

Study Overview

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Study Overview

This study contains 217 sequences from between 1998 and 2023. This sequence data came from 1 different countries.

Country	Number of Sequences
Philippines	217

Table 1. Numbers of sequences by area.

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 Nigerian sequences fall within the Africa 2 clade.

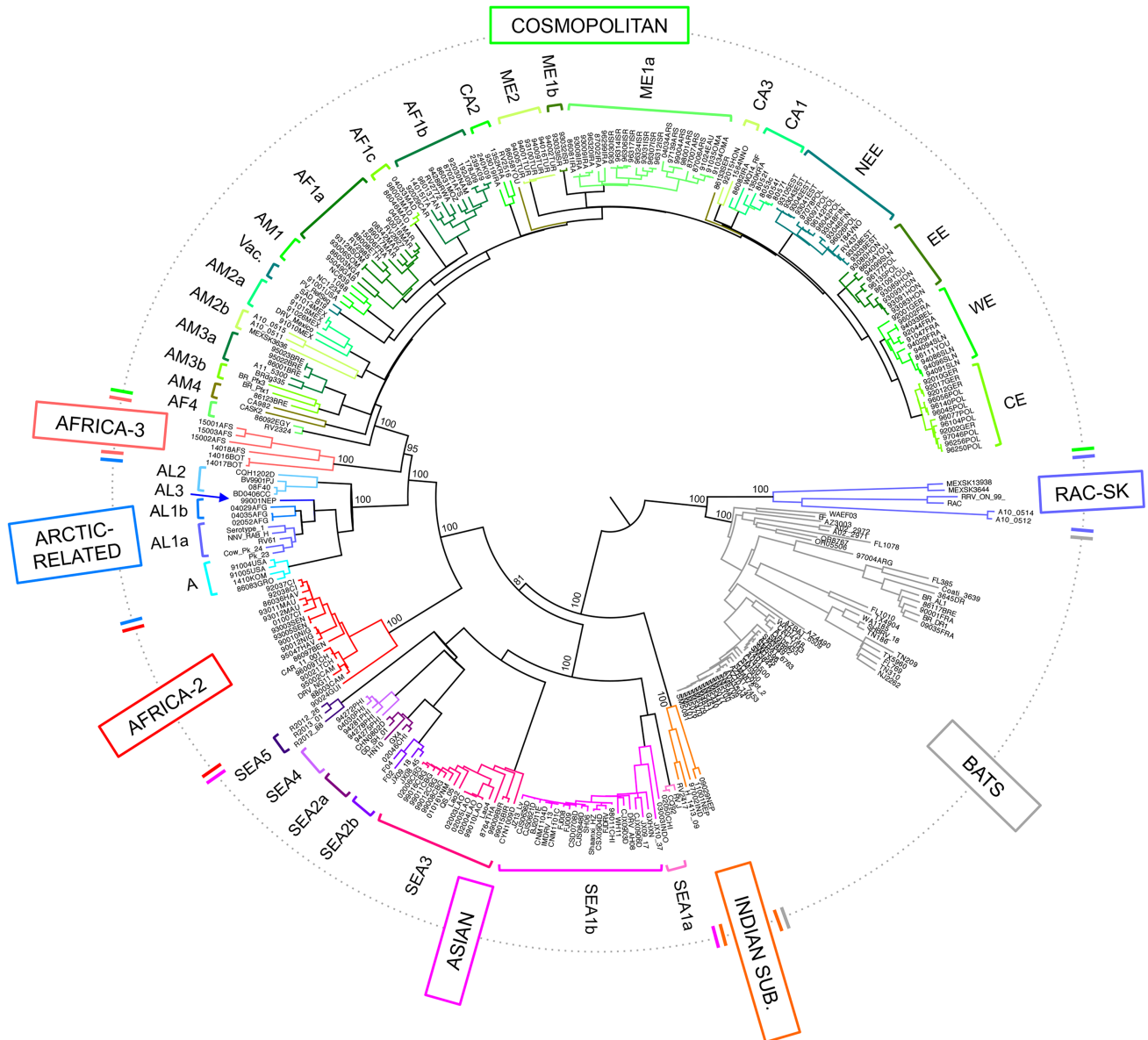


Figure 1. Global rabies clades. Phylogeny of all global rabies clades as defined by Troupin et al. (2016). *taken from* <https://doi.org/10.1371/journal.ppat.1006041> (<https://doi.org/10.1371/journal.ppat.1006041>)

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/10.1101/2021.10.13.464180>
(<https://doi.org/10.1101/2021.10.13.464180>)

A total of 11 lineages have been detected in this study. 3 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 6 existing lineages relevant to this study.

lineage	country	year_first	year_last	n_seqs	parent
Asian SEA4_A1	c("Japan", "Philippines")	1994	2020	54	Asian_A1
Asian SEA4_A1.1.2	c("Japan", "Philippines")	2006	2019	64	Asian SEA4_A1.1
Asian SEA4_A1.2	Philippines	1994	2019	22	Asian SEA4_A1
Asian SEA4_A1.1	Philippines	2012	2016	0	Asian SEA4_A1
Asian_A1	Taiwan	2012	2013	0	Asian
Asian		NA	NA	0	RABV

Table 2. Details of lineages relevant to this study. First and last years refer to the first and most recent years the lineage has been detected prior to this study.

There are 8 new lineages identified in this dataset.

lineage	country	year_first	year_last	n_seqs	parent
Asian SEA4_D1	Philippines	2022	2023	14	Asian SEA4_C1.1.1
Asian SEA4_C1.1.1	Philippines	2018	2023	7	Asian SEA4_C1.1
Asian SEA4_C1.1	Philippines	2007	2022	22	Asian SEA4_C1
Asian SEA4_C1	Philippines	1998	2022	7	Asian SEA4_A1.2.2
Asian SEA4_B1.1.1	Philippines	2014	2020	9	Asian SEA4_B1.1
Asian SEA4_B1.1	Philippines	2007	2022	8	Asian SEA4_B1
Asian SEA4_B1	Philippines	2006	2022	7	Asian SEA4_A1.1.2
Asian SEA4_A1.2.2	Philippines	2015	2016	3	Asian SEA4_A1.2

Table 3. 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.

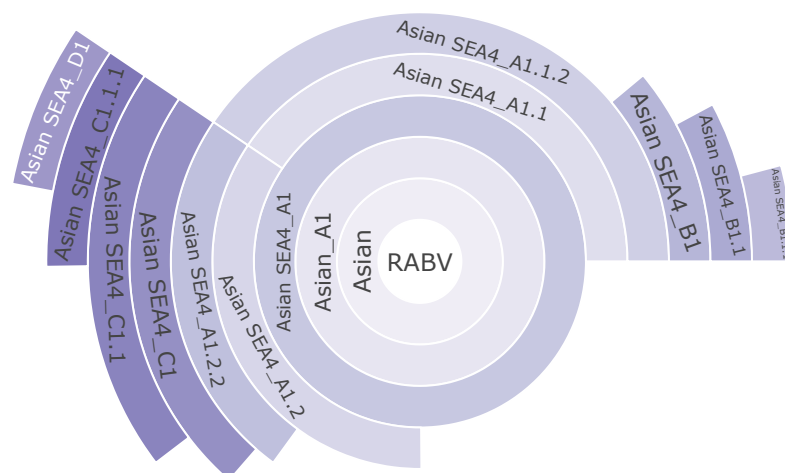


Figure 2. Sunburst plot showing hierarchal relationships of lineages. Bar length corresponds to number of sequences. Plot is interactive. Hover over bars to see details, and click to zoom in on sections.

Lineage Changes Over Time

The sequences span 25 years from 1998 to 2023. The year with the greatest number of sequences is 2022 with 39 sequences. The most prevalent lineage is Asian SEA4_A1.1.2 with 64 sequences.

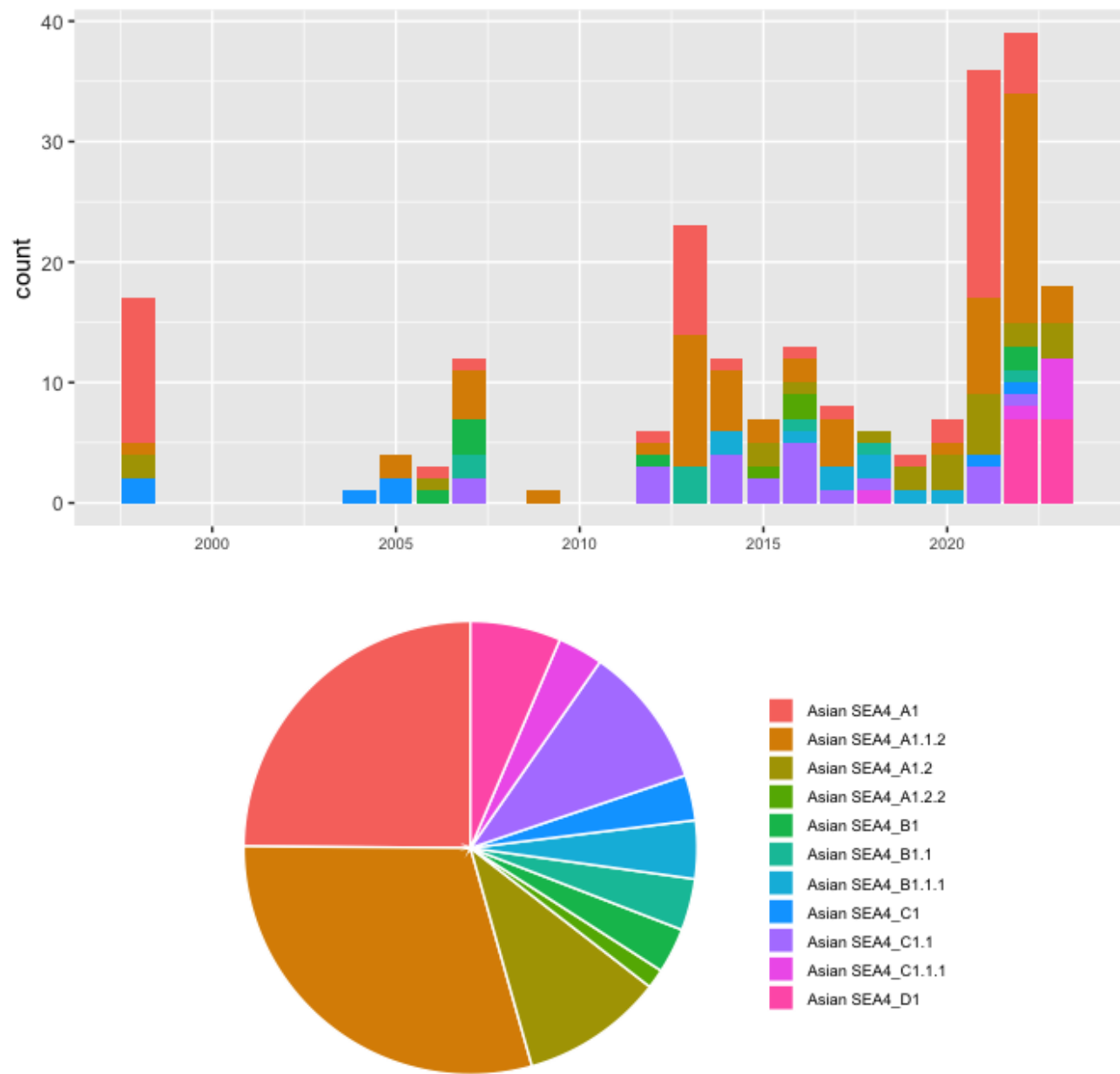


Figure 4. Above: Number of sequences per year, with bars split by lineage. Below: Pie chart indicating proportions of lineages.

Areas to Investigate

There are 7 potentially emerging or undersampled lineages within the lineages relevant to this study. This means that these lineages have between 5 and 9 sequences; not enough to be a full lineage, but are significantly diverse from their relatives. With more sequencing and more time, these are likely to become new lineages. Be aware these include ALL emerging or undersampled lineages within the relevant lineages in your dataset; not just your data. This is to show there may be gaps in the data.

lineage	tips	distance	country	year_first	year_last
Asian SEA4_A1.1.2_E1	5	0.0440821	Philippines	2022	2022
Asian SEA4_A1.1.2_E2	5	0.0440835	Philippines	2021	2022
Asian SEA4_A1.1.2_E3	5	0.0444111	Philippines	2022	2022
Asian SEA4_A1.2_E1	5	0.0422323	Philippines	2018	2019
Asian SEA4_C1.1.1_E1	5	0.0511130	Philippines	2022	2023
Asian SEA4_C1.1_E1	5	0.0460030	Philippines	2012	2014
Asian SEA4_B1.1.1_E1	7	0.0432379	Philippines	2017	2020

Table 5. Details of potentially emerging or undersampled lineages relevant to this study. First and last years refer to the first and most recent years the lineage has been detected.

There are 5 singletons of interest detected. These reflect highly divergent sequences that could indicate sequencing errors, or the start of new lineages, especially in undersampled areas. Be aware these include ALL singletons of interest within the relevant lineages in your dataset; not just your data. This is to show there may be general gaps in the data.

lineage	n_singletons	singleton_countries	singleton_years
Asian SEA4_A1	1	Philippines	2021
Asian SEA4_A1.1.2	1	Japan	2006
Asian_A1	2	Taiwan	2012
Asian SEA4_A1.2.2	1	Philippines	2015

Table 6. Summary of singletons of interest relevant to this study.

ID	closest relative	lineage	year	country
AB573763	AB573762	Asian SEA4_A1.1.2	2006	Japan
RADDL3-1045	RADDL1-16-166	Asian SEA4_A1.2.2	2015	Philippines
KF620487	MN857171	Asian_A1	2012	Taiwan
KF620488	KF620489	Asian_A1	2012	Taiwan
R7-21-161	R9-010	Asian SEA4_A1	2021	Philippines

Table 7. Details of individual singletons of interest relevant to this study.