

A newly introduced genotype of A(H1N2) swine influenza virus crosses the species barrier from pig to turkey in France

François-Xavier Briand¹, Amélie Chastagner², Martine Cherbonnel-Pansart¹, Claire Martenot¹, Pascale Massin¹, Yannick Blanchard³, Axelle Scoizec⁴, Sophie Le Bouquin-Leneveu⁴, Nicolas Rose⁴, Audrey Schmitz¹, Séverine Herve², Eric Niqueux¹, Gaëlle Simon², Béatrice Grasland¹

¹Agence nationale de sécurité sanitaire de l'alimentation, de l'environnement et du travail (Anses), Ploufragan, Unité Virologie Immunologie Parasitologie aviaire et Cunicole (VIPAC), France

²Agence nationale de sécurité sanitaire de l'alimentation, de l'environnement et du travail (Anses), Ploufragan, Unité Virologie Immunologie Porcine (VIP), France

³Agence nationale de sécurité sanitaire de l'alimentation, de l'environnement et du travail (Anses), Ploufragan, Unité Génétique virale et Biosécurité (GVB), France

⁴Agence nationale de sécurité sanitaire de l'alimentation, de l'environnement et du travail (Anses), Ploufragan, Unité épidémiologie, santé et bien-être (EPISABE), France

Corresponding Author: francois-xavier.briand@anses.fr

Abstract

Since February 2020, surveillance of influenza A viruses in pigs in France (carried out by the national Résavip network) has allowed the identification of numerous cases of infection by a new swine A(H1N2) influenza virus. This virus belongs to the swine lineage named "H1avN2 DK-EA" (HA clade 1C.2.4, NA included in the H3N2-Gent lineage and internal genes in the EA lineage) which has been described in Denmark in 2004. This genotype was detected for the first time in southwestern France in 2015, but had no longer been identified in France until 2020. A new introduction of this A(H1avN2) virus on the French territory from abroad is being suspected. Since its detection in Brittany in February 2020, this virus has been spreading very rapidly and widely across western France, currently affecting ten departments. It has become the predominant virus and has changed the distribution of the different swine influenza virus genotypes circulating in the western region, which had been rather stable since the late 1990s. In parallel with the epizootic in pig herds, 12 breeding turkey farms reported egg-drop symptoms in Brittany, in West of France, from April 2020 to March 2021. The presence of influenza A genome was demonstrated in each turkey farms. The viruses belonged to the H1avN2 DK-EA lineage and were confirmed in 11 of these 12 cases. NGS sequencing of A(H1avN2) virus genomes from pigs (n=77) and turkeys (n=11) allowed a comprehensive phylogenetic analysis. The results indicate that the H1avN2 DK-EA lineage viruses identified in both species were directly related for all eight segments and did not show any reassortment. A more refined phylogenetic analysis suggests at least three independent host jumps from pigs to turkeys. In addition, a phylogenetic cluster grouping the majority of virus sequences identified in turkeys (n=7) suggests a potential direct circulation between turkey farms. A comparative analysis at the protein sequence level between the sequences of this cluster and the other available sequences is in progress to identify possible markers of adaptation to the turkey species.