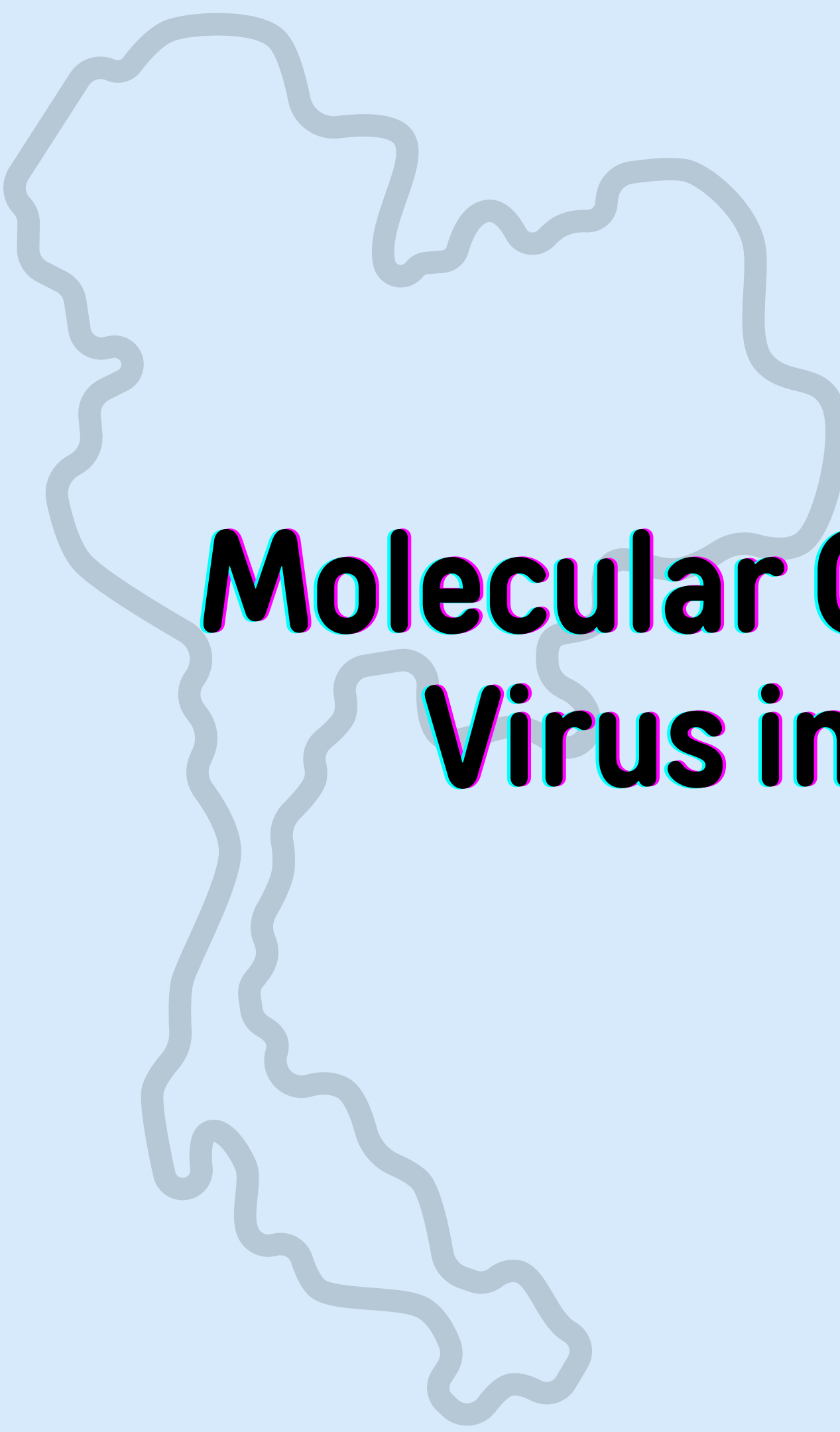




Molecular Characterization of Rabies Virus in Thailand, 2022–2025

Peerada Siriwatcharawong
National Institute for Animal Health, DLD

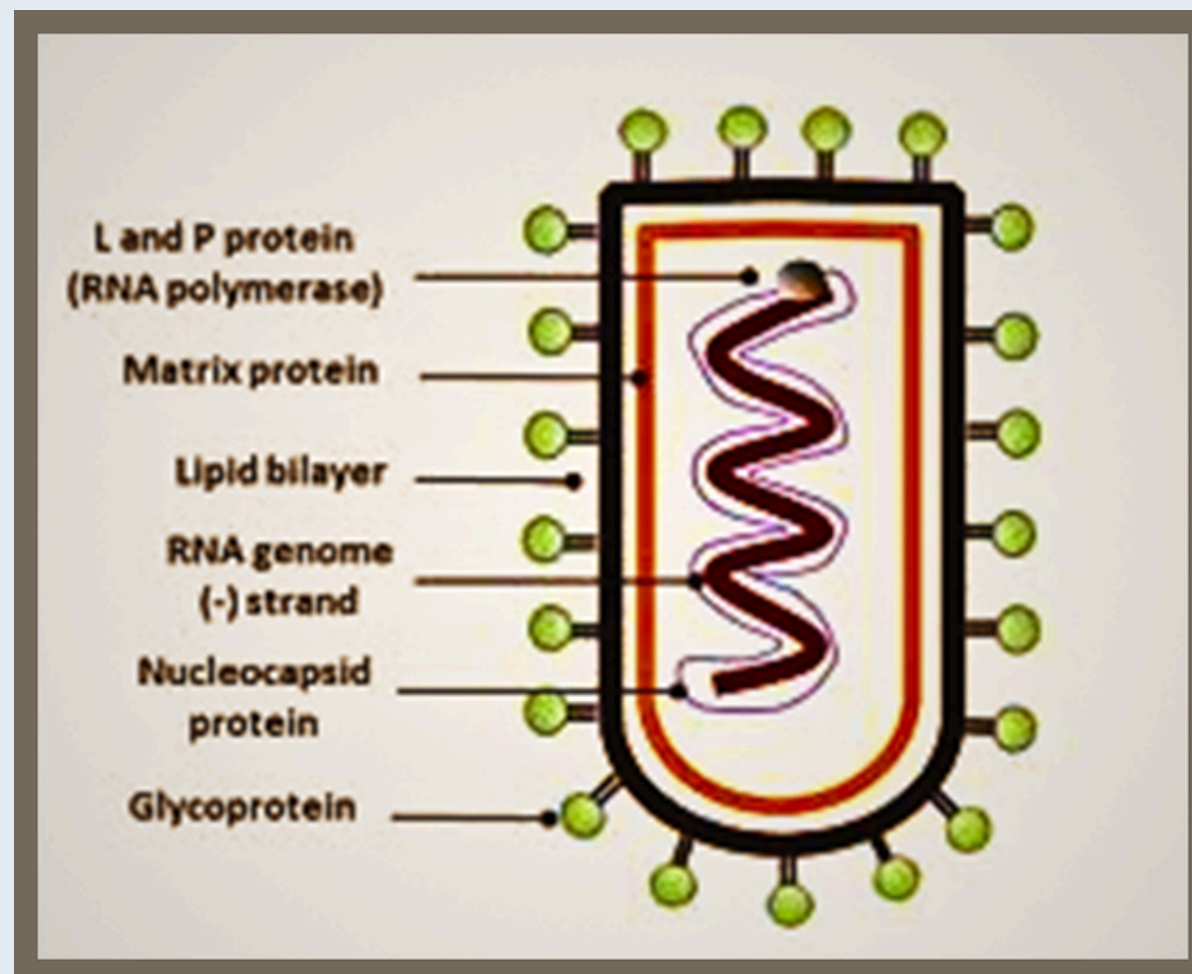


Molecular Characterization of Rabies Virus in Thailand, 2022–2025



Background

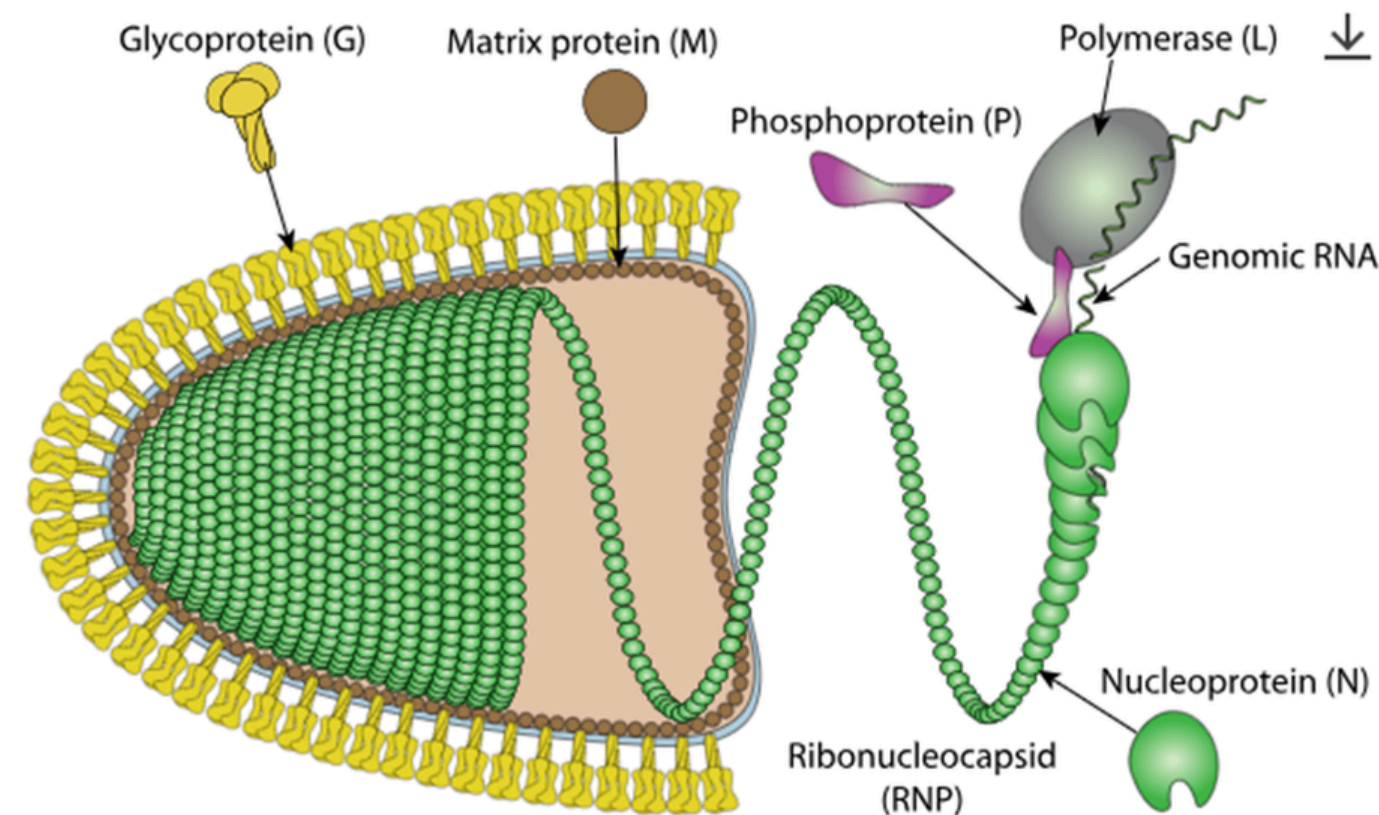
Rabies virus



Lyssavirus (taxid:11286)

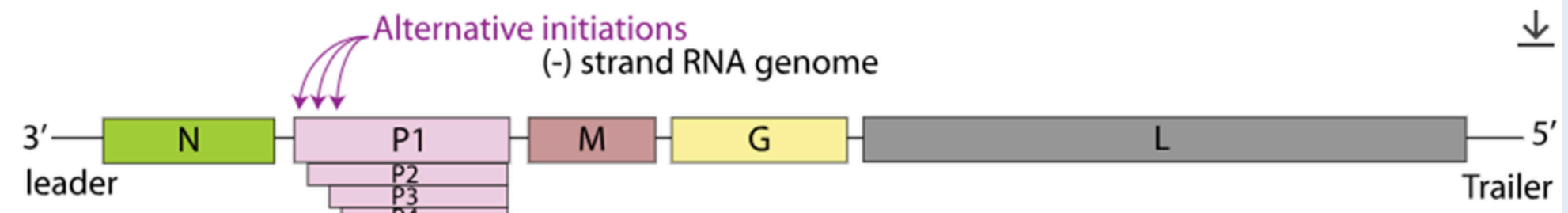
Lyssavirus is a genus of ssRNA- viruses in the family *Rhabdoviridae* that infect neurons of mammals. Rabies virus (RabV) infections in humans are associated with Rabies fatal encephalitis.

VIRION



Enveloped, bullet shaped. 180 nm long and 75 nm wide.

GENOME



TAXONOMY

Group V: Negative sense ssRNA viruses

Realm: *Riboviria*
Kingdom: *Orthornavirae*
Phylum: *Negarnaviricota*
Subphylum: *Haploviricotina*
Class: *Monjiviricetes*
Order: *Mononegavirales*
Family: *Rhabdoviridae*
Genus: *Lyssavirus*

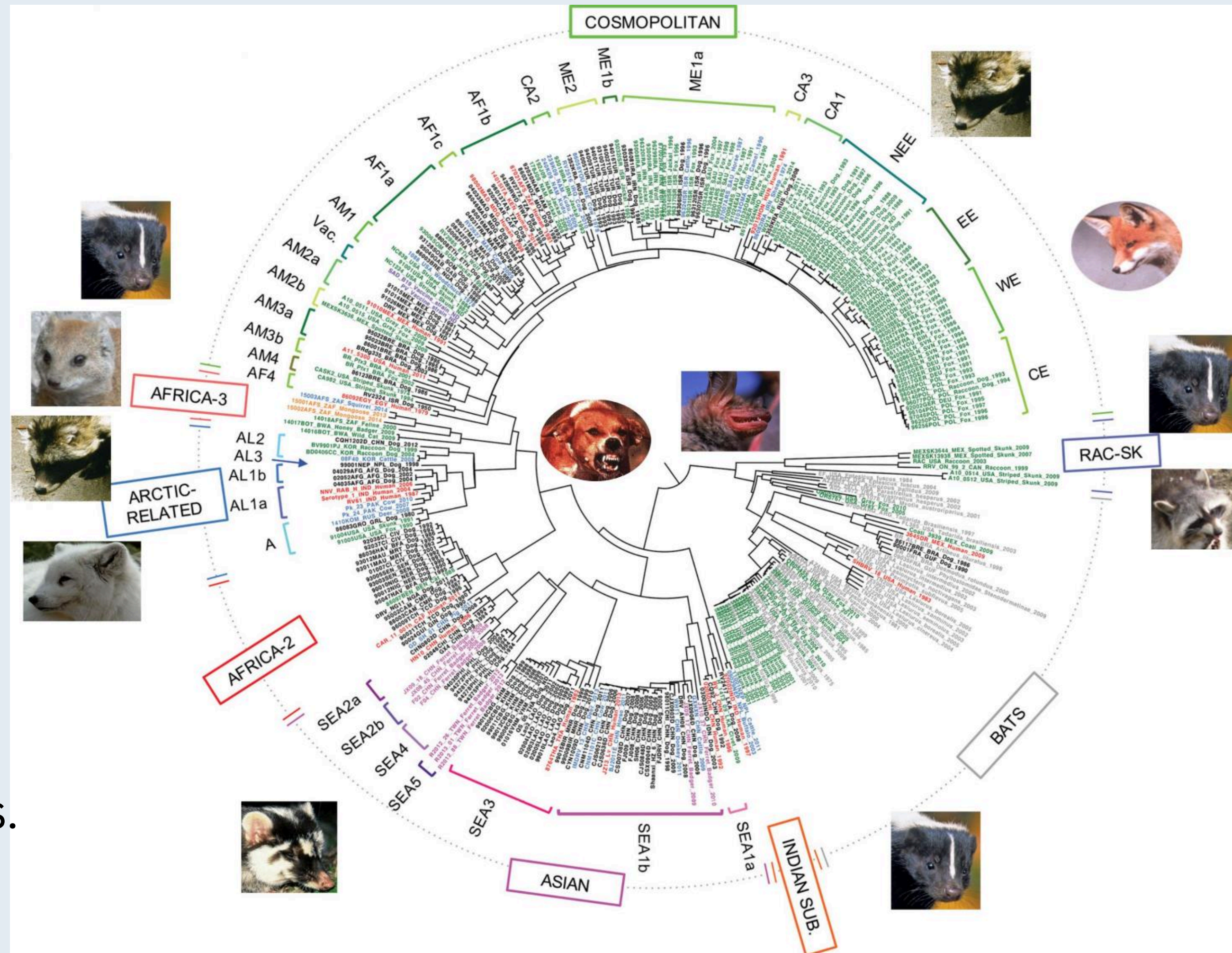
Two major groups of rabies virus

1. bat-related RABV

- RAC-SK
- bat clades

2. dog-related RABV

- Africa-2
- Africa-3
- Arctic-related
- Asian
- Indian subcontinent
- Cosmopolitan clades.



Molecular Characterization of Rabies Virus in Thailand, 2022–2025



- Project Goal:

Analyze up-to-date epidemiological data and genetic characteristics of rabies viruses in animals within Thailand. Utilize this information to develop comprehensive strategies for controlling, preventing, and ultimately eradicating rabies in the country.



- Objectives:

1. To update the epidemiological of rabies viruses from animals in Thailand which will be used as information for planning effectively to prevent and control rabies.
2. To update the genetic characteristics of rabies viruses from animals in Thailand.

Pilot Project: Whole Genome Sequencing

Design targeted primer for Rabies



Experiment to find the optimal PCR conditions

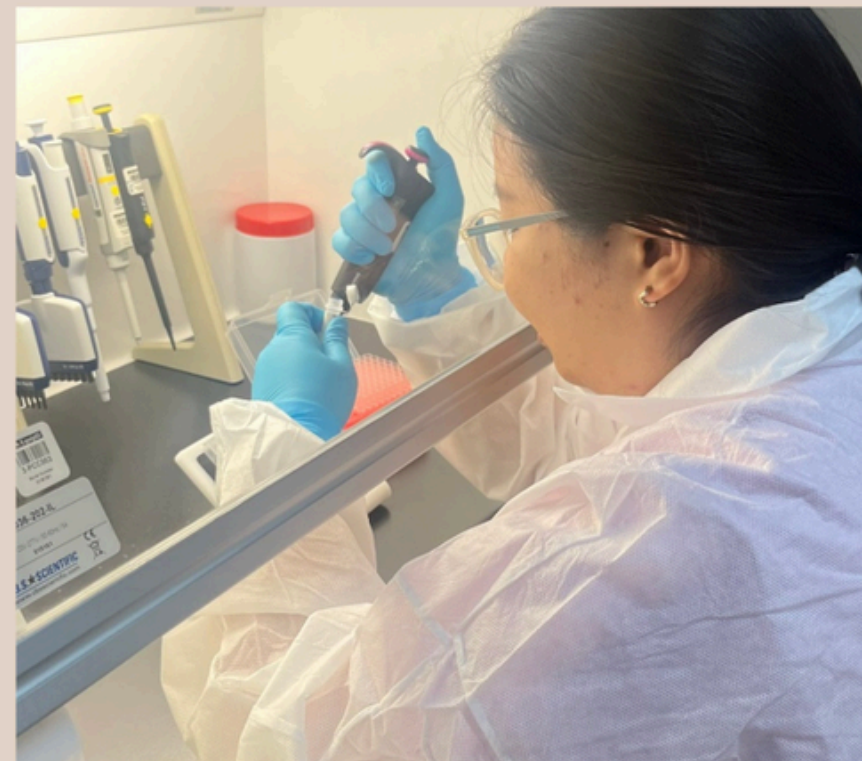
(sample from NIAH → extraction → PCR)



Genome sequencing (Oxford nanopore)



The goal is to include 5–6 samples, representing each region of Thailand.



Core Plan

Animal brain samples: positive with DFA from NIAH & VRDCs



RNA Extraction & Case confirmation by
Real-time RT-PCR



Select high-quality samples with low Ct value
covering the entire country of Thailand



PCR & Genome sequencing (ONT) 100 samples



Summary and analysis of data



Organize stakeholder meetings to close the project



& Infographic media publication on NIAH website

December 2024
pilot study at DGHP,
CDC, Thailand

Total
samples

Rabies DFA +	Dog	Cat	Cattle	Bafalo	Sheep	Golden jakal (Fox)	Total
NIAH	10						10
VRDS Lampang	12						12
VRDC Phitsanulok	7						7
VRDC Khon Khan	12					2	14
VRDC Surin	6		8	4			18
VRDC Chonburi	8	3	5		1		17
VRDC Rachaburi	7						7
VRDC Nakorn Si Thammarat	10		5				15
Total	72	3	18	4	1	2	100

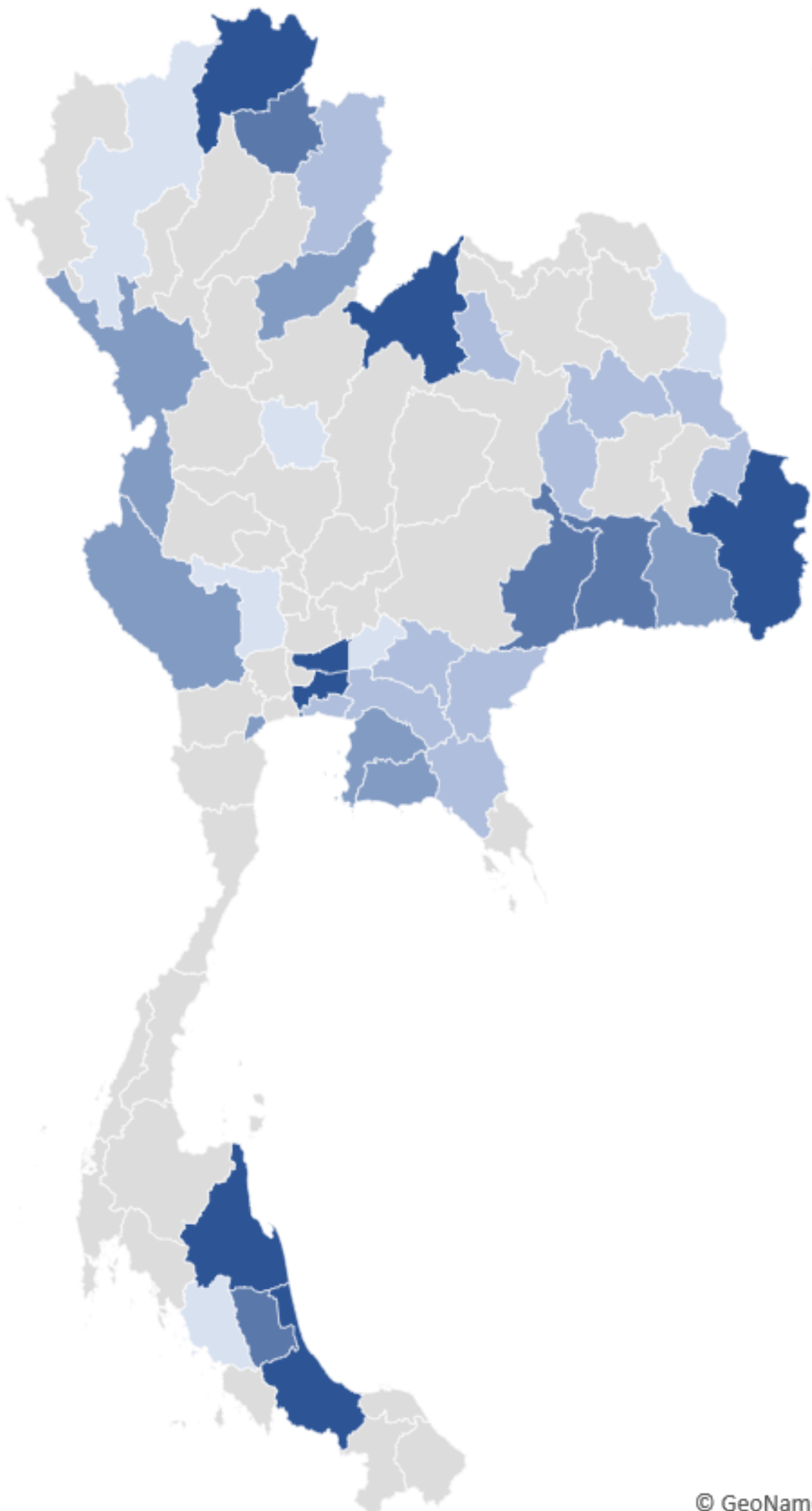
MappingNameAmount

Bangkok	5
Krabi	
Kanchanaburi	3
Kalasin	2
Kamphaeng Phet	
Khon Kaen	
Chanthaburi	2
Chachoengsao	2
Chonburi	3
Chainat	
Chaiphum	
Chumphon	
Chiang Mai	1
Chiang Rai	5
Trang	1
Trat	
Tak	3
Nakhon Nayok	1
Nakhon Pathom	
Nakhon Phanom	1
Nakhon Ratchasima	
Nakhon Si Thammarat	5
Nakhon Sawan	
Nonthaburi	
Narathiwat	
Nan	2
Bueng Kan	
Buriram	4
Pathum Thani	5
Prachuap Khiri Khan	
Prachinburi	2
Pattani	
Phra Nakhon Si Ayutthaya	
Phayao	4
Phang Nga	
Phatthalung	4
Phichit	1
Phitsanulok	
Phetchaburi	
Phetchabun	
Phrae	
Phuket	
Maha Sarakham	2
Mukdahan	2
Mae Hong Son	
Yasothon	
Yala	
Roi Et	
Ranong	
Rayong	3
Ratchaburi	
Lopburi	
Lampang	

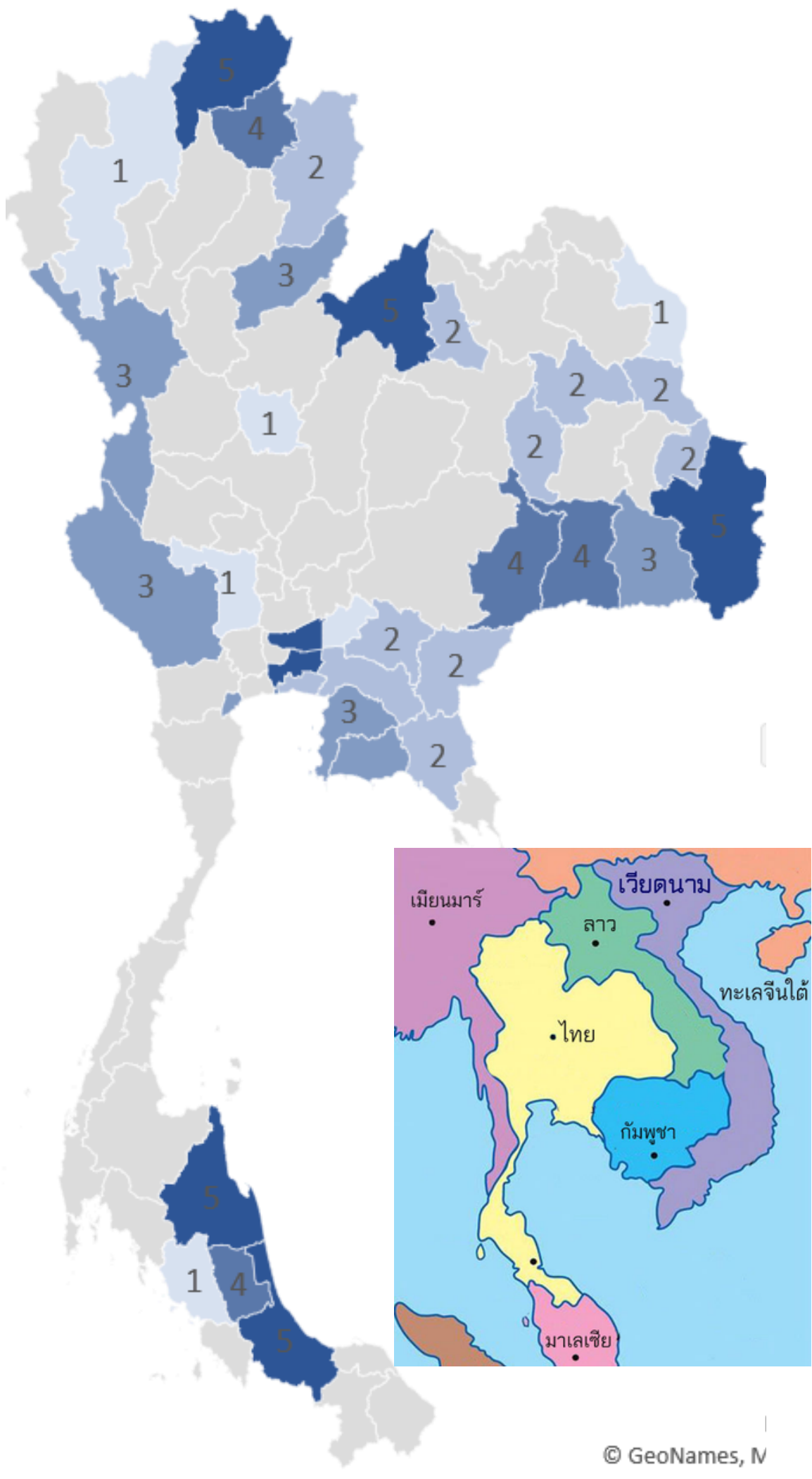
Lamphun	
Loei	5
Sisaket	3
Sakon Nakhon	
Songkhla	5
Satun	
Samut Prakan	2
Samut Songkhram	3
Samut Sakhon	
Sa Kaeo	2
Saraburi	
Sing Buri	
Sukhothai	
Suphan Buri	1
Surat Thani	
Surin	4
Nong Khai	
Nong Bua Lamphu	2
Ang Thong	
Amnat Charoen	2
Udon Thani	
Uttaradit	3
Uthai Thani	
Ubon Ratchathani	5

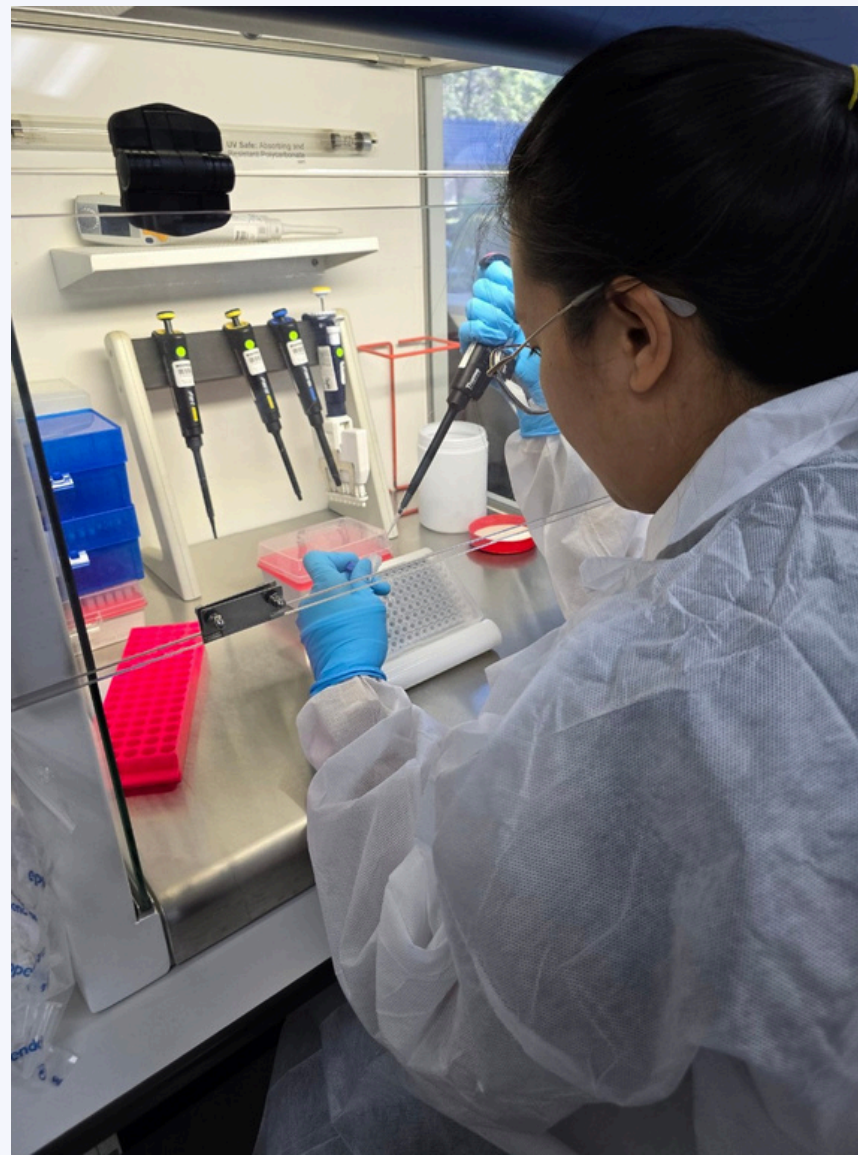
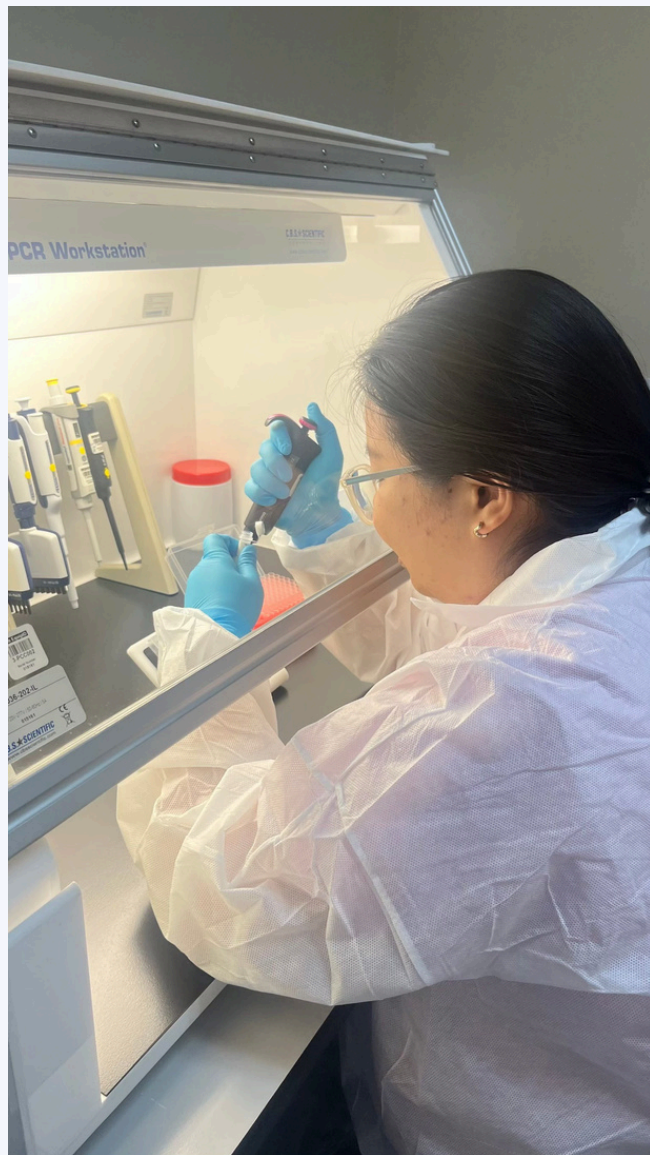
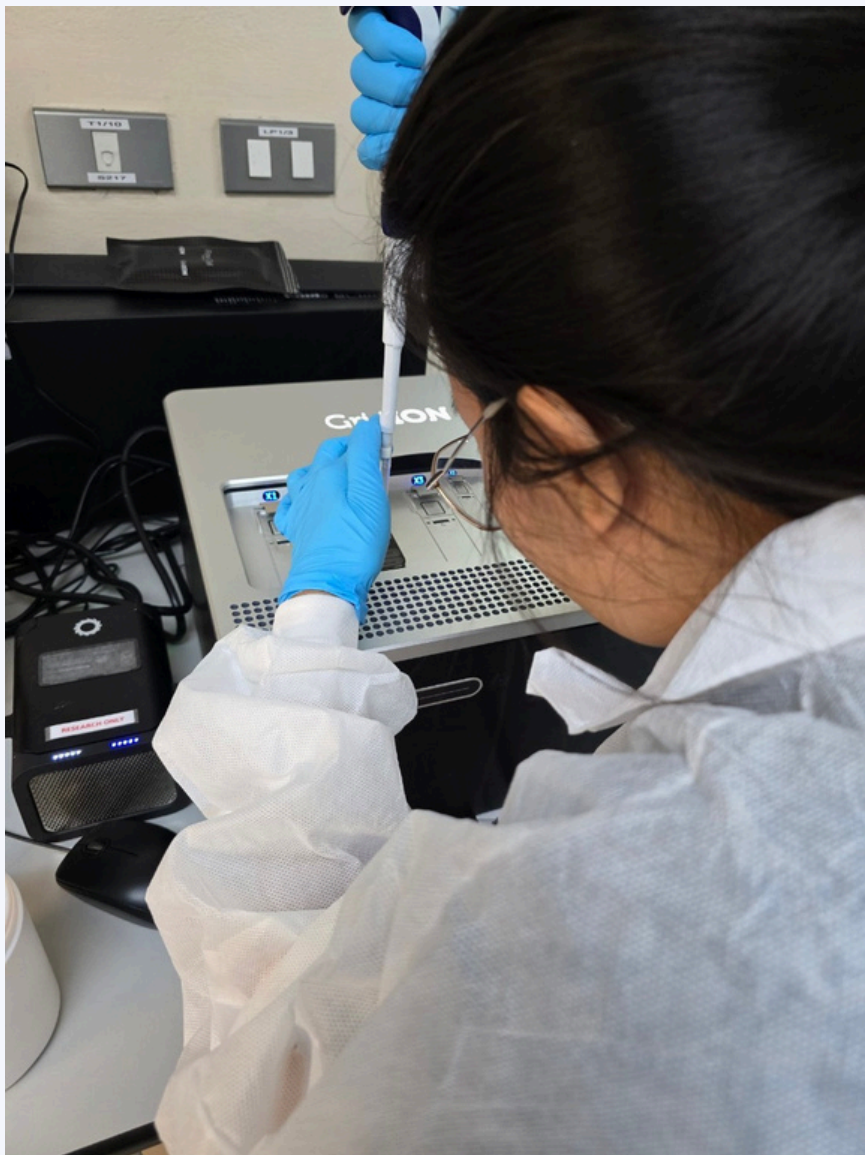
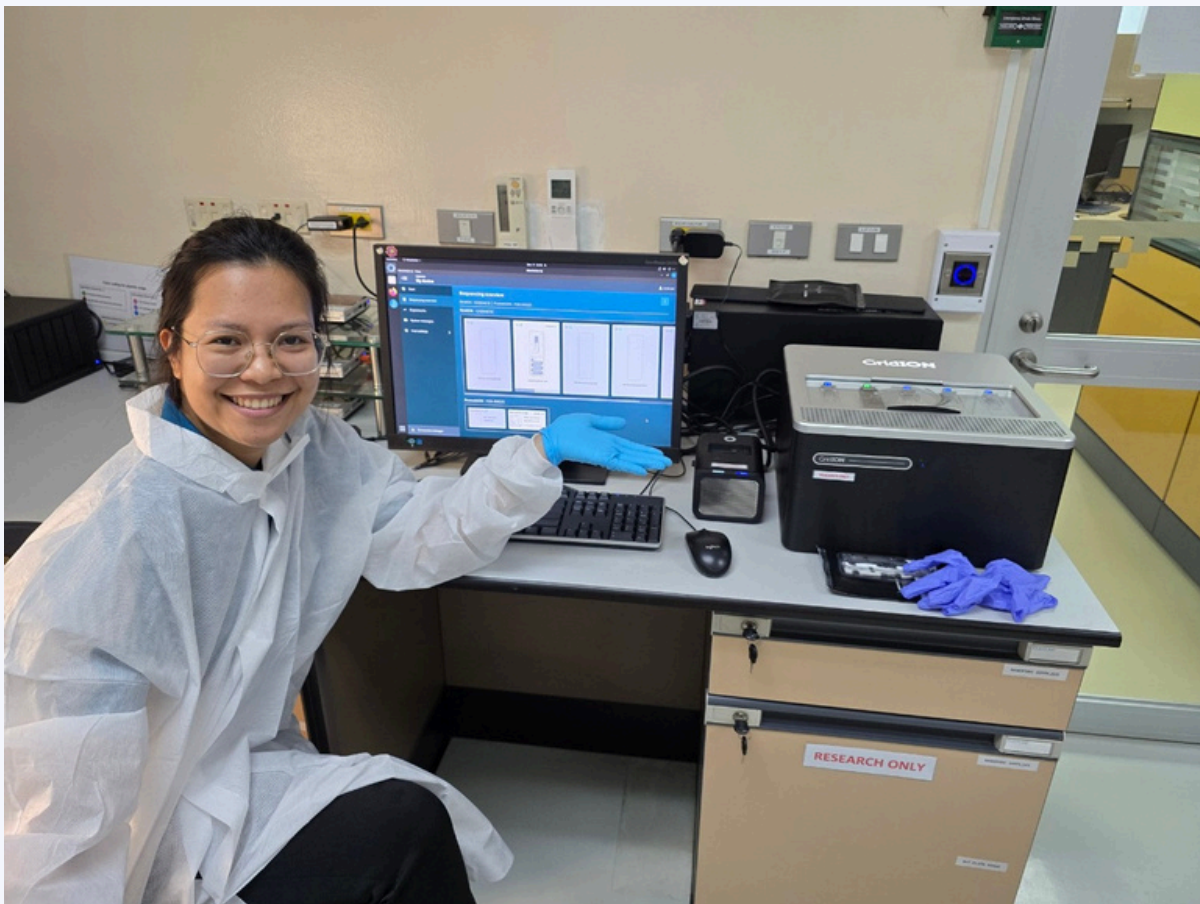
100

100 samples
from 35 provinces

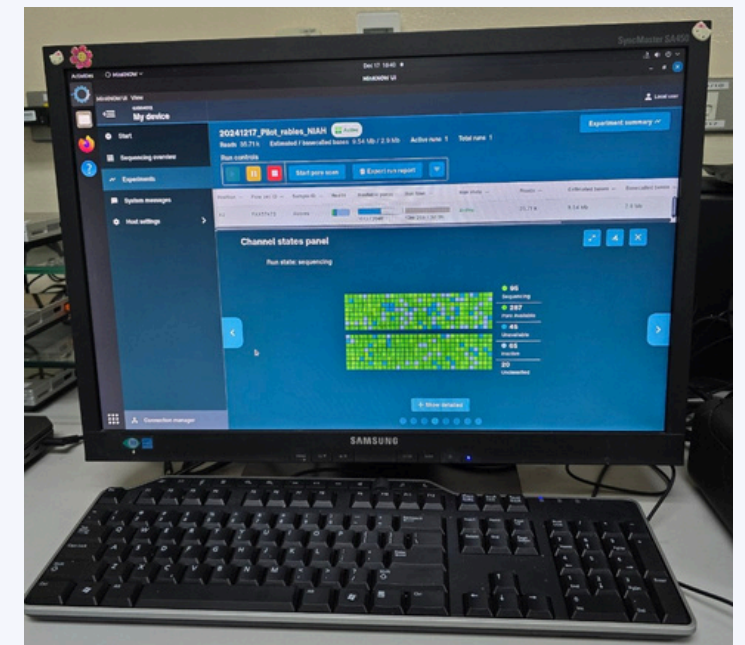


Amount

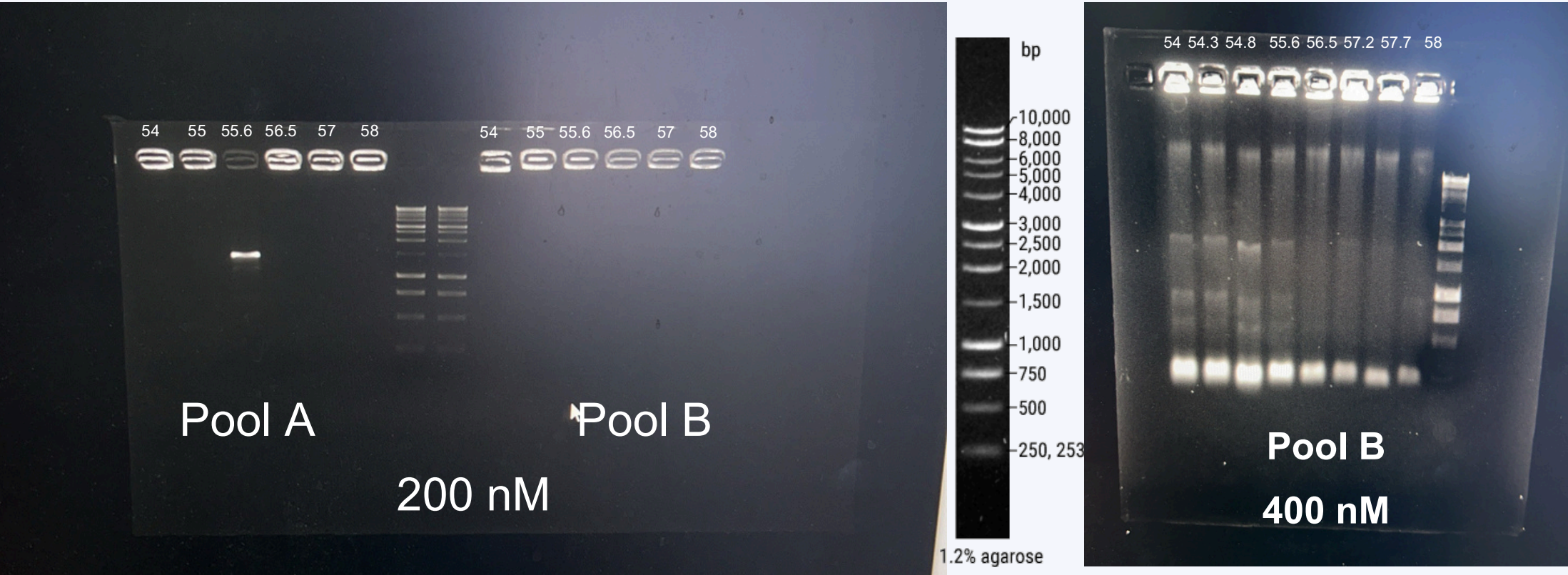




Pilot study at DGHP, CDC Thailand



Optimize primer concentration



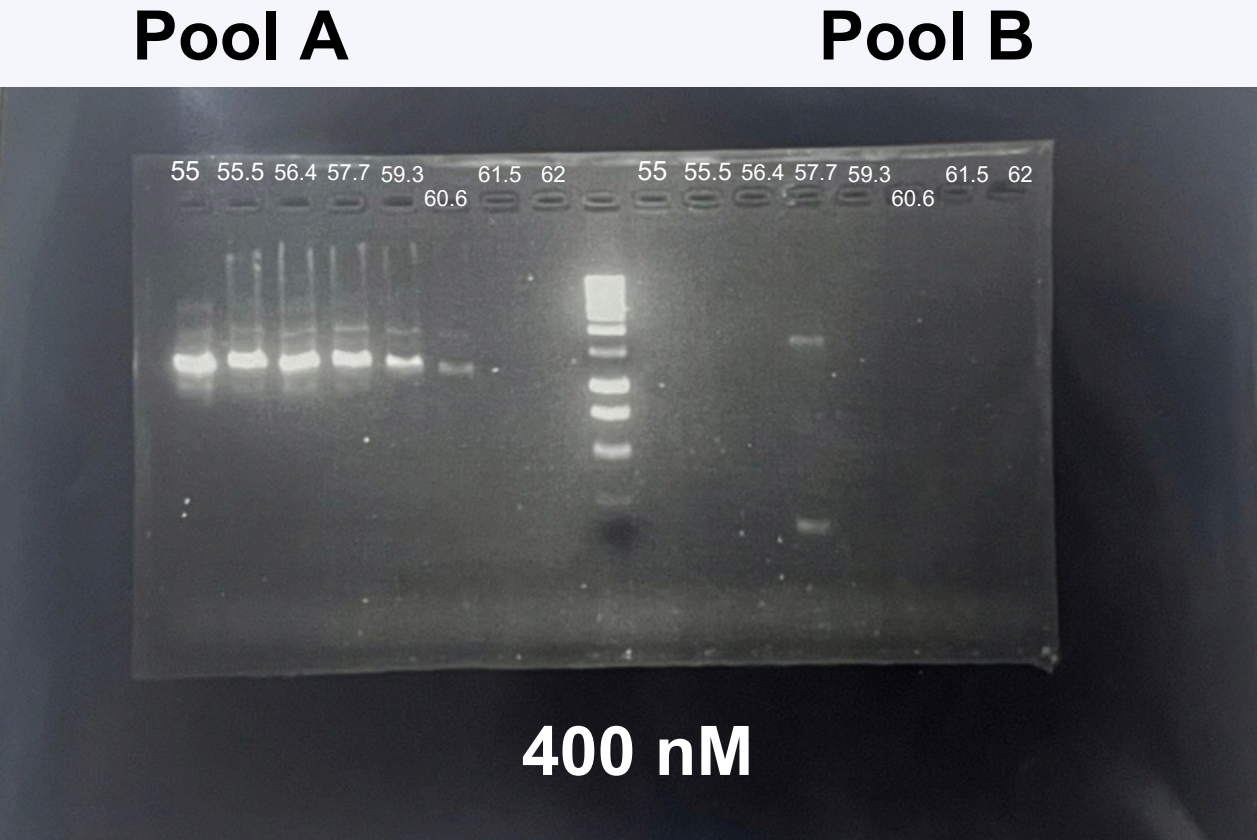
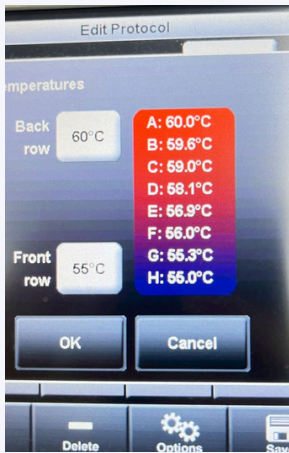
RT-PCR Component (25 uL/rxn)

2X reaction Mix	10 uL
Superscript III/Platinum Taq	1 uL
Primer pool A or B	0.5 (200nM) or 1 uL (400 nM)
RNA template	5 uL
Nuclease free water	up to 25 uL

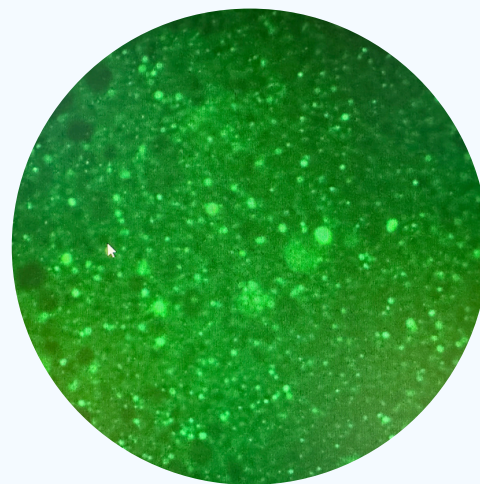
- Thermal cycler**
- cDNA synthesis and pre-denaturation (1 cycle)**
55 °C 30 minutes
94 °C 2 minutes
 - PCR step (35 cycles)**
94 °C 30 seconds
55-62 °C 30 minutes
68 °C 1 minutes
 - Final Extension (1 cycle)**
68 °C 5 mins



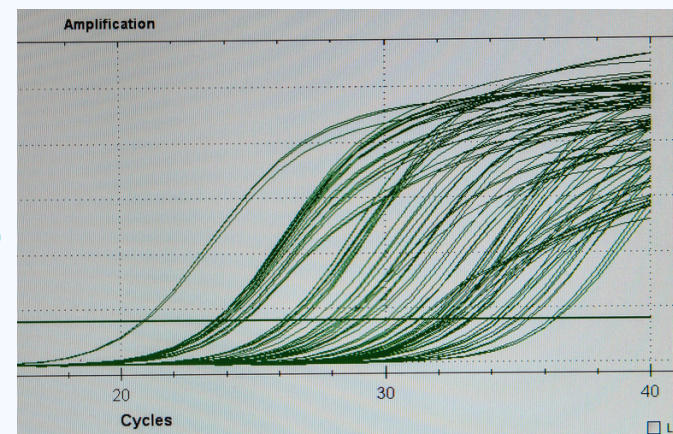
- Thermal cycler**
- cDNA synthesis and pre-denaturation (1 cycle)**
55 °C 30 minutes
94 °C **5 minutes**
 - PCR step (35 cycles)**
94 °C 30 seconds
55-62 °C **1 minute**
68 °C **1.30 minutes**
 - Final Extension (1 cycle)**
68 °C **8 minutes**



Material & Methods



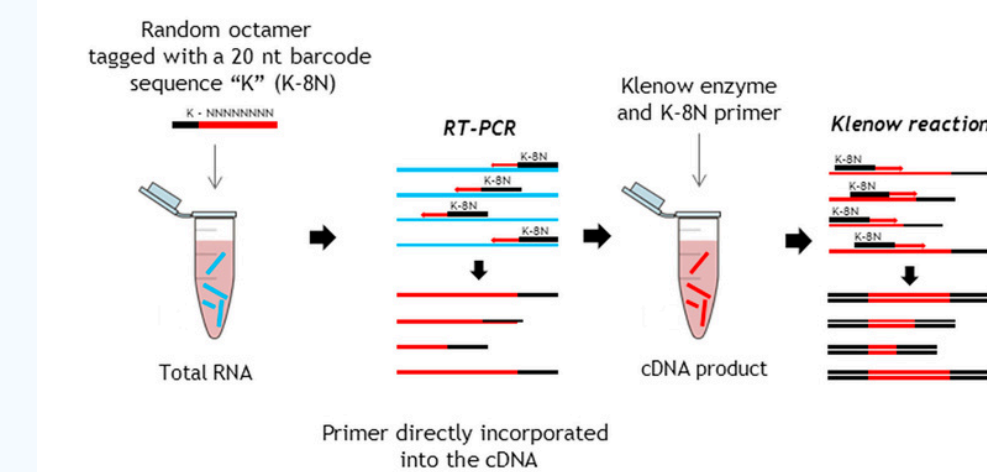
samples confirmed positive for rabies by DFA test



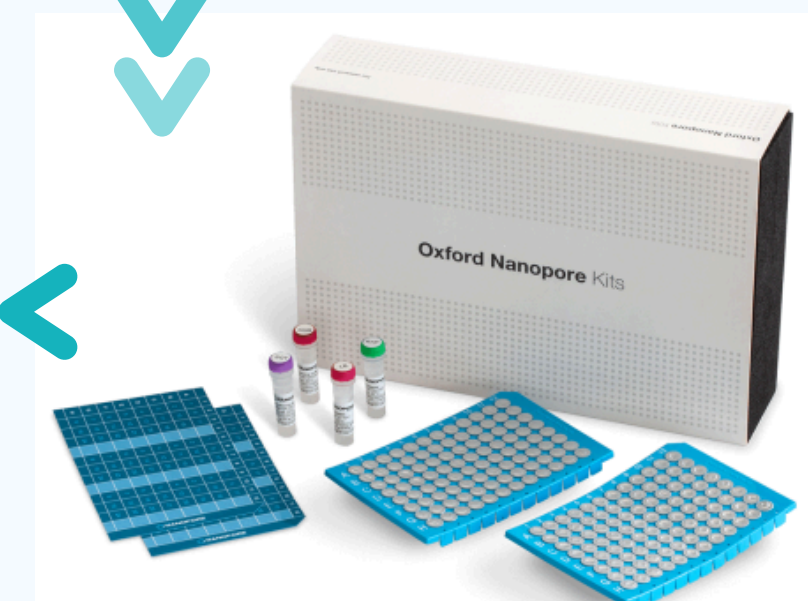
RNA was extracted and confirmed by real-time PCR.



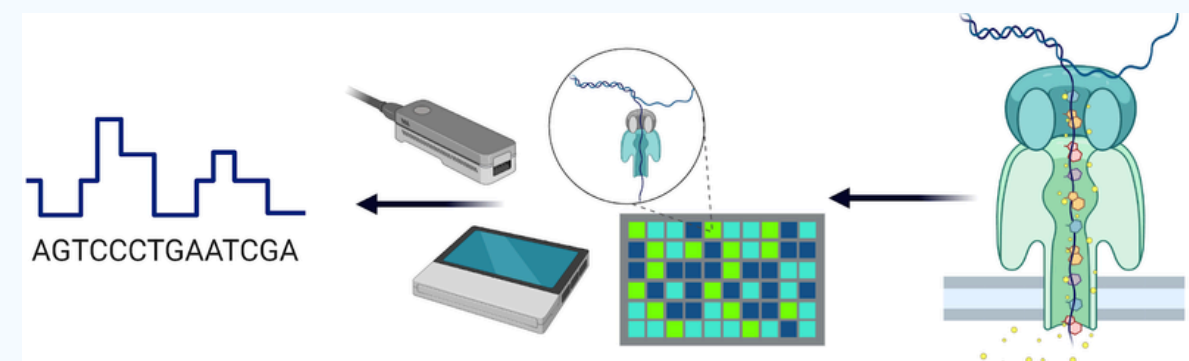
Sequence-independent, single-primer amplification (SISPA)



Enrichment by SISPA-technique



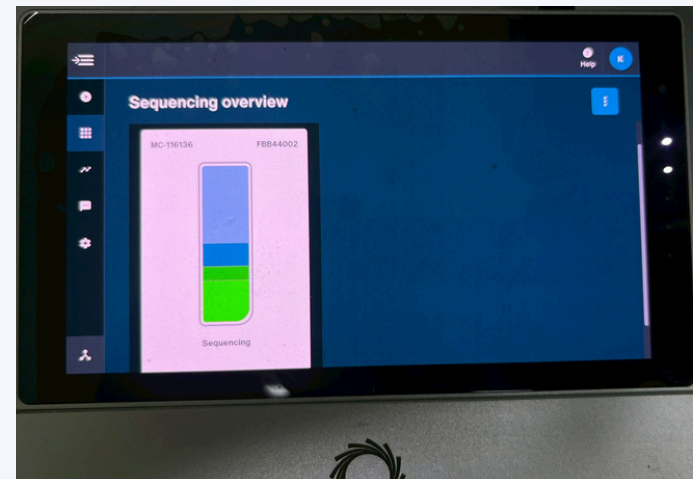
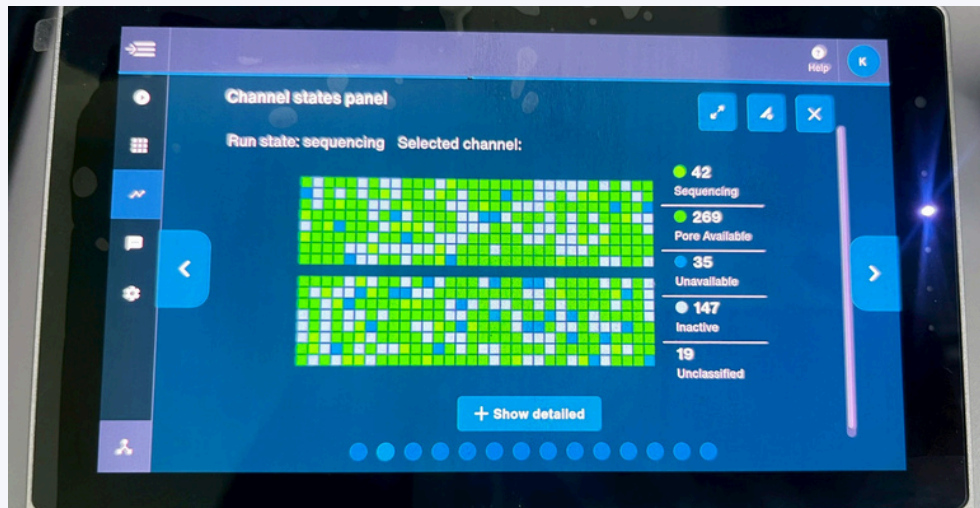
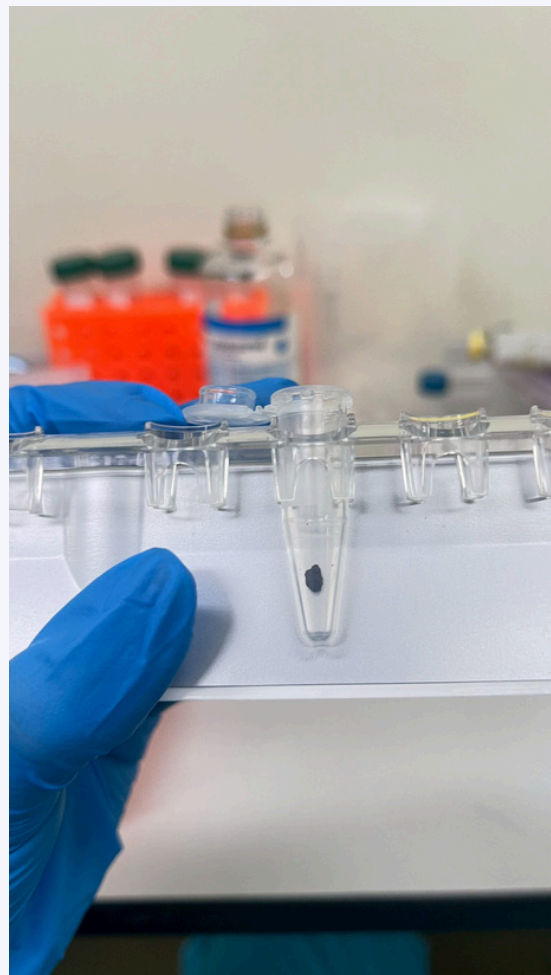
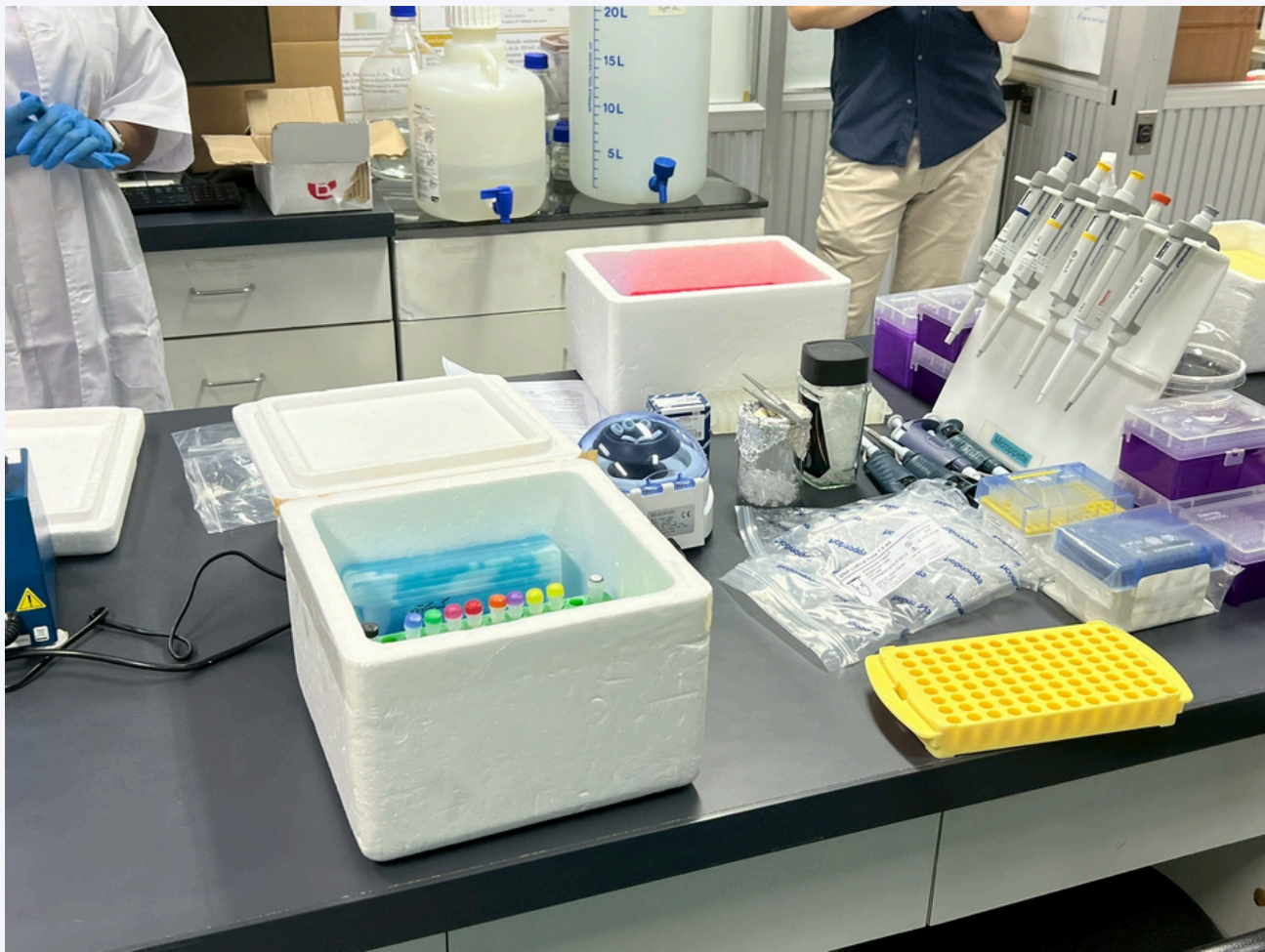
Library preparation (Rapid Barcoding kit)



sequencing by Oxford Nanopore (Mk1c)



Bioinformatics analysis: Command line



N gene

Asian SEA 1

Asian SEA 2

Asian SEA 3

Cosmopolitan

Arctic

Africa-3

Africa-2

Bat Rac-SK

G gene

Asian SEA 2

Asian SEA 1

Asian SEA 3

Cosmopolitan

Africa-3

Arctic

Africa-2

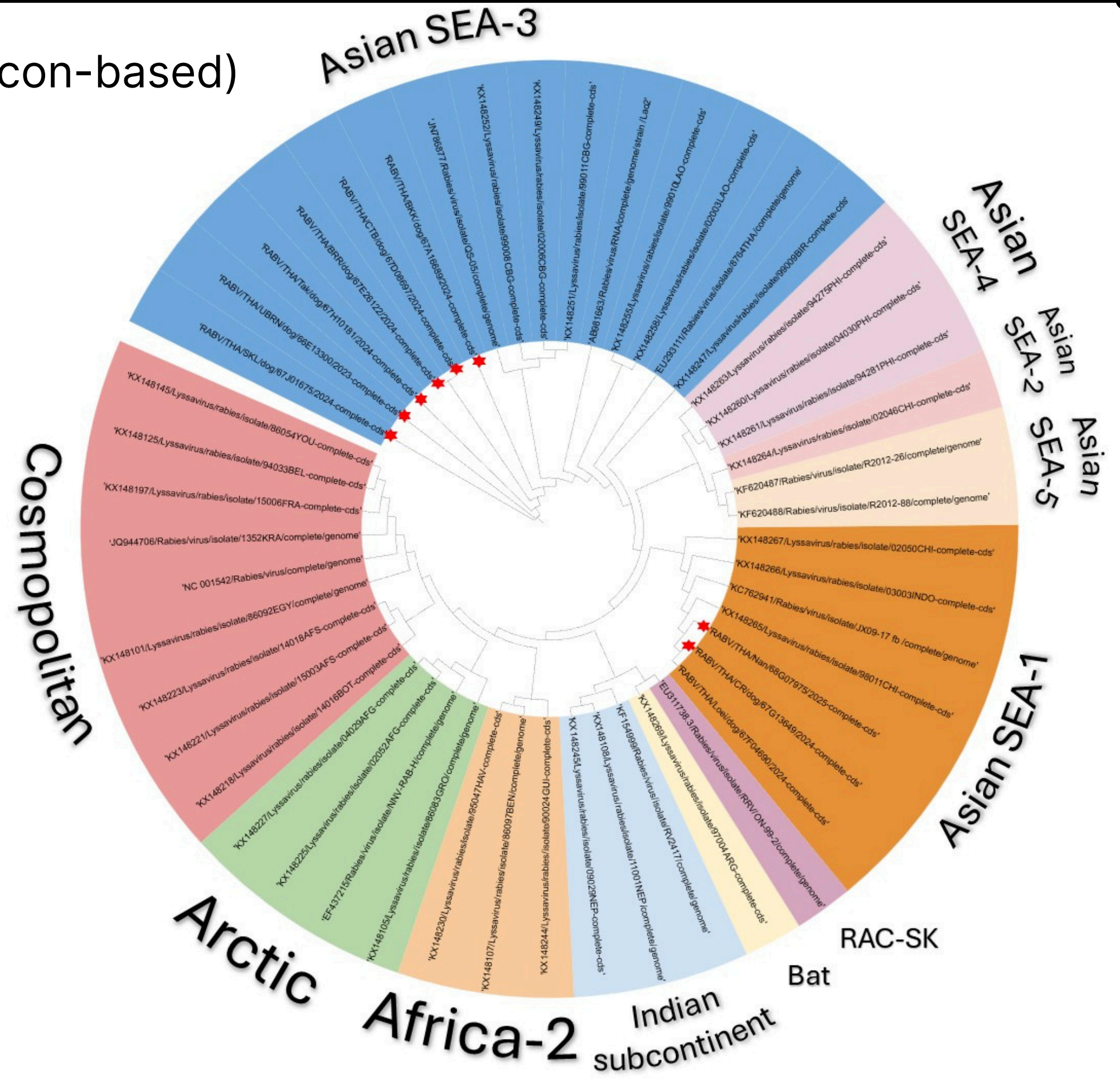
Bat Rac-SK

Whole genome sequencing (WGS)

No.	Sample ID	Specimen type	Ct value	Date collected (DD-MM-YYYY)	Location (Province)	% Identity (Accession no.)
1	RABV/THA/Nan/dog/68G01975/2025-complete-cds	Brain	14.5	17/02/2025	Nan	99.52% Lyssavirus rabies D171 viral cRNA, complete genome/ Viet Nam (LC867589.1)
2	RABV/THA/CR/dog/67G13649/2024-complete-cds	Brain	13.38	28-08-2024	Chiang Rai	99.48% Lyssavirus rabies D159 viral cRNA, complete genome/ Viet Nam (LC867588.1)
3	RABV/THA/BKK/dog/67A16689/2024-complete-cds	Brain	14.44	3/12/2024	Bangkok	98.50% Lyssavirus rabies isolate RABV/TH/382/2010, complete genome, Thailand (ON808418.1)
4	RABV/THA/UBRN/dog/66E13300/2023-complete-cds	Brain	17.08	20-02-2023	Ubon Ratchathani	99.45% Lyssavirus rabies isolate RABV/TH/382/2010, complete genome, Thailand (ON808418.1)
5	RABV/THA/CTB/dog/67D08697/2024-complete-cds	Brain	18.68	14-03-2024	Chanthaburi	99.37% Lyssavirus rabies isolate Y127, partial genome, Cambodia; Kampong Sambuor (OP515296.1)
6	RABV/THA/BRR/dog/67E26122/2024-complete-cds	Brain	12.72	16-10-2024	Buri Ram	99.49% MAG: Lyssavirus rabies isolate human/Thailand/RB11/2023, complete genome, Thailand; Surin (PP700503.1)
7	RABV/THA/Tak/dog/67H10181/2024-complete-cds	Brain	15.98	12/5/2024	Tak	99.54% Lyssavirus rabies isolate RABV/TH/382/2010, complete genome, Thailand (ON808418.1)
8	RABV/THA/SKL/dog/67J01675/2024-complete-cds	Brain	16.67	19-01-2024	Song Kla	99.42% Lyssavirus rabies isolate RABV/TH/382/2010, complete genome, Thailand (ON808418.1)

Phylogenetic tree

Whole Genome Sequencing (amplicon-based)



Antigenic site epitopes of G-gene

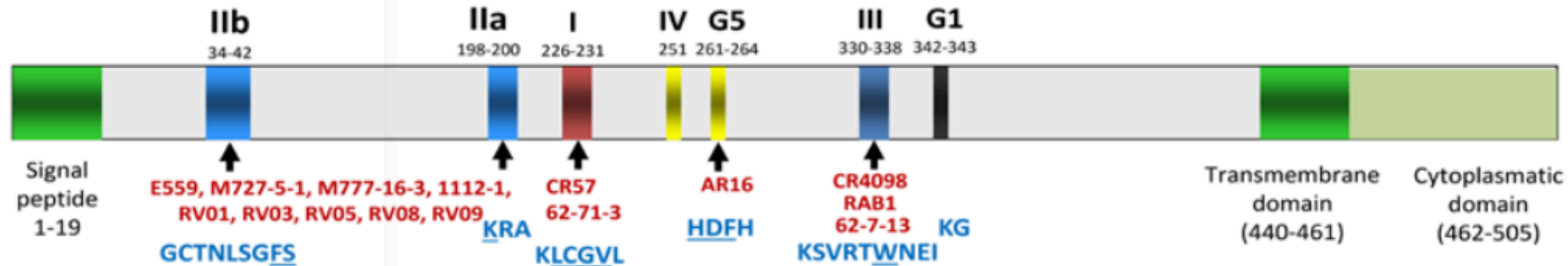
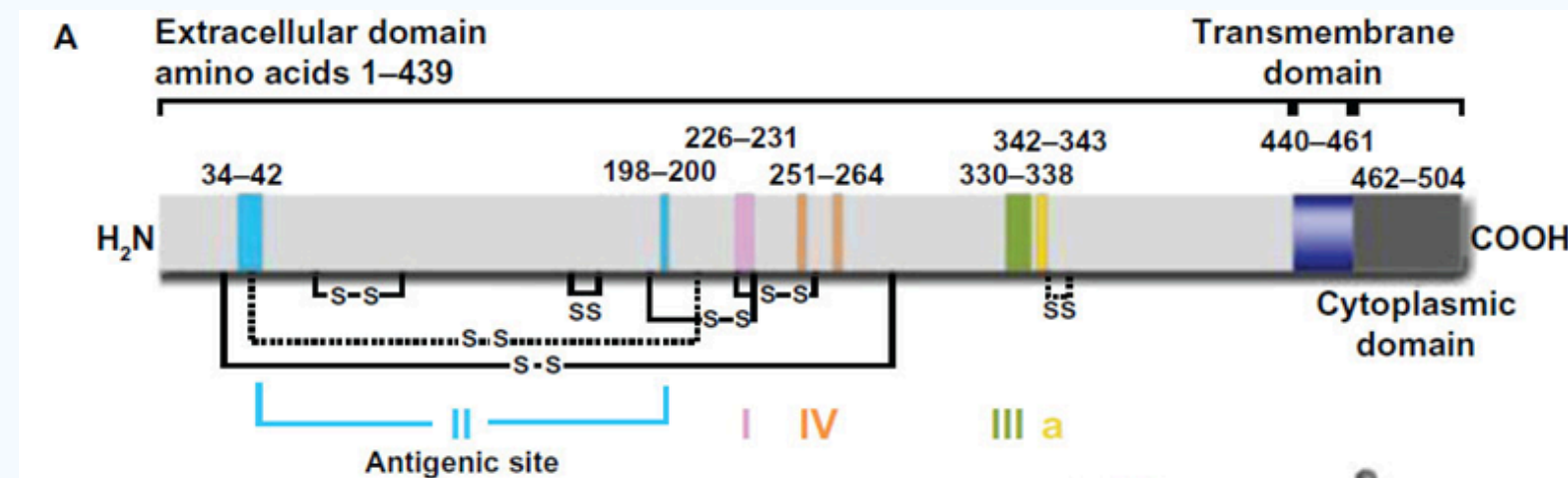
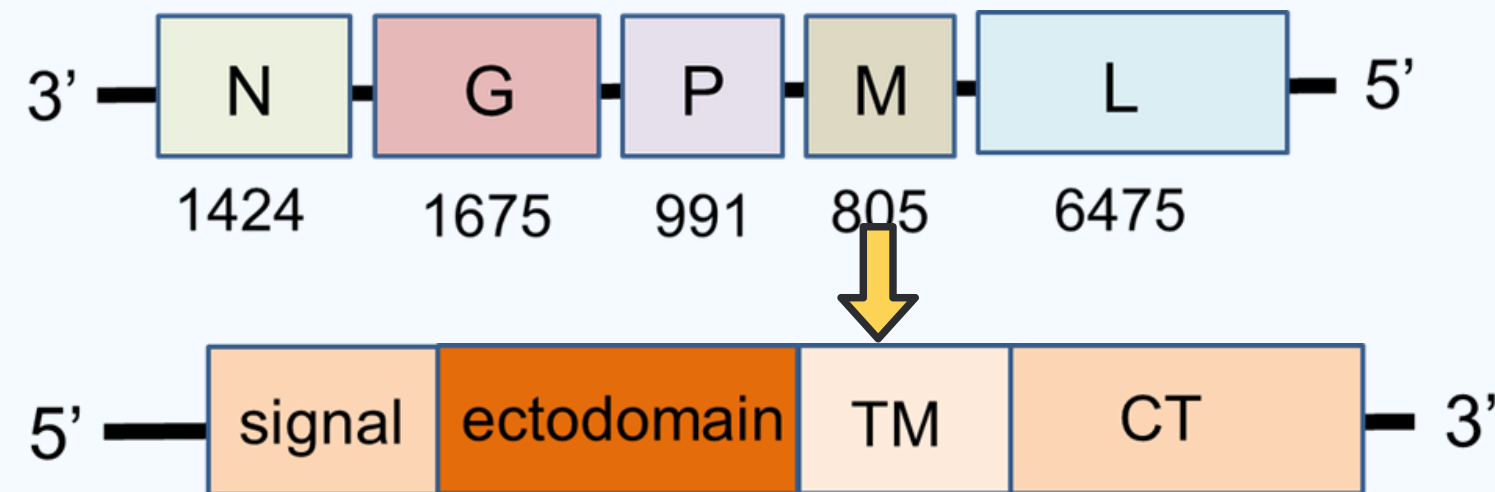
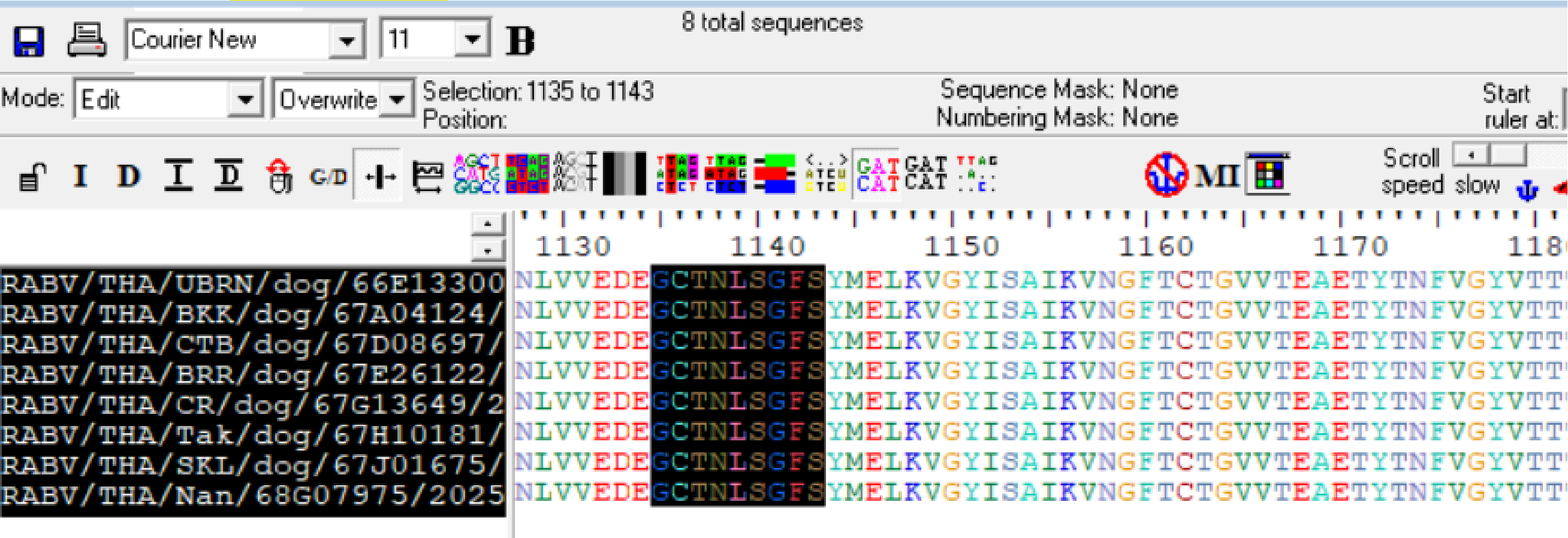


Figure 1: Schematic representation of the RV glycoprotein. Major antigenic sites and their amino acid positions are shown above the bar. Arrows indicate MAb epitopes within antigenic sites. The MAbs addressed in this study are shown in red. Consensus amino acid sequences of the antigenic sites are shown in blue. Underlined residues are invariable.

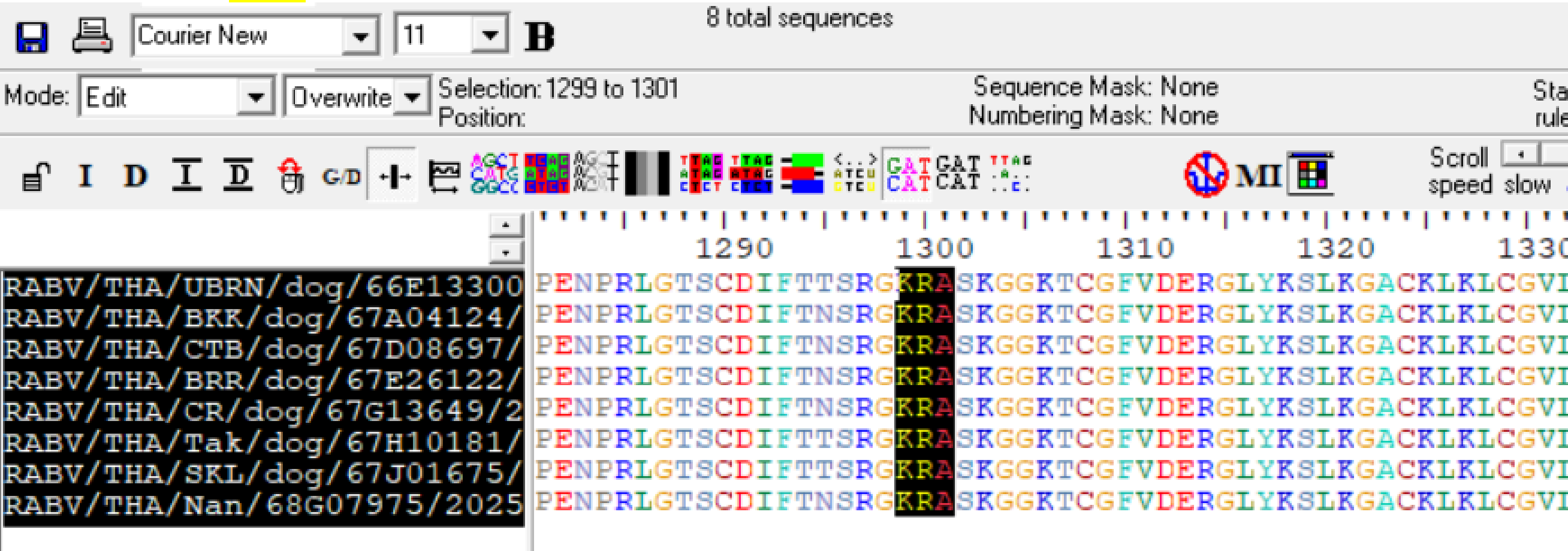


Epitopes	Position	AA seq.
IIb	34-42	GCTNLSG <u>F</u> S
IIa	198-200	<u>K</u> RA
I	226-231	K <u>L</u> C <u>G</u> V <u>L</u>
IV	251	W
G5	261-264	<u>H</u> D <u>F</u> H
III	330-338	KSVRT <u>W</u> NEI
G1	342-343	KG

Epitope IIb: GCTNLSGFS



Epitope IIa: KRA



Epitope I: KLCGVL

8 total sequences

Mode: Edit Overwrite Selection: 1327 to 1332 Position: Sequence Mask: None Numbering Mask: None Start ruler a

Scroll speed slow

	1310	1320	1330	1340	1350
RABV/THA/UBRN/dog/66E13300	KGGKTCGFVDERGLYKSLKGACKL	KLCGVL	GLRLMDGTWAAIQTSDEAKWCPP		
RABV/THA/BKK/dog/67A04124/	KGGKTCGFVDERGLYKSLKGACKL	KLCGVL	GLRLMDGTWVAIQTSDEIKWCSP		
RABV/THA/CTB/dog/67D08697/	KGGKTCGFVDERGLYKSLKGACKL	KLCGVL	GLRLMDGTWAAIQTSDEAKWCPP		
RABV/THA/BRR/dog/67E26122/	KGGKTCGFVDERGLYKSLKGACKL	KLCGVL	GLRLMDGTWAAIQTSDEAKWCPP		
RABV/THA/CR/dog/67G13649/2	KGGKTCGFVDERGLYKSLKGACKL	KLCGVL	GLRLMDGTWVAIQTSDEIKWCSP		
RABV/THA/Tak/dog/67H10181/	KGGKTCGFVDERGLYKSLKGACKL	KLCGVL	GLRLMDGTWAAIQTSDEAKWCPP		
RABV/THA/SKL/dog/67J01675/	KGGKTCGFVDERGLYKSLKGACKL	KLCGVL	GLRLMDGTWAAIQTSDEAKWCPP		
RABV/THA/Nan/68G07975/2025	KGGKTCGFVDERGLYKSLKGACKL	KLCGVL	GLRLMDGTWVAIQTSDEIKWCSP		

Epitope IV: W

8 total sequences

Mode: Edit Overwrite Selection: 1352 Position: Sequence Mask: None Numbering Mask: None Start ruler .

Scroll speed slow

	1320	1330	1340	1350	1360	137
RABV/THA/UBRN/dog/66E13300	SLKGACKL	KLCGVL	GLRLMDGTWAAIQTSDEAKW	CPPDQLVNIHDFRSDEIEH		
RABV/THA/BKK/dog/67A04124/	SLKGACKL	KLCGVL	GLRLMDGTWVAIQTSDEIKW	CSPDQLVNLHDFHSDEIEH		
RABV/THA/CTB/dog/67D08697/	SLKGACKL	KLCGVL	GLRLMDGTWAAIQTSDEAKW	CPPDQLVNIHDFRSDEIEH		
RABV/THA/BRR/dog/67E26122/	SLKGACKL	KLCGVL	GLRLMDGTWAAIQTSDEAKW	CPPDQLVNIHDFRSDEIEH		
RABV/THA/CR/dog/67G13649/2	SLKGACKL	KLCGVL	GLRLMDGTWVAIQTSDEIKW	CSPDQLVNLHDFHSDEIEH		
RABV/THA/Tak/dog/67H10181/	SLKGACKL	KLCGVL	GLRLMDGTWAAIQTSDEAKW	CPPDQLVNIHDFRSDEIEH		
RABV/THA/SKL/dog/67J01675/	SLKGACKL	KLCGVL	GLRLMDGTWAAIQTSDEAKW	CPPDQLVNIHDFRSDEIEH		
RABV/THA/Nan/68G07975/2025	SLKGACKL	KLCGVL	GLRLMDGTWVAIQTSDEIKW	CSPDQLVNLHDFHSDEIEH		

Epitope G5: HDFH --> HDFR (Histidine --> Arginine)

8 total sequences

Mode: Edit Overwrite Selection: 1362 to 1365 Position: Sequence Mask: None Numbering Mask: None Start ruler at:

Scroll speed slow

	1350	1360	1370	1380	1390	1
RABV/THA/UBRN/dog/66E13300	SDEAKWCPPDQLVNI	HDFR	SDEIEHLVVEELVKKREECLDALESIMTTKSVSF			
RABV/THA/BKK/dog/67A04124/	SDEIKWCSPDQLVNL	HDFH	SDEIEHLVVEELVKKREECLDALETIMTTKSVSF			
RABV/THA/CTB/dog/67D08697/	SDEAKWCPPDQLVNI	HDFR	SDEIEHLVVEELVKKREECLDALESIMTTKSVSF			
RABV/THA/BRR/dog/67E26122/	SDEAKWCPPDQLVNI	HDFR	SDEIEHLVVEELVKKREECLDALESIMTTKSVSF			
RABV/THA/CR/dog/67G13649/2	SDEIKWCSPDQLVNL	HDFH	SDEIEHLVVEELVKKREECLDALETIMTTKSVSF			
RABV/THA/Tak/dog/67H10181/	SDEAKWCPPDQLVNI	HDFR	SDEIEHLVVEELVKKREECLDALESIMTTKSVSF			
RABV/THA/SKL/dog/67J01675/	SDEAKWCPPDQLVNI	HDFR	SDEIEHLVVEELVKKREECLDALESIMTTKSVSF			
RABV/THA/Nan/68G07975/2025	SDEIKWCSPDQLVNL	HDFH	SDEIEHLVVEELVKKREECLDALETIMTTKSVSF			

Epitope III: KSVRTWNEI --> KSIRTWNEI (Valine --> Isoleucine)

8 total sequences

Mode: Edit Overwrite Selection: 1431 to 1439 Position: Sequence Mask: None Numbering Mask: None Start ruler at:

Scroll speed slow

	1420	1430	1440	1450	1460	147
RABV/THA/UBRN/dog/66E13300	IFNKTLM EADAHYK	SVRTWNEI	IPSKGCLRVGGRCHPHVNGVFFNGIILGPDGH'			
RABV/THA/BKK/dog/67A04124/	IFNKTLM EADAHYK	SIRTWNEI	IPSKGCLRVGGRCHPHVNGVFFNGIILGPDGH'			
RABV/THA/CTB/dog/67D08697/	IFNKTLM EADAHYK	SVRTWNEI	IPSKGCLRVGGRCHPHVNGVFFNGIILGPDGH'			
RABV/THA/BRR/dog/67E26122/	IFNKTLM EADAHYK	SVRTWNEI	IPSKGCLRVGGRCHPHVNGVFFNGIILGPDGH'			
RABV/THA/CR/dog/67G13649/2	IFNKTLM EADAHYK	SIRTWNEI	IPSKGCLRVGGRCHPHVNGVFFNGIILGPDGH'			
RABV/THA/Tak/dog/67H10181/	IFNKTLM EADAHYK	SVRTWNEI	IPSKGCLRVGGRCHPHVNGVFFNGIILGPDGH'			
RABV/THA/SKL/dog/67J01675/	IFNKTLM EADAHYK	SVRTWNEI	IPSKGCLRVGGRCHPHVNGVFFNGIILGPDGH'			
RABV/THA/Nan/68G07975/2025	IFNKTLM EADAHYK	SIRTWNEI	IPSKGCLRVGGRCHPHVNGVFFNGIILGPDGH'			

Epitope G1: KG

8 total sequences

Mode: Edit Overwrite Selection: 1443 to 1444 Position: Sequence Mask: None Numbering Mask: None Start ruler at:

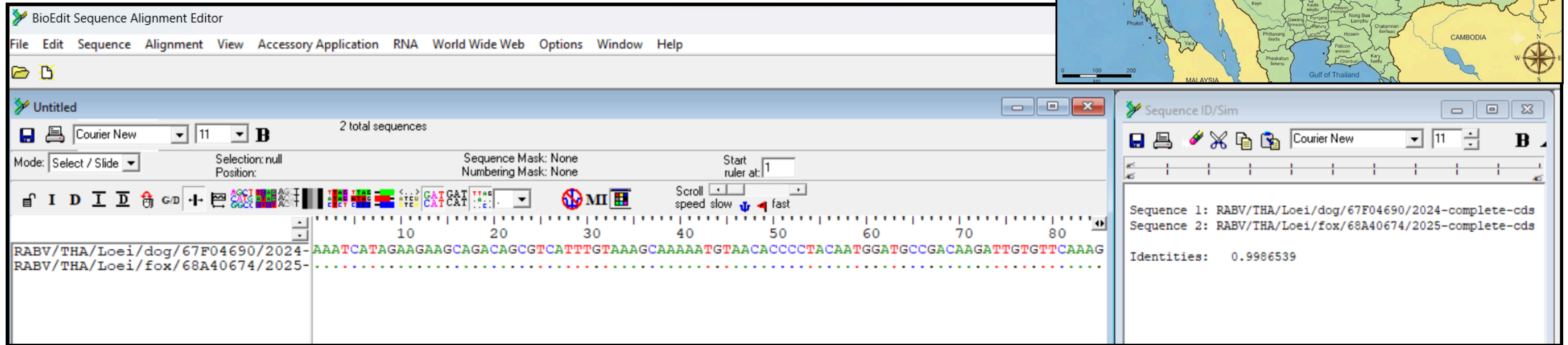
Scroll speed slow

Restor

	1420	1430	1440	1450	1460
RABV/THA/UBRN/dog/66E13300	IFNKTLMEADAHYKSVRTWNEIIPS	KG	CLRVGGRCHPHVNGVFFNGIILGPDGH		
RABV/THA/BKK/dog/67A04124	IFNKTLMEADAHYKSIRTWNEIIPS	KG	CLRVGGRCHPHVNGVFFNGIILGPDGH		
RABV/THA/CTB/dog/67D08697	IFNKTLMEADAHYKSVRTWNEIIPS	KG	CLRVGGRCHPHVNGVFFNGIILGPDGH		
RABV/THA/BRR/dog/67E26122	IFNKTLMEADAHYKSVRTWNEIIPS	KG	CLRVGGRCHPHVNGVFFNGIILGPDGH		
RABV/THA/CR/dog/67G13649/2	IFNKTLMEADAHYKSIRTWNEIIPS	KG	CLRVGGRCHPHVNGVFFNGIILGPDGH		
RABV/THA/Tak/dog/67H10181	IFNKTLMEADAHYKSVRTWNEIIPS	KG	CLRVGGRCHPHVNGVFFNGIILGPDGH		
RABV/THA/SKL/dog/67J01675	IFNKTLMEADAHYKSVRTWNEIIPS	KG	CLRVGGRCHPHVNGVFFNGIILGPDGH		
RABV/THA/Nan/68G07975/2025	IFNKTLMEADAHYKSIRTWNEIIPS	KG	CLRVGGRCHPHVNGVFFNGIILGPDGH		

Mutation	Antigenic site	Type	Likely effect on virulence	Likely effect on vaccine
HDFH → HDFR	G5	Conservative (basic→basic)	Minimal	Minimal, vaccine still effective
KSVRTWNEI → KSI ^R RTWNEI	III	Conservative (hydrophobic→hydrophobic)	Minimal	Minimal, vaccine still effective

SEA1 Rabies virus: Dog–Fox Genetic Link



“Both isolates belong to the SEA1 subclade and share 99.87% nucleotide identity (12 nucleotide differences), indicating a very close genetic relationship.”

“These findings are consistent with viruses circulating within the same transmission lineage, with possible recent cross-species transmission between dog and fox.”



GenBank ▼

GenBank: LC867588.1

[FASTA](#) [Graphics](#)

Go to: 

LOCUS	LC867588	11886 bp	cRNA	linear	VRL 08-JUL-2025
DEFINITION	Lyssavirus rabies D159 viral cRNA, complete genome.				
ACCESSION	LC867588				
VERSION	LC867588.1				
KEYWORDS	.				
SOURCE	Lyssavirus rabies				
ORGANISM	Lyssavirus rabies				

REFERENCE	1
AUTHORS	Harada,M., Nguyen,T.T., Okutani,A., Inoue,S. and Maeda,K.
TITLE	Four genetically distinct types of rabies virus exist in Vietnam, including the SEA1 and SEA3 subclades within Asian clade
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 11886)
AUTHORS	Okutani,A. and Harada,M.
TITLE	Direct Submission
JOURNAL	Submitted (15-APR-2025) Contact: Akiko Okutani National Institute of Infectious Disease, Japan Institute for Health Security, Veterinary Science; 1-23-1 Toyama, Shinjyuku, Tokyo 162-8640, Japan

```
COMMENT      ##Genome-Assembly-Data-START##
Assembly Method      :: CLC Genomics Workbench v. 23.0.2
Genome Coverage      :: 462.68x
Sequencing Technology :: Illumina iSeq
##Genome-Assembly-Data-END##
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FEATURES	LOCATION/QUALIFIERS
source	1..11886 /organism="Lyssavirus rabies" /mol_type="viral cRNA" /strain="D159" /isolation_source="brain" /host="Canis lupus familiaris" /db_xref="taxon: 11292 " /geo_loc_name="Viet Nam" /collection date="2011"



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Job Title

RABV/THA/Loei/dog/67F04690/2024-complete-cds

RID

SVU765C9016
[Search expires on 07-21 17:22 pm](#)
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Program

BLASTN
[Citation ▼](#)

Database

core_nt
[See details ▼](#)

Query ID

lclQuery_61985855

Description

RABV/THA/Loei/dog/67F04690/2024-complete-cds

Molecule type

dna

Query Length

11886

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Organism

☐ exclude

[+ Add organism](#)

Percent Identity

to

E value

to

Query Coverage

to

Sequences producing significant alignments

☒ select all
100 sequences selected

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[Distance tree of results](#)
[MSA Viewer](#)

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per Ident	Acc. Len	Accession
☒	Lyssavirus rabies D159 viral cRNA complete genome	Lyssavirus rabies	21795	21795	100%	0.0	99.76%	11886	LC067588.1
☒	Lyssavirus rabies H201 viral cRNA complete genome	Lyssavirus rabies	21595	21595	100%	0.0	99.46%	11890	LC067577.1



Descriptions

Graphic Summary

Alignments

Taxonomy

Sequences producing significant alignments

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Select columns

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☒ select all 100 sequences selected

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[MSA Viewer](#)

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☒	Lyssavirus rabies D159 viral cRNA, complete genome	Lyssavirus rabies	21795	21795	100%	0.0	99.76%	11886	LC867588.1
☒	Lyssavirus rabies H201 viral cRNA, complete genome	Lyssavirus rabies	21595	21595	100%	0.0	99.46%	11898	LC867577.1

GenBank: LC867577.1

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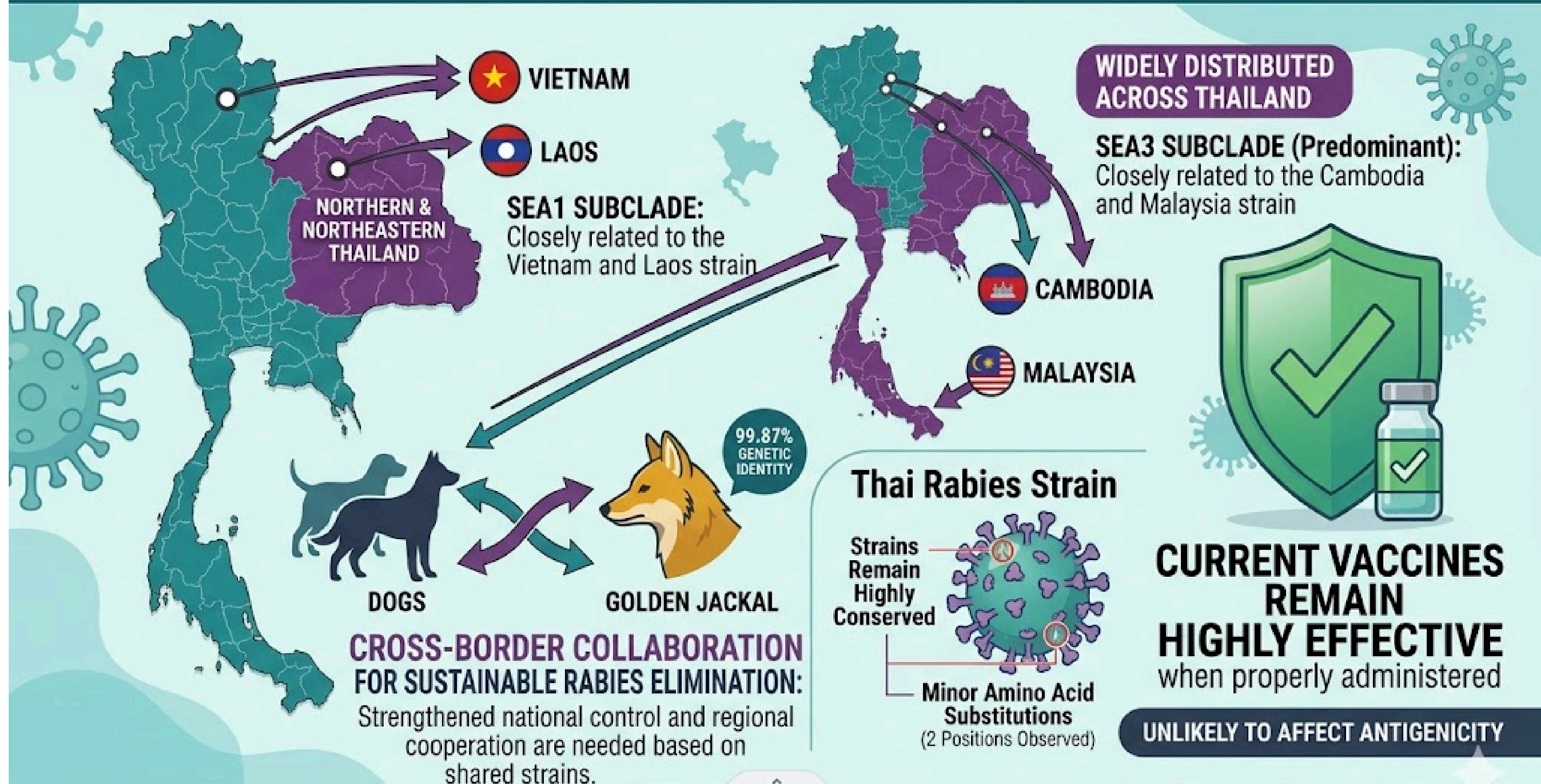
Go to:

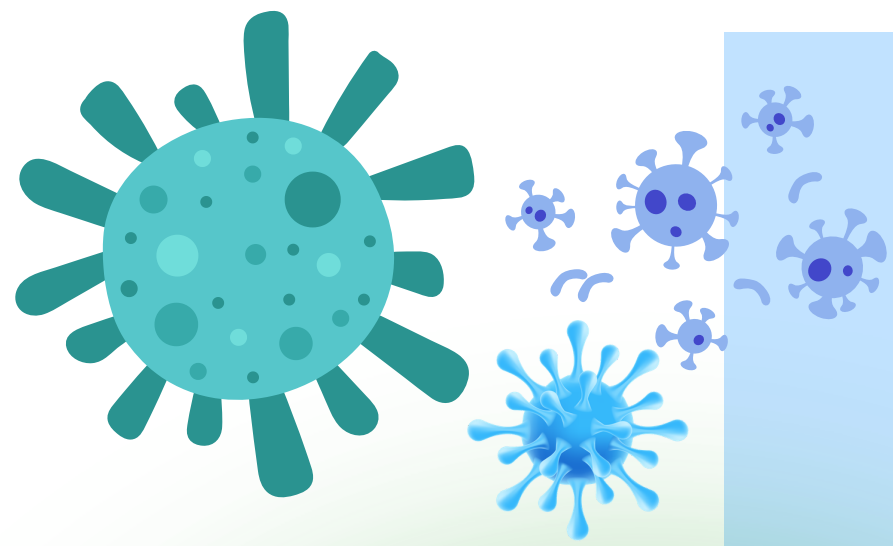
LOCUS LC867577 11898 bp cRNA linear VRL 08-JUL-2025
DEFINITION Lyssavirus rabies H201 viral cRNA, complete genome.
ACCESSION LC867577
VERSION LC867577.1
KEYWORDS .
SOURCE Lyssavirus rabies
ORGANISM [Lyssavirus rabies](#)
Viruses; Riboviria; Orthornavirae; Negarnaviricota;
Haploviricotina; Monjiviricetes; Mononegavirales; Rhabdoviridae;
Alpharhabdovirinae; Lyssavirus.

```
REFERENCE 1
AUTHORS Harada,M., Nguyen,T.T., Okutani,A., Inoue,S. and Maeda,K.
TITLE Four genetically distinct types of rabies virus exist in Vietnam,
including the SEA1 and SEA3 subclades within Asian clade
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 11898)
AUTHORS Okutani,A. and Harada,M.
TITLE Direct Submission
JOURNAL Submitted (15-APR-2025) Contact: Akiko Okutani National Institute of
Infectious Disease, Japan Institute for Health Security, Veterinary
Science; 1-23-1 Toyama, Shinjyuku, Tokyo 162-8640, Japan
COMMENT ##Genome-Assembly-Data-START##
Assembly Method :: CLC Genomics Workbench v. 23.0.2
Genome Coverage :: 47.98x
Sequencing Technology :: Illumina MiSeq
##Genome-Assembly-Data-END##
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FEATURES	Location/Qualifiers
source	1..11898 /organism="Lyssavirus rabies" /mol_type="viral cRNA" /strain="H201" /isolation_source="brain of suckling mouse inoculated with patient saliva" /host="Homo sapiens" /db_xref="taxon: 11292 " /geo_loc_name="Viet Nam" /collection_date="2020"

RABIES VIRUSES IN THAILAND: SUBCLADES, TRANSMISSION, & VACCINES





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- **Nannapat Pengchan**
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