

PRRSV-2 Detection and Phylogenetic Classification from Swine in Northern Thailand Using ORF5 Gene

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Abstract

Background: Porcine reproductive and respiratory syndrome virus (PRRSV) causes severe reproductive failures and respiratory illness in pigs worldwide. The type 2 genotype (PRRSV-2) is prevalent in North American and Asia, and ORF5 gene sequencing has been used to classify PRRSV-2 into multiple genetic lineages. In Thailand, PRRSV-2 has circulated for decades, and recent studies found Thai isolates belonging to at least five lineages (L1, L5, L8, L9, L10). Notably, lineage 10 appears to be Thai-specific, as global sequence data show L10 sequences exclusively from Thailand.

Objectives: This study aimed to detect PRRSV-2 in pig blood samples from northern Thailand (2025) and to determine the genetic lineage of any detected virus. Specifically, we sought to amplify and sequence the PRRSV ORF5 gene from positive samples and classify the viruses by phylogenetic analysis.

Methods: Two porcine blood samples were screened for PRRSV using a real-time reverse-transcription PCR assay. For each PRRSV-positive sample, the ORF5 gene was amplified by RT-PCR; PCR products were purified and subjected to Sanger sequencing. The resulting ORF5 sequences were aligned with global reference sequences and phylogenetic analysis was performed using the maximum-likelihood method in IQ-TREE with the GTR+G model. Branch support was assessed using ultrafast bootstrap and SH-aLRT with 1,000 replicates each.

Results: Both samples tested positive for PRRSV-2, and their ORF5 sequences clustered firmly within lineage 10. This Thai-specific lineage has low intra-lineage diversity. Each sequence showed >99% nucleotide identity to a reference lineage-10 strain (GenBank AF494042.1), indicating very high similarity. These findings are consistent with prior reports that circulating Thai PRRSV-2 strains group in lineage 10.

Conclusion: We report detection of PRRSV-2 lineage 10 in pigs from northern Thailand, highlighting the persistence of this Thai-specific lineage. ORF5-based phylogenetic analysis proved effective for classifying the virus. This integrated molecular approach improves understanding of PRRSV-2 diversity and underscores the importance of ongoing surveillance to guide control measures.

Keywords: PRRSV-2, ORF5 gene, Phylogenetic classification, Lineage 10, Thailand

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