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Influenza A(H1N1)pdm09 virus in pigs, Togo, 2013

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Background and Methods

Very little is known on influenza virus and even more so on swine influenza virus (SIV) circulation in Africa. Antibodies reacting with human H1 and H3 influenza viruses have been reported in Egyptian and Nigerian swine sera [1,2] and a few SIV cross-reacting with human H1 and H3 serotypes have been isolated in Nigeria [3]. Since A/H1N1pdm09 became pandemic in human, the virus started to emerge in swine in La Réunion Island in 2009 [4], in Cameroon in 2010 [5], and in Nigeria in 2010 [6]. With the presence of swine swabs collected in Togo through 2012 had been positive for Influenza A virus (irrespective of the subtype), but had any serum tested positive for influenza antibodies [7], swine influenza surveillance continued and influenza virus was detected in 2013. We aim at understanding influenza virus circulation and transmission in the region.

325 nasal swabs were collected from freshly slaughtered pigs in a slaughterhouse near Lomé in June (see map). Samples were collected once a month every month from October 2012 through January 2014. RNA was extracted and influenza A specific one-step real-time RT-PCR (RT-PCR) was carried out. Virus was isolated on MDCK cells and Sanger sequencing was performed. Phylogeny was performed with ML algorithms on Mega.

Results

Influenza A virus genome was detected in 2.5 to 12.3% of the samples (screened by pools of 5 swabs: 8/65 positive pools) collected in February, from June through September, and in November 2013. A(H1N1)pdm09 virus was identified by RT-PCR in all the positive pools.

A virus isolate was obtained from a representative specimen, A/swine/Togo/ON32/2013 (H1N1), and fully sequenced (GenBank accession numbers: KM386872-KM386883).

The virus harbored 8 genes clustering with A/H1N1pdm09 virus gene. The sequences of A/swine/Togo/ON32/2013 were compared gene by gene with the closest blast hit for which a full genome was available: A/Texas/JMM_52/2012, with all the sequences from human (H1N1)pdm09 viruses from West and Central Africa available in GenBank, and with all the available African swine (H1N1)pdm09 virus sequences.

For the 8 genes, A/swine/Togo/ON32/2013 grouped with A/Texas/JMM_52/2012 as shown on the Figure with high supporting bootstrap values (92, 97, 100, 99, 99, and 100 for HA, PB2, PB1, PA, NP, NA, M, and NS, respectively, Figures A to H).

Interestingly, the HA gene sequence of A/Côte d’Ivoire/1529/2012 was also closely related to A/swine/Togo/ON32/2013 and A/Texas/JMM_52/2012 (Figure A). The full genome sequence of this swain strain was not available on GenBank for further comparison.

Discussion

Is there a seasonality in swine (H1N1)pdm09 circulation in West Africa?

- Combination of activity and animal mobility factors might be responsible for the absence of influenza virus in the backyard sector of Côte d’Ivoire, Benin, and Togo [7].
- The lower the temperature and relative humidity, the higher aerosol transmission in a laboratory setting [8].
- SIV isolated in Nigeria more frequently from November through January, when the dry harmattan wind is present [6].
- In Togo, SIV prevalence did not increase in the harmattan season. This could be explained by a low animal density (10,000 and 249,000 tons of pork meat produced in 2012 in Togo and Nigeria, respectively (FAOSTAT)).

Could swine (H1N1)pdm09 in Togo originate from a human to swine transmission event?

- First report of human (H1N1)pdm09 in Togo: October 2010: sporadic circulation (no seasonality) since then (WHO).
- High HA sequence similarity between A/swine/Togo/ON32/2013 (H1N1) and A/Côte d’Ivoire/1529/2012 (H1N1) (Figure A).
- Free roaming of pigs: a significant risk factor for spillover of human influenza virus from human to swine [9].

Swine production in Togo: small farms and free range pigs, little to no importation from abroad: a setup poorly favorable to sustained SIV transmission.

A/swine/Togo/ON32/2013(H1N1) harbored a pure (H1N1)pdm09 genotype, while (H1N1)pdm09 in swine has evolved in America, Europe and Asia towards complex genotypes with numerous reassortment events.

Conclusion and perspectives

We identified (H1N1)pdm09 viruses in swine in Togo in 2013 after years without animal influenza virus detection in the region. Phylogenetic analyses showed that A/swine/Togo/ON32/2013(H1N1) was more closely related to (H1N1)pdm09 viruses circulating in human in 2012-2013 in the region and worldwide than to swine virus, suggesting a human to swine transmission of the pathogen. Surveillance studies need to be however pursued in the region to better understand the virus transmission and evolution and the interspecies transmission.

References:

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