

TITLE

EPIDEMIOLOGICAL SURVEILLANCE AND CHARACTERIZATION OF INFLUENZA A VIRUSES (IAV) IN SPANISH AND PORTUGUESE PIG FARMS

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CONTENT

Background and Objectives

The aim of this study was to determine the diversity of IAV from clinical outbreaks in pig farms of Spain and Portugal as well as from active surveillance.

Material & Methods

Nasal swabs (NS; 10-20 animals/farm) were collected from 141 outbreaks of respiratory disease compatible with swine influenza. Additionally, 20 NS from suckling piglets, weaners and fatteners were collected in 17 farms. Presence of IAV and lineage determination were initially assessed by RT-qPCR. For 39 isolates genotyping of IAV was determined after sequencing with the Illumina MiSeq® Plattform.

Results

IAV was confirmed in 93/141 (65.9%) outbreaks of which 48 happened in weaners. In active surveillance, 14/17 (82.3%) farms were positive for IAV. The most commonly detected lineages were H1avN2 (28.03%) and H1avN1av (15.89%). Since October 2018, H1 and N1 of the 2009 pandemic lineage have been detected in (3 cases) for the first time in the last 2 years. Six different genotypes (A, B, C, D, M and N) have been identified so far. Nonetheless, 4 cases did not fit into the European classification system and contained one or more genes derived from human lineages.

Discussion & Conclusion

The present results show that IAV is widely spread in pig farms causing both outbreaks and apparently subclinical infections. The most frequent lineage, H1avN2 was undetected in Spain until 2013, indicating a rapid spread within the pig population. The recent re-emergence of H1 and N1 2009 pandemic, and the high presence of human-IAV origin genes detected by genotyping emphasise the close relationship between human and swine influenza. Also, genotyping is the cornerstone for understanding the circulation dynamics and variations of this virus in swine. As this is an ongoing research, more results are expected within the next months.