

Phylogenetic analysis of A(H5N8) viruses characterized during the beginning of the highly pathogenic avian influenza epizootic in France in late 2020

François-Xavier Briand¹, Pascale Massin¹, Claire Martenot¹, Martine Cherbonnel-Pansart¹, Katell Louboutin¹, Rachel Busson¹, Chantal Allee¹, Carole Guillemoto¹, Florent Souchaud¹, Isabelle Pierre¹, Yannick Blanchard¹, Nicolas Etteradossi¹, Anne Van De Wiele², Axelle Scoizec¹, Sophie Le Bouquin-Leneveu¹, Severine Rautureau³, Yves Lambert³, Audrey Schmitz¹, Eric Niqueux¹, Béatrice Grasland¹

¹Agence nationale de sécurité sanitaire de l'alimentation, de l'environnement et du travail, Ploufragan, France

²Office français de la biodiversité, Vincennes, France

³Direction Générale de l'Alimentation, France

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

Abstract

Russia, Kazakhstan, and Europe have been facing a highly pathogenic H5 avian influenza (HPAI) epizootic since August 2020. Currently, at least 5 subtypes of HPAI A(H5N8), A(H5N1), A(H5N3), A(H5N4) and A(H5N5) have been identified; subtype A(H5N8) being the most represented with 10 genotypes. All these viruses exhibited an HA segment belonging to clade 2.3.4.4b of the A/Goose/Guangdong/1/96 lineage. In France, the majority of HPAI viruses have been detected in duck farms (n=490 as of March 29, 2021), in southwestern France (n=476). A very large diffusion in of HPAI A(H5N8) farms had already described 2016-2017. Whole genome sequencing was performed on viruses from the first domestic (n=21) and wild (n=4) outbreaks detected from 16/11/2020 to 26/12/2020 in France from various departments: Haute-Corse, South Corsica, Bouches-du-Rhône, Meurthe-et-Moselle, Calvados, Loire-Atlantique, Deux-Sèvres, Landes and Hautes-Pyrénées. Despite the wide geographical distribution of these samples, the nucleotide sequence comparison of the genomes indicates that all the sequenced viruses belong to clade 2.3.4.4.b of HPAI A(H5N8). They are also all of the same genotype and their nucleotide sequences are very close. Phylogenetic analysis of the sequences indicates that the viruses detected in Haute-Corse and South Corsica (n=7) are closely related to each other suggesting a single introduction of HPAI A(H5N8) in this area from geese originated from Northern France. Similarly, the virus sequences detected in southwestern France (n=11) are all directly related and distinct from the previous group suggesting a single introduction of HPAI A(H5N8) into this area probably through contact with wild birds. The other complete viral genomes identified in the farms of the other departments seem to indicate rather punctual and limited introductions of the virus in farms, probably via wild birds (n=3).