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REFINING GENETIC CLASSIFICATION OF GLOBAL TYPE 1 PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS AND CHARACTERIZATION OF THEIR GEOGRAPHIC DISTRIBUTIONS

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Background and Objectives

PRRSV-1 is predominantly prevalent in Europe, yet it is also detected in North America and Asia. Previous investigations, utilizing ORF5 sequences, categorized PRRSV-1 into four subtypes. Subtype 1 further underwent classification into 12 clades (A-L) or three lineages, with lineage 1 encompassing clades 1A-1G and lineage 3 encompassing clades 3A-3G. However, neither system has been widely accepted for use.

Material and Methods

Here, we proposed a statistically supported PRRSV-1 genetic classification system based on 10,400 global PRRSV-1 ORF5 sequences spanning the years 1991-2023.

Results

We replaced “subtype” with “lineage”, and, subsequently, PRRSV-1 was classified into four lineages (L1-L4) with L1 including 18 sublineages (L1.1 to L1.18). This classification system is flexible for expansion if additional lineages, sublineages, or more granular classifications are needed. Geographic distributions of global PRRSV-1 at lineage and sublineage levels were investigated. A small number of PRRSV-1 sequences were classified in lineages L2, L3, and L4 and were exclusively found in Eastern Europe. In contrast, lineage L1 exhibited widespread distribution, circulating in North America, Asia, and across Europe. In Europe, 17 out of 18 sublineages (excluding L1.13) within L1 were identified. In North America, only sublineage L1.1 was detected. In Asia, sublineages L1.1, L1.2, L1.6, L1.10, L1.11, L1.13 (confined to China), and L1.17 were identified. This study also determined the classification and ORF5 nucleotide identity of six commercial PRRSV-1 vaccines (Porcilis L1.1, Unistrain L1.2, Pyrsvac-183 L1.2, Ingelvac PRRS Flex EU L1.3, ReproCyc PRRS EU L1.3, and Suvaxyn L1.11) against each lineage and sublineage and the detection frequency of vaccine-like viruses. The phylogeny based on whole-genome sequences demonstrated a slightly different tree topology compared to that based on ORF5 sequences due to recombination. Recombination of PRRSV-1 was observed at intra-sublineage and inter-sublineage levels. A set of PRRSV-1 ORF5 reference sequences representing global diversity and these refined classifications are available for future diagnostic and epidemiological applications.

Discussion and Conclusion

This study provides a benchmark, delineating the current genetic diversity of PRRSV-1, and the revised ORF5-based classification system can be used to characterize the genetic and phenotypic evolution of PRRSV-1.