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INFLUENZA A VIRUSES SUBTYPES IN NURSERY AND FINISHING PIGS IN THE SOUTH OF BRAZIL

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Background and Objectives

Influenza A virus (IAV) is a zoonotic RNA virus that causes respiratory diseases in commercial pig farming in Brazil, with a prevalence estimated at 70%. Swine can be infected with various subtypes, including H1N1, H1N2, H3N2, and reassortment, including human IAV. This study aimed to understand IAV subtypes in swine herds of an agroindustry in South Brazil through subtyping and genomic sequencing.

Material and Methods

Nasal swabs and swine lungs were collected from nursery and finishing pigs in Santa Catarina and Rio Grande do Sul (RS) States between April and December 2021. A total of 1988 samples were screened for IAV using RT-qPCR, and positive samples were selected for subtyped by multiplex RT-PCR viral, SPF eggs isolation and sequenced. IAV genes (8 segments) sequenced by Illumina MiSeq System™ had their complete genome analyzed.

Results

IAV was detected in 16.65% of 331 samples, with Zone A having 27.68% of positive samples. All farms from each zone were significantly different for the presence of IAV. Lungs from clinical cases resulted in 84.21% positivity for IAV RNA, compared to nasal swabs (16%). Multiplex RT-qPCR subtyped 110 IAV isolates, and 57.27% HA or NA were identified: H1N1pan (3.51%) and one H1huN1pan subtype samples. H3hu was the most frequent (27 samples), followed by N1pan, H1hu, H1pan, and N2hu. Zone A was the most diverse and the only one where the N2hu subtype was detected. Eleven samples were completed sequenced and in 5/11 there were co-infection with at least 2 different IAV. The results demonstrated several introductions of human H3N2 subtypes and at least two different clusters of H1N1 subtypes (Brazil and USA).

Discussion and Conclusion

The study showed IAV infection detection in the studied pig farms in all four zones. The H3hu subtype gene presented the highest predominance, found mostly in RS. However, the N1pan glycoprotein gene was well distributed in both states. These results provide important information on IAV circulation in swine herds, helping to better interpret its epidemiology and provide control tools for each region. Coinfection of different or genetically distant subtypes was confirmed by sequencing, demonstrating the interaction of human and swine origin IAV in the evaluated farms.