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TITLE

USE OF BIOPORTAL IN A PRRSV OUTBREAK IN A SPANISH FARM

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CONTENT

Background and objectives

New introduction of isolates and the evolving dynamics of the PRRS virus can be monitored by the consistent sequence of the diagnosis. Thus, the aim of this work is monitoring the isolates in a farm level by using Bioportal software.

Materials and Methods

The study was conducted in a 775 sows farrow-to- wean farm located in Zaragoza (Spain). Since the last outbreak in December 2015 the farm was under a 5 step process PRRS control program. An ORF5 PRRS virus resident strain sequence "A" was identified. The heterology with the "Lelystad" PRRS virus strain was 13.9% and 15% with the Ingelvac PRRSFLEX EU® vaccine.

From May 2016 to June 2018 no virus was detected in 30 due-to-wean piglets monthly sampled. In July 2018 PRRSv PCR positive serum samples from aborted sows were detected and ORF5 sequence was obtained. The Bioportal software was used for epidemiological analyze purposes. Results

Compared to the farm resident strain the recent sequence heterology was 16.8% and 3.8% with the closest sequence from a sow farm of the same production system. The heterology was ranged between 10.9% and 14.2% among all licensed PRRS vaccines in Spain. A new wild-type virus strain was introduced in the herd. When the benchmark was performed within the entire Spanish Bioportal database (1829 sequences), we found a range between 0.8% and 3% heterology with strains detected in farms from five other swine companies located up to 250 km distance. Some of them shared the same pig transportation company.

Discussion and Conclusions

Bioportal was a crucial tool to track easily a newly introduced PRRSv sequence in a negative farm by comparisons within a huge sequences database. The main conclusion is that pig transportation represents a very high risk factor for PRRSv dissemination among different production systems in Spain.

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