2026
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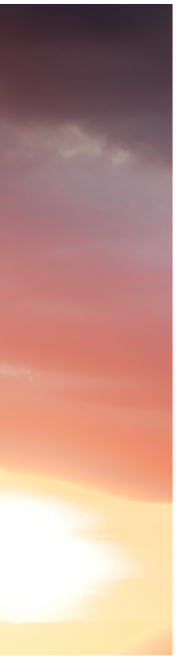
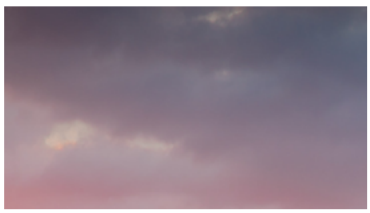
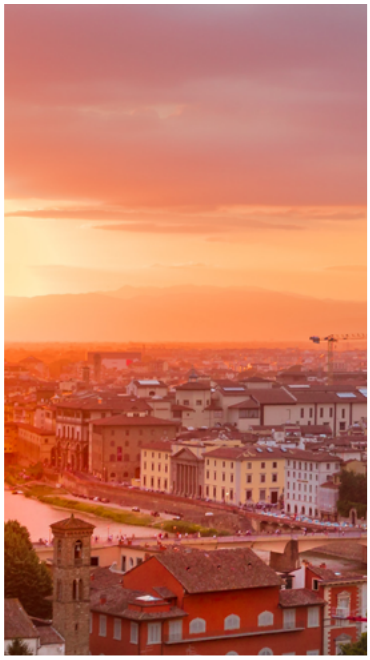
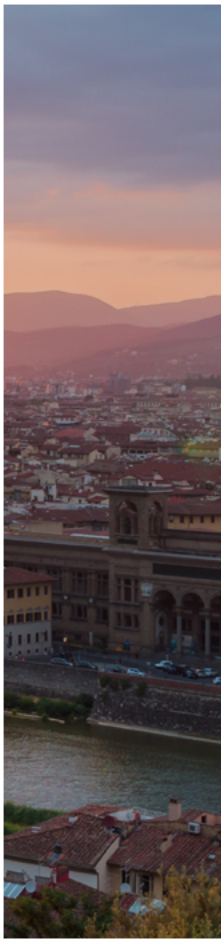
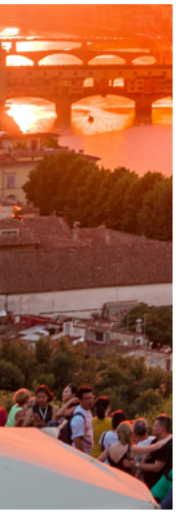
ESPHM
17th EUROPEAN SYMPOSIUM
OF PORCINE HEALTH MANAGEMENT

PROCEEDINGS

May 13-15, 2026
Florence, Italy

VVD-PP-17

GENETIC DIVERSITY OF PCV2 IN SWINE FARMS OF JALISCO, MEXICO

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Background and Objectives

PCV2 is responsible for Porcine Circovirus Diseases, has a substantial impact on swine productivity. Effective control depends on early diagnosis, consistent vaccination, and strong biosecurity measures, all of which influence the genetic diversity of the virus. The ORF2 gene, which encodes the capsid protein, is highly variable and has contributed to genotype shifts observed globally. This study aimed to PCV2 detection and to describe the genetic variability of circulating strains in swine farms in Jalisco, Mexico.

Material and Methods

From 2022 to 2023, 80 farms participating in the "Sanidad Jalisco" program were assessed across four regions classified by swine population density (A-9.46, B3-135.4, B1-210.36 and B2-261.65 pigs/km^2). A total of 4,207 serum samples were pooled into 844 groups and tested by qPCR targeting ORF2. Pools with Ct<30 were selected for full ORF2 amplification (765 bp) followed by Sanger sequencing. Genetic analyses were conducted using MEGA v12.

Results

A total of 70 sequences were obtained and submitted to GenBank under accession numbers PV235521 to PV235590. PCV2 molecular detection was higher in high-density regions, with region B2 showing the highest positivity at 39.9%. ORF2 sequencing revealed a predominance of genotype D (73%), followed by genotype A (27%). Additionally, several sequences clustered closely with strains previously associated with increased pathogenicity.

Discussion and Conclusion

Based on the observations made throughout the study, PCV2 occurrence in high-density regions appears to be largely driven by insufficient vaccination coverage and weak biosecurity practices. The dominance of genotype D, along with the detection of variants potentially linked to increased pathogenicity, underscores the need for continuous molecular monitoring and the adoption of region-specific control strategies. This genetic variability is consistent with national reports and reinforces the importance of integrating epidemiological and molecular data to enhance surveillance efforts. Acknowledgments: SADER-CONACYT -2017-6-292826. SIGI 1281834685.