasted with the high similarity observed among avian-like H1N1 viruses. Genome sequencing revealed for four strains the novel combination of the human-like HAH1 gene of H1N2 viruses and the NAN1 gene of avian-like H1N1 viruses. Sequencing of the six internal genes showed that they were all of avian origin, closely related to those of avian-like H1N1. Three reassortants were isolated in 2001 and 2005 in the same farm and were genetically and antigenically closely related. The fourth one, isolated in 2006, presented a particular antigenic reaction pattern and had a deletion of one amino acid belonging to the receptor-binding pocket. The identification of these novel H1N1 reassortants highlights the importance of continuous disease-based surveillance in order to monitor their evolution and possible adaptation to the pig population. Although viral factors necessary for interspecies transmission are still unknown, the particular deletion in HAH1 of one reassortant, also observed in recent human H1N1 strains, could be likely to increase the chances of generating transmissible viruses.