



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

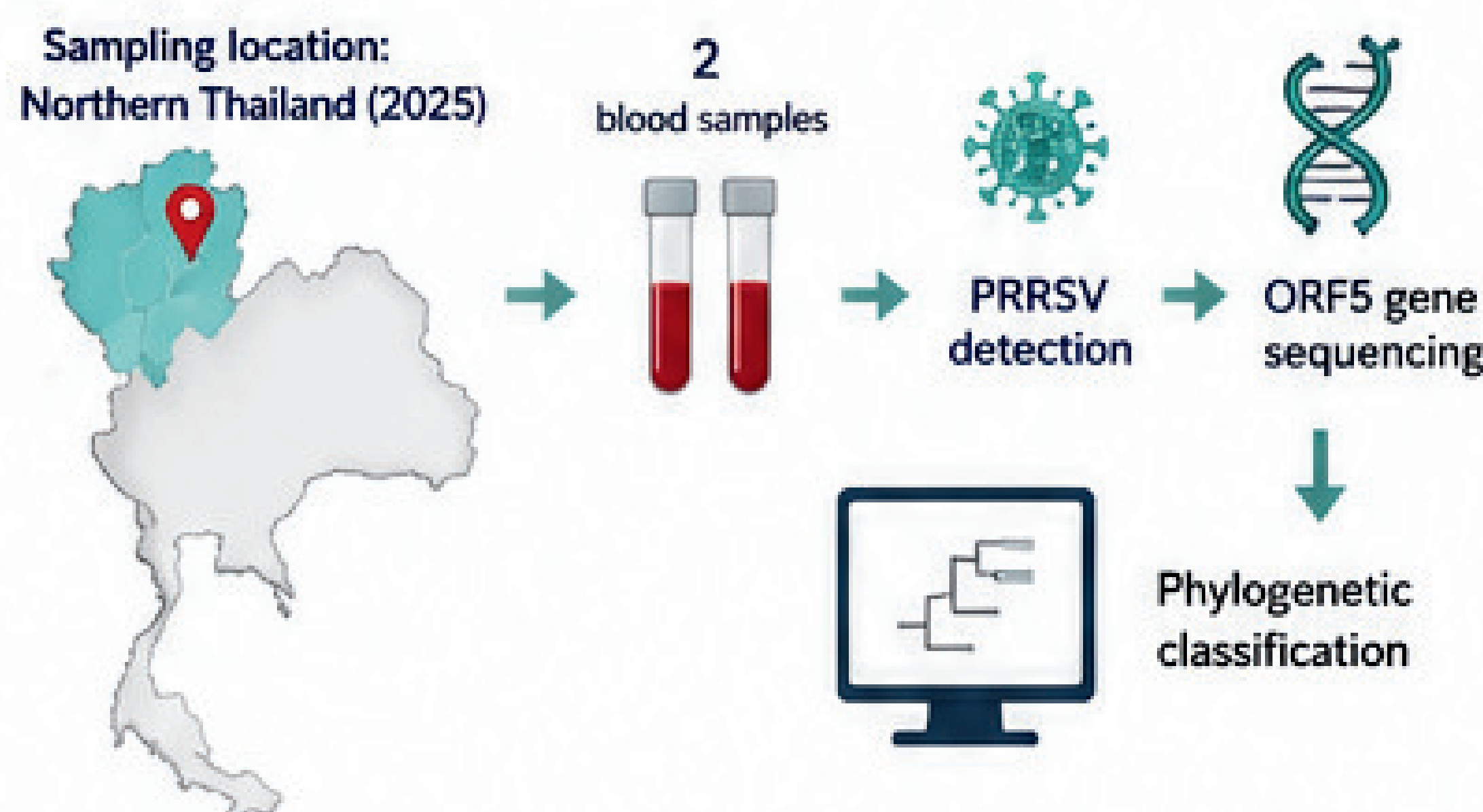
We report detection of PRRSV-2 lineage 10 in pigs from northern Thailand, highlighting the persistence of this Thai-specific lineage. ORF5-based phylogenetic analysis proved effective for classifying the virus. This integrated molecular approach improves understanding of PRRSV-2 diversity and underscores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

Keywords

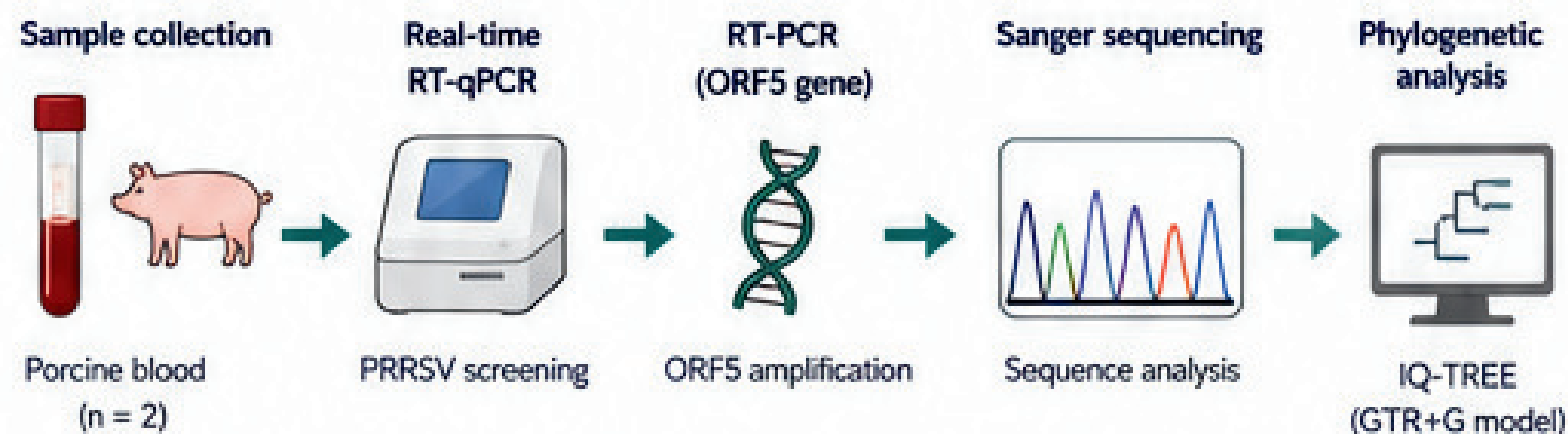
PRRSV-2, ORF5 gene, phylogenetic classification, lineage 10, Thailand

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overview



Material and Methods

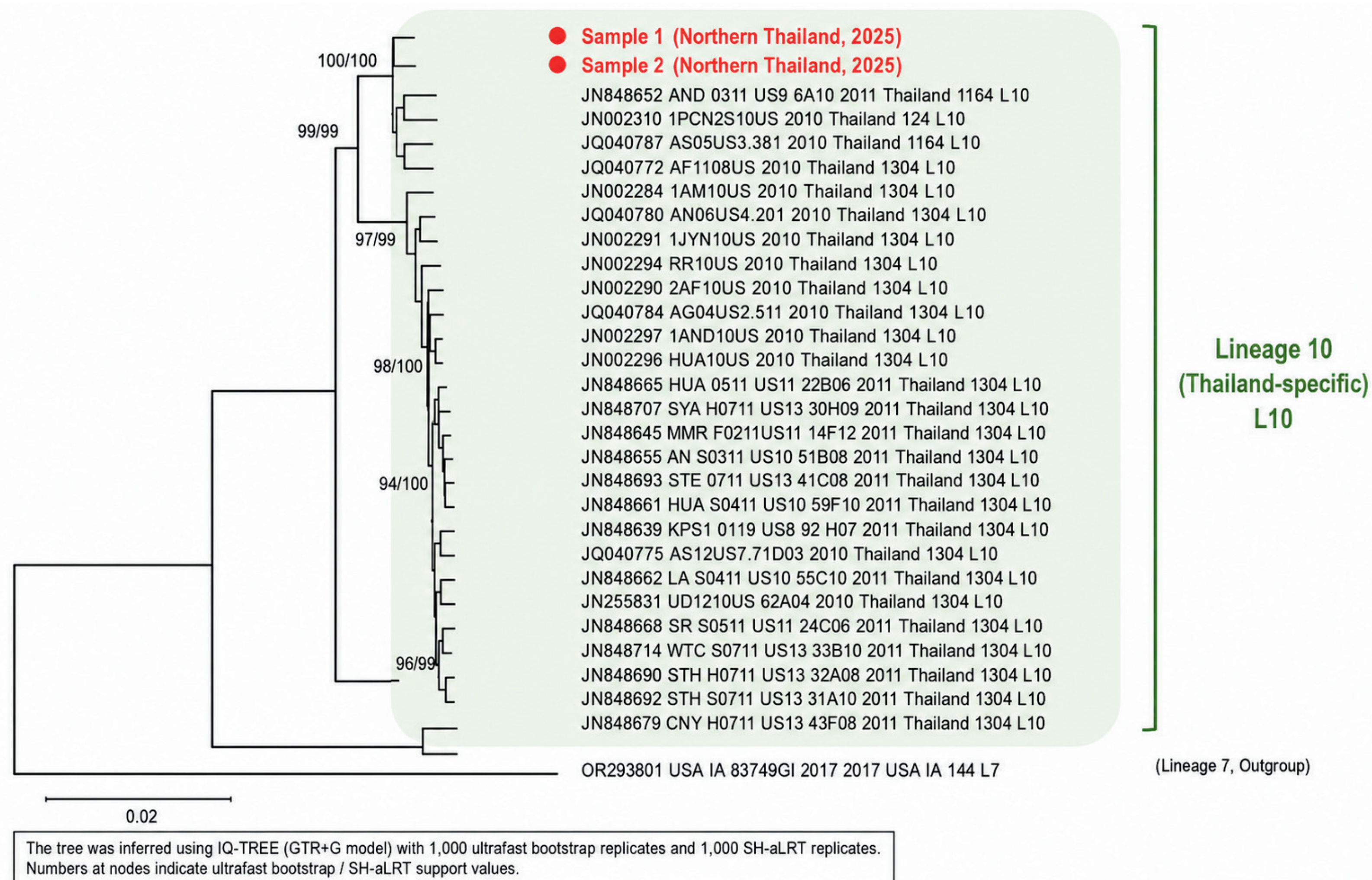


Results

Sample ID	Ct value	Result	PRRSV Type
NP25-01	21.32	Positive	PRRSV-2
NP25-02	22.18	Positive	PRRSV-2

Sample ID	Nucleotide identity (%)
NP25-01	>99.5%
NP25-02	>99.4%

Phylogenetic Analysis



Reference

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