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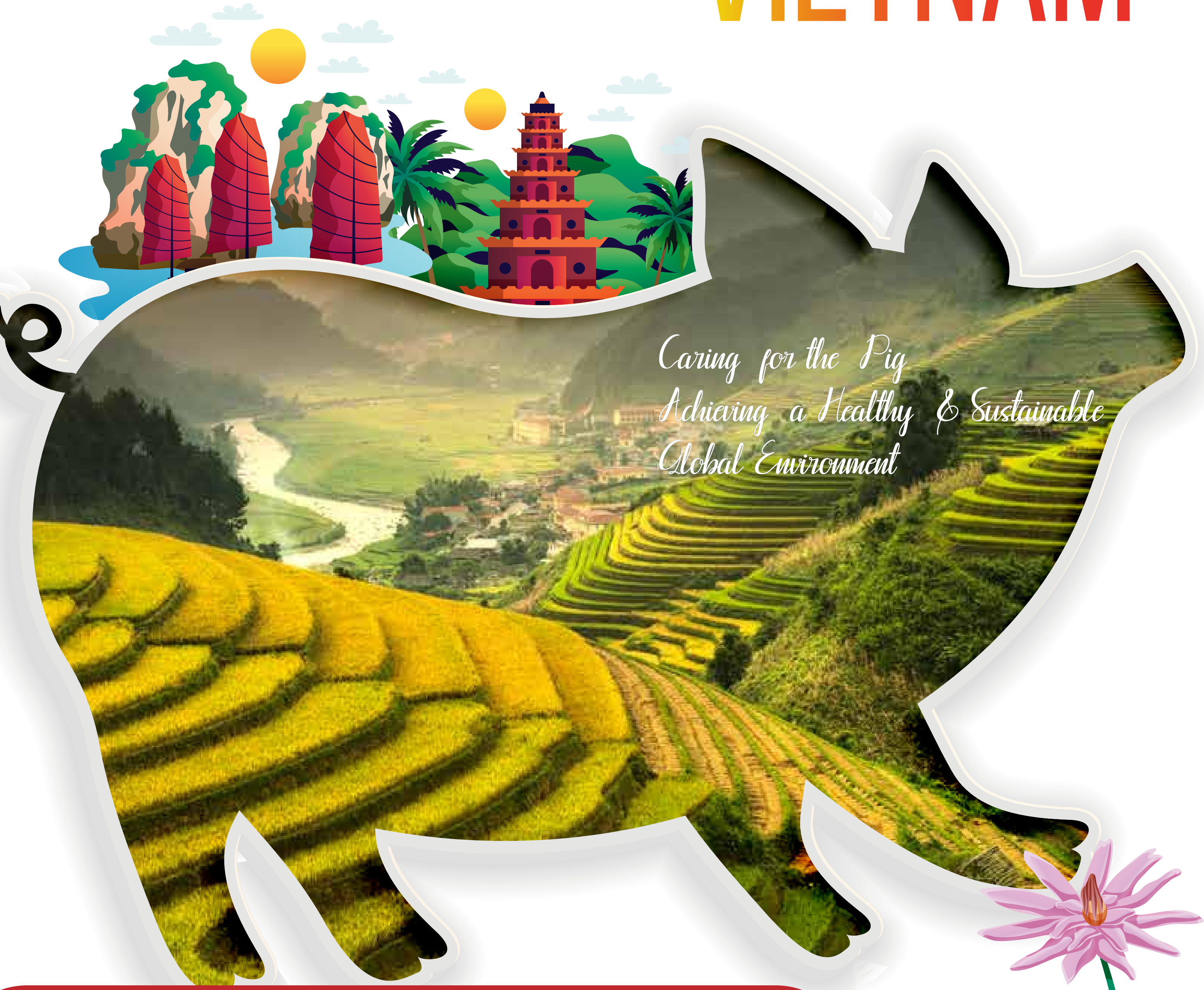
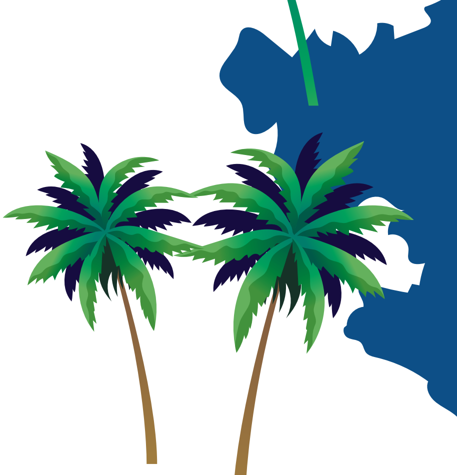


PROCEEDINGS



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RISK FACTORS AND GENETIC DIVERSITY OF PCV2 IN SWINE FARMS OF JALISCO, MEXICO

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Introduction and Objectives

Porcine circovirus type 2 (PCV2) is the causal agent of Porcine Circovirus Diseases, which significantly affect farm productivity. Its control relies on timely diagnosis, vaccination, and biosecurity, which also shape viral genetic diversity. The ORF2 gene, encoding the capsid protein, is highly variable and has driven genotype shifts worldwide. This study aimed to identify risk factors associated with PCV2 detection and characterize the genetic variability of circulating strains in swine farms from Jalisco, Mexico.

Materials and Methods

Between 2022 and 2023, 80 farms enrolled in the “Sanidad-Jalisco” program were evaluated across four animal-density regions. A total of 4,207 serum samples were grouped into 844 pools and tested by qPCR targeting ORF2 (Ct < 35 as positive). Management information was collected and analyzed using 2 × 2 contingency tables, Chi-square tests, and Odds Ratios (95% CI). Samples with Ct < 30 were selected for full ORF2 (765 bp) amplification and Sanger sequencing. Genetic analyses were performed with MEGA v11.

Results and Discussion

PCV2 molecular detection was higher in high-density regions, particularly in B2 (39.9%). Incomplete vaccination programs and inadequate biosecurity practices were the main risk factors associated with viral DNA detection. In region B2, lack of access control and entry of non-disinfected vehicles were strongly associated with PCV2 detection (OR = 21.5 and 19.3, respectively). Pigs without circovirus vaccination had higher odds of PCV2 molecular detection (OR = 6) compared with vaccinated animals. ORF2 sequencing identified 51/70 (73%) sequences as PCV2d and 19/70 (27%) as PCV2a. Nucleotide divergence analysis showed low intra-genotype variability in PCV2d (0.0 - 3.9%) and broader divergence in PCV2a (0.3–15.0%), associated with two subclades and detection of a recombinant strain classified as genotype A with parental A and D lineages. Inter-genotype divergence ranged from 13% to 31%. All PCV2d sequences exhibited lysine at position 234 of the capsid protein (N234K), a molecular signature previously linked to increased viral load and PCVAD-compatible lesions in experimental models.

Conclusion

In high-density areas, PCV2 occurrence is mainly linked to inadequate vaccination and weak biosecurity. The predominance of PCV2d and the presence of potentially pathogenic variants reinforce the need for continuous molecular surveillance and region-specific control strategies.

Keywords: Biosecurity, Molecular epidemiology, ORF2 divergence, Porcine circovirus type 2, PCV2d.

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