

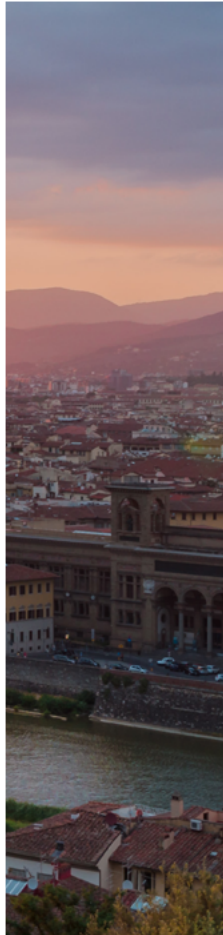
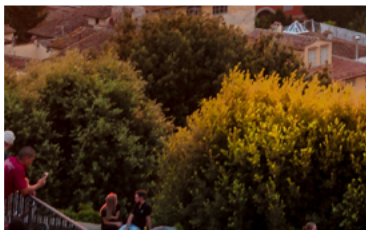
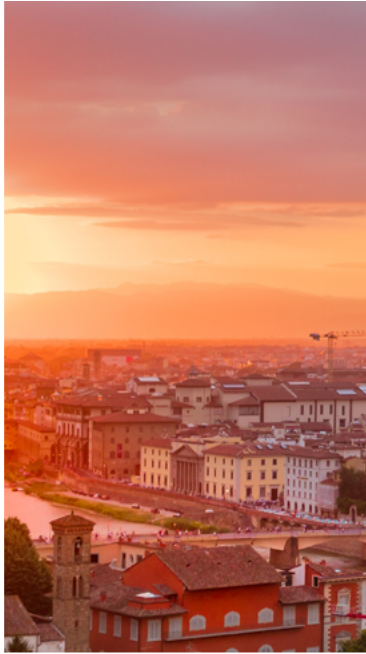
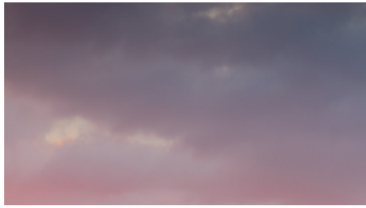


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17<sup>th</sup> EUROPEAN SYMPOSIUM  
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PROCEEDINGS

May 13-15, 2026  
Florence, Italy

## VIRAL DISEASES

VVD-PP-42

### MOLECULAR DIVERSITY PRRSV IN SWINE FARMS OF JALISCO, MEXICO

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#### Background and Objectives

PRRSV continues to be one of the most significant health challenges in swine production, especially in areas with high animal density. Sequencing the ORF5 region remains a key tool for evaluating viral diversity and understanding evolutionary dynamics. Additionally, identifying farm-level risk factors is essential for establishing effective control measures. The objective of this study was to PRRSV detection and to describe the genetic diversity of circulating strains in swine farms across Jalisco, Mexico.

#### Material and Methods

Between 2022 and 2023, sampling was conducted on 80 farms distributed across four regions categorized by swine population density (A-9.46, B3-135.4, B1-210.36 and B2-261.65 pigs/km<sup>2</sup>). A total of 4,207 serum samples were obtained from different production stages and subsequently grouped into 844 pools for ORF7 qRT-PCR testing. Pools with Ct values <30 were selected for ORF5 amplification via endpoint RT-PCR, followed by Sanger sequencing.

#### Results

Positive pools were most frequently detected in weaning (61.1%), followed by growing (40.4%) and lactation (38.2%). The highest positivity occurred in region B2 (44.6%), the area with the greatest pig density. A total of 39 ORF5 sequences were obtained and assigned to lineages L1A, L1C, L1I, L2, L5A, L8C, and L8D (GenBank Accession PV235482 to PV235520). L1A accounted for 53.8% of the sequences and showed low intra-lineage diversity (3.6%).

#### Discussion and Conclusion

The detection of several co-circulating lineages demonstrates heterogeneous viral movement across the region. Overall, PRRSV circulation in Jalisco appears to be driven mainly by high pig density, insufficient biosecurity, and inconsistent vaccination practices. The predominance of lineage L1A, together with the concurrent presence of additional lineages, indicates ongoing viral introduction and underscores the need to reinforce access control and optimize vaccination programs to mitigate the epidemiological impact of the virus. This work was supported by IPVS Association México 2014 A. C. SIGI 1520226989.