

Molecular Characterization of Rabies Virus in Thailand, 2022-2025

Peerada Siriwatcharawong^{1,*}, Kulyarat Bhakha¹, Ratchadaporn Wongsombut¹,
Janejira Santo¹, Nannapat Pengjan¹ and Nantaporn Wandee¹

Abstract

Background: Rabies remains a fatal zoonotic disease and a significant public health concern in Thailand. Understanding the epidemiological patterns and genetic diversity of circulating rabies virus strains is essential for effective surveillance and control. Analysis of the nucleoprotein (N) and glycoprotein (G) genes, together with whole genome sequencing (WGS) of selected isolates, enables detailed characterization of circulating viruses and supports improved rabies monitoring and control strategies in Thailand.

Objective: To characterize the genetic features of rabies virus in Thailand and generate updated molecular data, including information related to antigenicity (G gene) and molecular characteristics of key viral genes (N, P, M, and L), to support rabies surveillance and contribute to effective prevention and control strategies.

Methods: Rabies virus-positive brain samples from animals collected in Thailand during 2022–2025 were confirmed by the Direct Fluorescent Antibody (DFA) test and real-time RT-PCR. Viral RNA was extracted, and the N and G genes were amplified by RT-PCR and sequenced using Oxford Nanopore technology in 100 samples. In addition, WGS was performed on eight representative samples using the same platform. The obtained sequences were compared with reference and vaccine strains from GenBank and analyzed using standard bioinformatics tools to identify genetic variations and construct phylogenetic trees.

Results: Phylogenetic analysis of the N and G genes showed that rabies virus strains circulating in Thailand belong to the Asian clade. Viruses in the northern and upper northeastern regions ($n = 17$) were mainly classified into the SEA1 subclade, while the SEA3 subclade ($n = 83$) was distributed across the country. WGS of representative samples showed consistent clustering with the N and G gene analyses. The Thai strains were genetically related to viruses reported from neighboring countries in the GenBank. In addition, the virus detected in a golden jackal was highly similar to strains circulating in domestic dogs in Loei Province. Comparative analysis suggested that current rabies vaccines remain effective against the circulating strains.

Conclusion: This study provides updated information on the genetic characteristics of rabies viruses circulating in Thailand. The findings demonstrate that the circulating strains belong to the Asian clade and are genetically related to viruses reported in neighboring countries. The detection of genetically similar rabies viruses in wildlife and domestic animals also highlights the potential role of wildlife in rabies transmission. These results support ongoing rabies surveillance and indicate that current vaccines remain effective for rabies prevention and control.

Keywords: Rabies, Whole genome sequencing, N gene, G gene, Vaccine

¹ Virology Section, National Institute of Animal Health, Department of Livestock Development, Bangkok, Thailand

* Corresponding author; E-mail: peerada_s@outlook.com