

Study Overview

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# Mindoro Lineage Dynamics

## Study Overview

This study contains 52 sequences from between 2021 and 2023. This sequence data came from 21 different places.

Place	Number of Sequences
Lipa	1
General Trias	1
Lucena City	1
Batangas City	1
Tayabas	1
Calapan	2
Victoria	1
Puerto Galera	5
Baco	6
Mansalay	3
Bongabong	2
Gloria	1
Pinamalayan	1

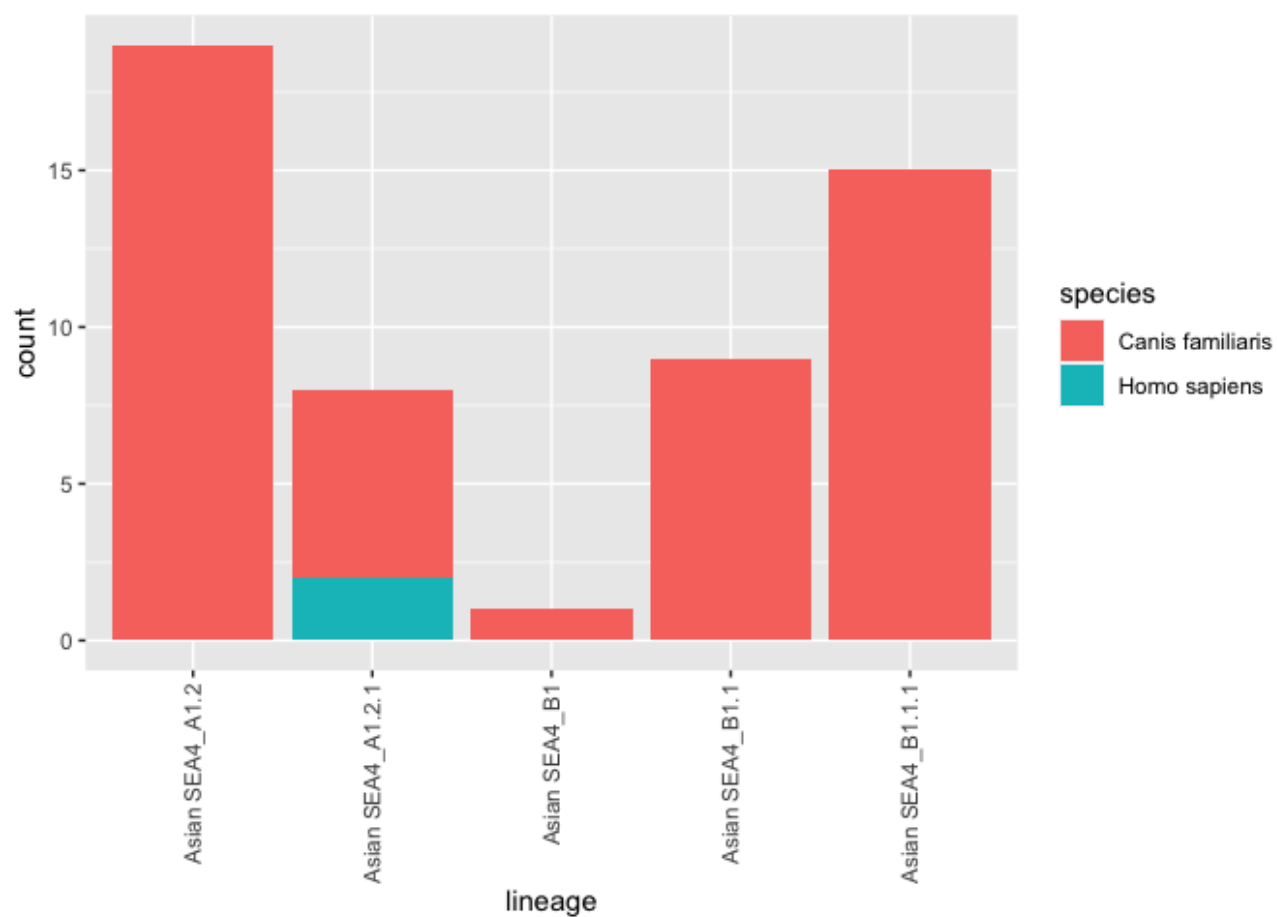
Place	Number of Sequences
Pola	1
Roxas	1
Alcantara	3
Odiongan	7
Santa Maria	7
San Agustin	5
San Andres	1
Calintaan	1

**Table 1. Numbers of sequences by province.**

This sequence data came from 2 different hosts. 96.15% of these are from dogs.

Host	Number of Sequences
Canis familiaris	50
Homo sapiens	2

**Table 2. Numbers of sequences from different hosts.**



**Figure 1. Host numbers by lineage**

# Lineages Overview

Several well-defined RABV clades circulate globally, within two major phylogenetic groups; bat-related and dog-related. The dog-related group is split into 6 different clades according to Troupin et al. (2016). These clades are: Africa 2, Africa 3, Cosmopolitan, Arctic, Asian and Indian. The majority of Philippine sequences fall within the Asian clade.

The MAD DOG (Method for Assignment, Definition and Designation Of Global lineages) tool is an updated lineage designation and assignment tool for rabies virus based on the dynamic nomenclature used for SARS-CoV-2 by Rambaut et al. (2020). This tool defines sequences beyond the clade and subclade level, allowing increased definition. Application of this tool can be used to generate detailed information to inform control efforts and monitor progress towards the elimination of rabies virus.

Details of the tool can be found at <https://doi.org/10.5281/zenodo.5503916>  
(<https://doi.org/10.5281/zenodo.5503916>)

For more information see: <https://doi.org/10.1371/journal.ppat.1010023>  
(<https://doi.org/10.1371/journal.ppat.1010023>)

Overall 5 lineages have been detected in this study. 2 lineages are included here that have not been seen in this study, but are direct parents of lineages in this study, so are included for relevant evolutionary investigations. There are 3 existing lineages relevant to this study.

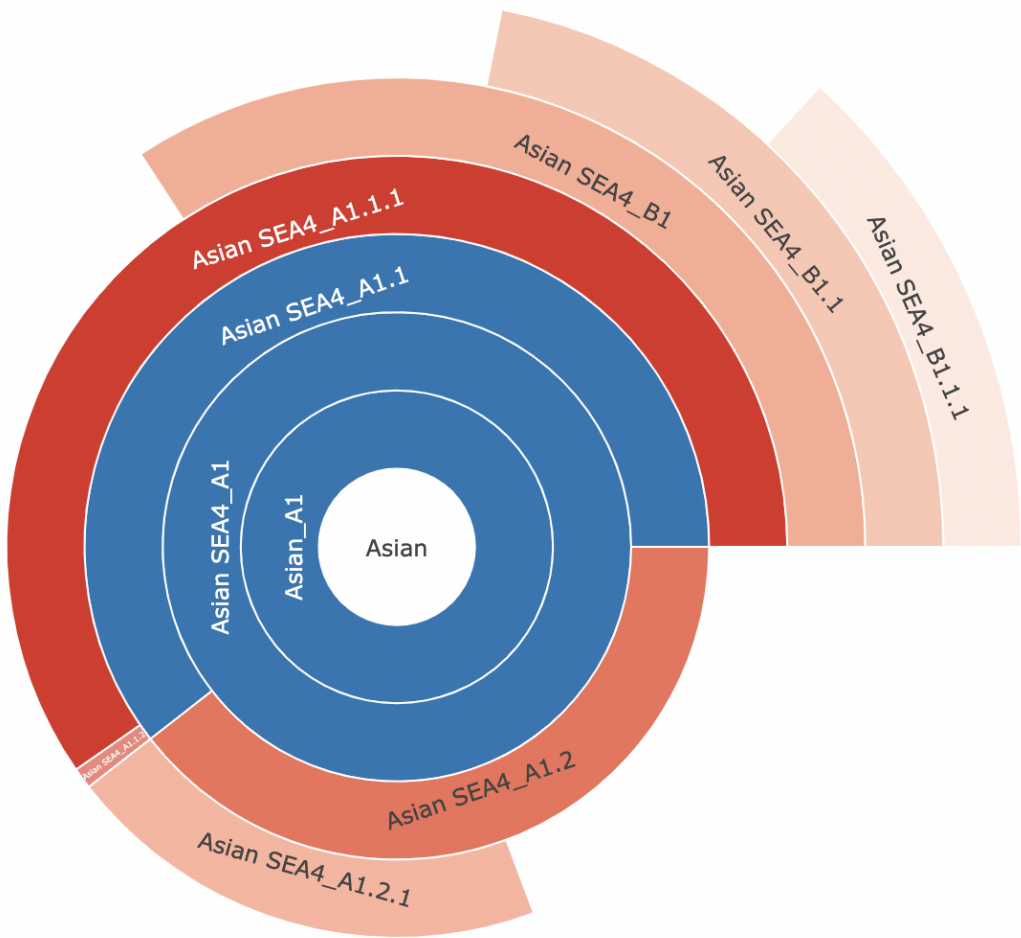
country	year_first	year_last	n_seqs	parent
Philippines	2012	2016	29	Asian SEA4_A1.1
Philippines	2013	2019	1	Asian SEA4_A1.1
Philippines	2012	2019	22	Asian SEA4_A1

**Table 3.** Details of lineages relevant to this study. First and last years refer to the first and most recent years the lineage has been detected.

There are 4 new lineages identified in this dataset.

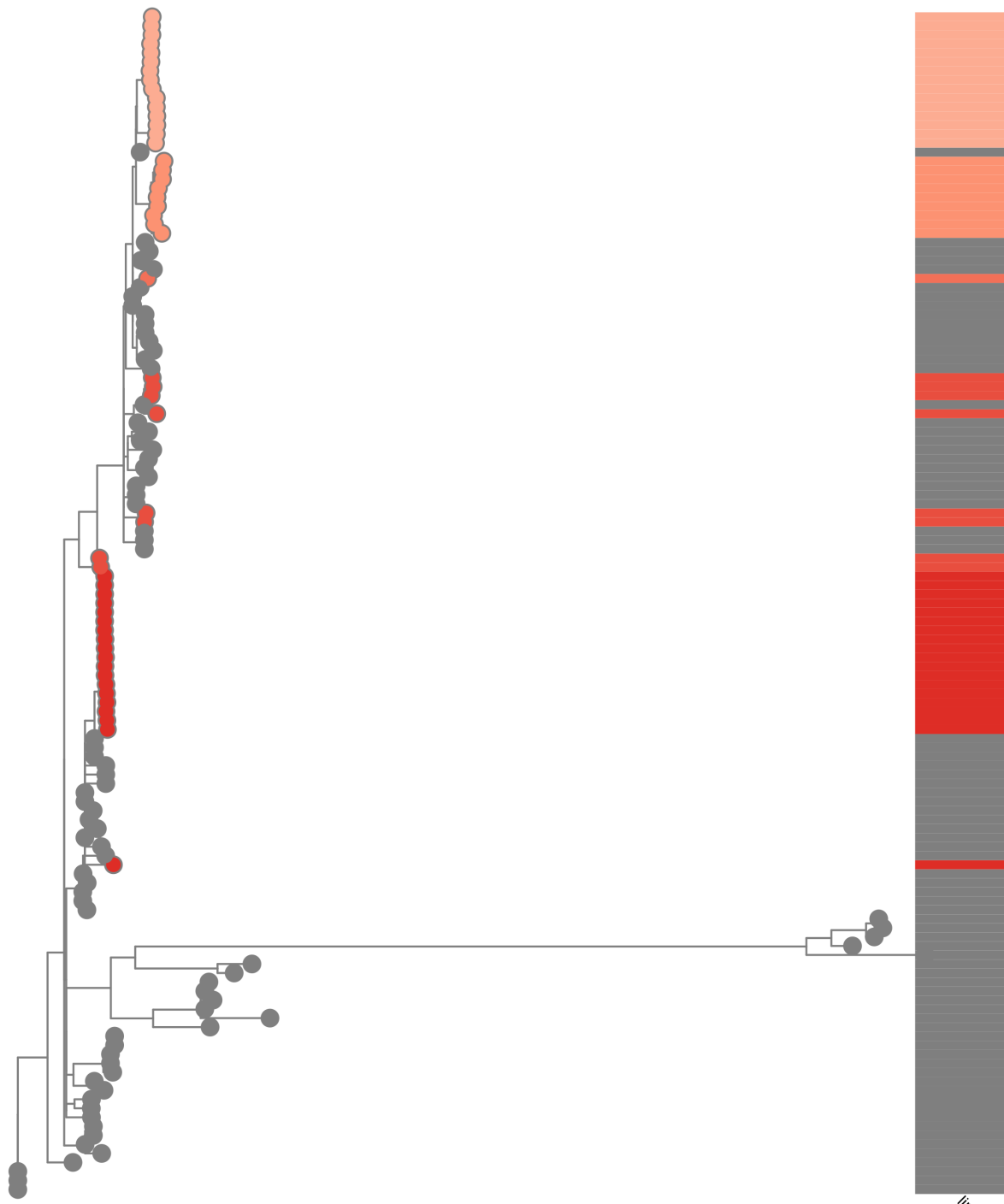
lineage	country	year_first	year_last	n_seqs
Asian SEA4_A1.2.1	c("Japan", "Philippines")	2006	2023	23
Asian SEA4_B1	Philippines	2012	2022	14
Asian SEA4_B1.1	Philippines	2012	2022	10
Asian SEA4_B1.1.1	Philippines	2021	2022	15

**Table 4.** Details of new lineages identified in this study. First and last years refer to the first and most recent years the lineage has been detected.



sunburst

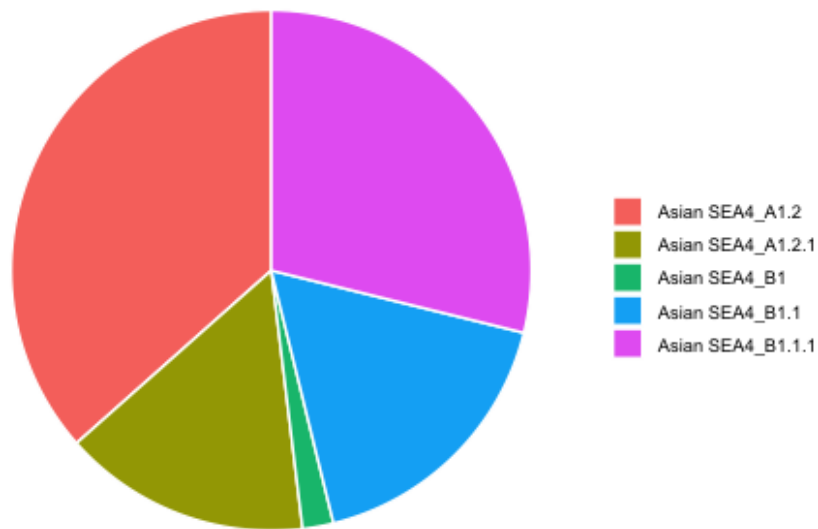
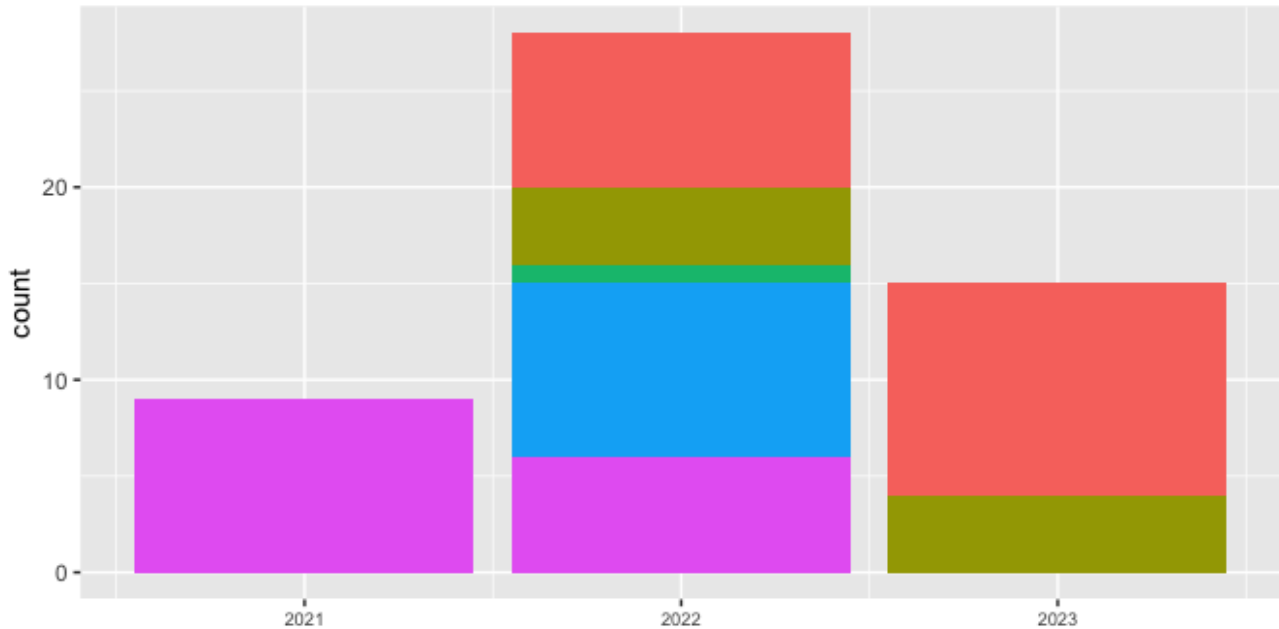
**Figure 2. Sunburst plot showing evolutionary relationships of lineages**



**Figure 3. Maximum likelihood tree with tips coloured by lineage, and bar showing lineage positions**

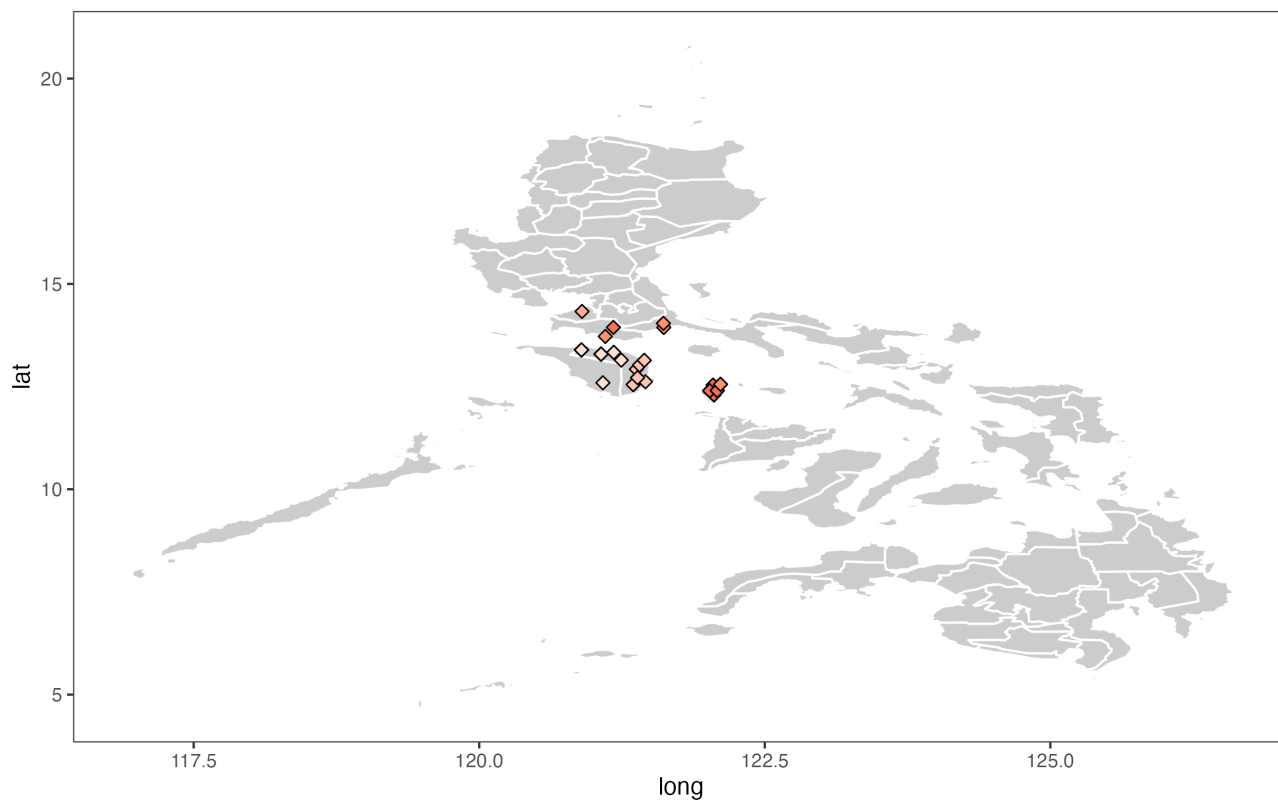
# Lineage Changes Over Time

The sequences span 2 years from 2021 to 2023. The year with the greatest number of sequences is 2022 with 28 sequences. The most prevalent lineage is Asian SEA4\_A1.2 with 19 sequences.



**Figure 4.** Above: Number of sequences per year, with bars split by lineage. Below: Pie chart indicating proportions of lineages. All lineages are prefixed by the clade.

# Sequence Locations



**Figure 5. Locations of samples included in the study**