THE 28TH INTERNATIONAL PIG VETERINAR SOCIETY CONGRESS

16-19 June 2026

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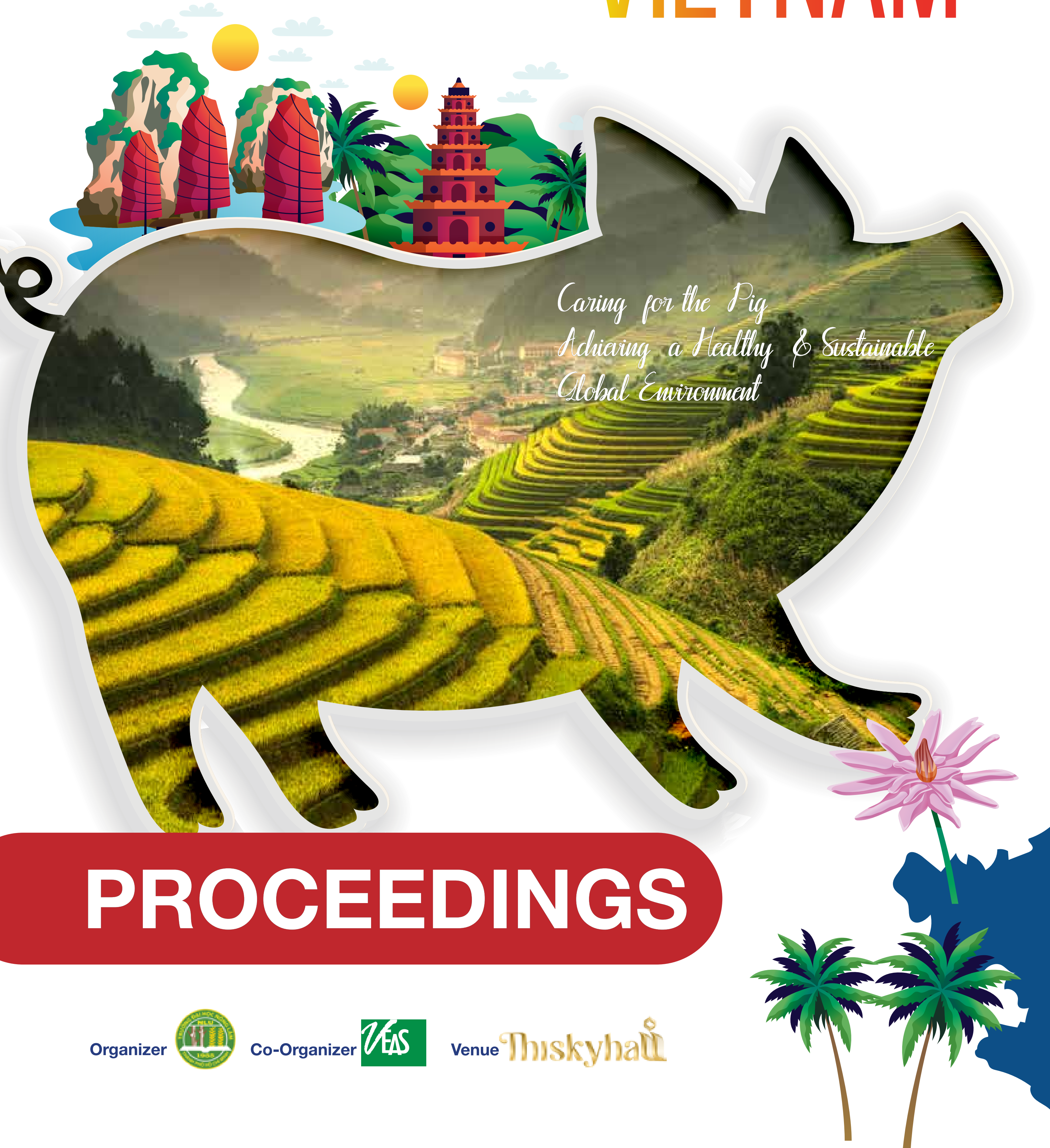

PROCEEDINGS

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IPVS 2026 - Topic 1: Virology and Viral Diseases (VVD) - PO0970

MOLECULAR DIVERSITY AND FARM-LEVEL RISK FACTORS ASSOCIATED WITH PRRSV CIRCULATION IN SWINE REGIONS OF JALISCO, MEXICO

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Introduction and Objectives

PRRS virus remains one of the main health challenges for swine production, particularly in high-density systems. ORF5 sequencing is essential to assess viral variability and evolutionary patterns, while identifying risk factors supports the design of effective control strategies. This study aimed to identify the main risk factors associated with PRRSV detection and characterize the genetic diversity of circulating strains in swine farms of Jalisco, Mexico.

Materials and Methods

From 2022 to 2023, 80 farms were sampled across four density-based regions (A, B1, B2, B3). A total of 4,207 serum samples were collected by production stage and grouped into 844 pools for ORF7 qRT-PCR. Farm-level information on management, biosecurity, vaccination, facilities, pest control, and waste handling was analyzed using 2 × 2 contingency tables, Chi-square tests, and Odds Ratios (95% CI). Pools with $Ct < 30$ were used to amplify ORF5 by endpoint RT-PCR, followed by Sanger sequencing and analysis in MEGA 11.

Results and Discussion

Positive pools were more frequent in weaning (61.1%), growing (40.4%), and lactation (38.2%). Region B2, the area with the highest pig density, showed the greatest positivity (44.6%). Thirty-nine ORF5 sequences were obtained and classified into lineages L1A, L1C, L1I, L2, L5A, L8C, and L8D. Lineage L1A represented 53.8% of sequences and showed low within-group diversity (3.6%), although multiple co-circulating lineages indicate heterogeneous viral movement. Lack of control over farm access was the strongest risk factor associated with PRRSV detection, particularly in region B3 and semi-intensive systems. The absence of vaccination against key bacterial pathogens and PCV2 also increased the likelihood of viral detection, consistent with evidence that co-infections can enhance PRRSV replication and clinical impact.

Conclusion

High pig density, deficient biosecurity, and inconsistent vaccination practices favor PRRSV circulation in Jalisco. The predominance of L1A, alongside additional lineages, highlights the need to strengthen biosecurity and optimize vaccination programs to mitigate the epidemiological impact of the virus.

Keywords: Lineages, Jalisco, Mexico, PRRSV, Risk Factors.

Acknowledgements: The authors thank INIFAP for supported, IPVS Mexico Association 2014 A.C. SIGI No. 1520226989 and Jalisco farmers (URPJ).