

## Molecular Epidemiology

### **MEP01 Genetic and antigenic characterization of swine influenza virus in France: identification of novel H1N1 reassortants**

Gaëlle Kuntz-Simon<sup>1</sup>, Nathalie Franck<sup>1</sup>, Stéphane Queguiner<sup>1</sup>,  
Stéphane Gorin<sup>1</sup>, Eric Eveno<sup>2</sup>, François Madec<sup>2</sup>

<sup>1</sup>AFSSA-LERAPP, Swine Virology Immunology Unit, France, <sup>2</sup>AFSSA-LERAPP, Pig Epidemiology and Welfare Unit, France

Swine influenza virus (SIV) infections are a cause for concern due to induction of a highly contagious disease of the respiratory tract in pigs. They are also of public health interest because of possible transmission of SIV to humans. Moreover, pigs are susceptible to both human and avian influenza viruses and could serve as intermediate hosts for the generation of pandemic strains through reassortment or adaptation to the mammalian host. In order to guarantee effective surveillance of SIV in France, we examined genetic and antigenic variation in viruses isolated from 2000 to 2007 in Brittany, the leading pig-producing region. SIV of H1N1, H3N2 and H1N2 subtypes co-evolve in Europe but no H3N2 strain was isolated in our study. H1N1 and H1N2 viruses were represented in equal proportions. Genetic comparisons of HA genes showed a marked heterogeneity among H1N2 strains possessing human-like HAH1, which contrasted with the high similarity observed among avian-like H1N1 viruses. Surprisingly, four strains appeared as novel combinations of the human-like HAH1 gene of H1N2 viruses and the NAN1 gene of avian-like H1N1 viruses. The six internal genes were all of avian origin. 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 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 not well known, the deletion in HAH1 of one reassortant, also observed in recent human H1N1 strains, could be likely to increase the chances of generating transmissible virus.