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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. Besides their veterinary health interest, swine influenza virus (SIV) infections are also a matter of deep concern due to the possible pathogenic transmission to humans. Pigs are susceptible to infection with both avian and human influenza viruses. They could serve as an intermediate host for the adaptation of avian influenza viruses to the mammalian host, as well as for the generation of pandemic viruses through reassortment. Three major subtypes of influenza virus A, H1N1, H3N2 and H1N2, co-evolve in pigs worldwide. However, various lineages of each subtype can be distinguished depending on the world area. In Europe, H1N1 SIV originated from the transmission of an avian influenza virus to pigs in 1979. H3N2 strains have circulated in European pigs since the mid 1980s and are reassortants between an H3N2 strain of human origin and a swine avian-like H1N1 strain from which they inherited the internal genes. In the early 1990s, H1N2 viruses arose by genetic reassortment of human H1N1 viruses and swine reassortant H3N2 strains. Thus, H1N2 viruses possess a haemagglutinin (HA) gene closely related to that of human H1N1 strains that were circulating in the late 1970s. 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 H1N1 reassortants were isolated in 2001 and 2005 in the same farm and were genetically and antigenically closely related. By contrast, the fourth one, isolated in 2006 in another farm, presented a particular antigenic reaction pattern. Analysis of its HA deduced amino acid sequence revealed it had a deletion of one residue belonging to the receptor-binding pocket, a deletion that was also observed in recent human H1N1 strains. Identification of these novel H1N1 reassortants highlights the importance of continuous disease-based surveillance in order to monitor their evolution, their possible adaptation to the pig population and their increased chances of transmission to humans.