



VIRAL DISEASES

VVD-054

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

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Introduction

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

Material & Methods

Nasal swabs (NS; 10-20 animals/farm) were collected from 64 outbreaks of respiratory disease compatible with swine influenza. Additionally, 20 NS from suckling piglets, weaners and fatteners were collected in 10 randomly selected farms. Presence of IAV and subtyping were initially assessed by RT-qPCR. For 11 isolates genotyping of IAV was determined after sequencing with the Illumina MiSeq® Plattform.

Results

IAV suspicion was confirmed in 49/64 outbreaks of which 33 happened in weaners. Detected subtypes were: H1N1, H1N2, H3N2 and H3N1. In active surveillance, 9/10 farms were positive for IAV -always H1 viruses- (6 maternities, 7 nurseries and 2 fattening units, with average prevalences of 44%, 37% and 6%, respectively). Globally, six different lineages were detected being H1avN2 (25.0%) and H1avN1av (21.4%) the most frequently ones. H1 or N1 of the 2009 pandemic lineage were not found. Regarding the genotyping, 5/11 isolates belonged to genotypes M and N, which contain the Matrix gene of the 2009 human pandemic H1N1 virus.

Discussion & Conclusion

The present results indicate that IAV is widely spread in pig farms of Spain causing both outbreaks and apparently subclinical infections. The most frequent lineage, H1avN2, was not present in Spain until 2013 a fact that indicates a rapid spread within the pig population. The common presence of reassortants, including human pandemic gene segments, emphasize the need for genotyping to get a precise picture of the molecular epidemiology of IAV.