

## Background

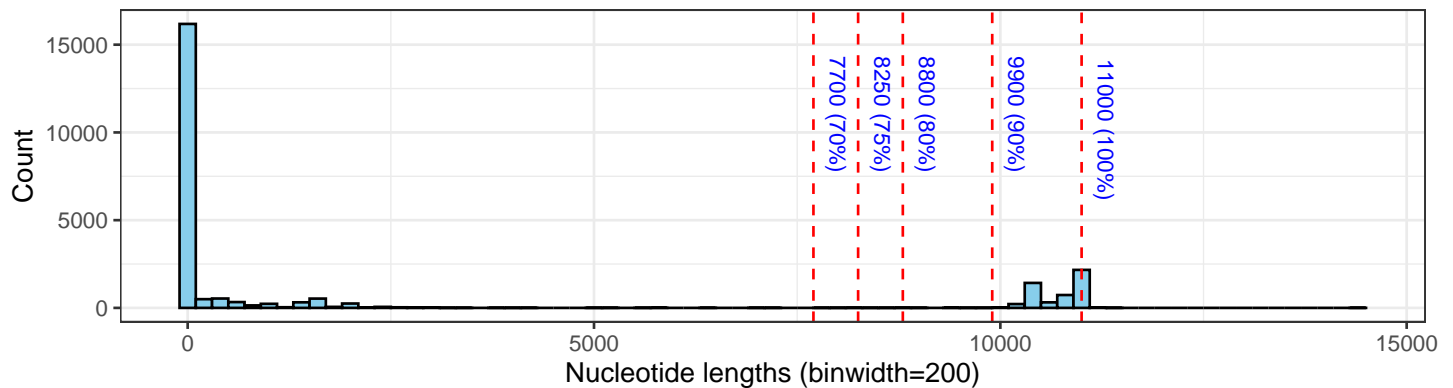
CDC website: <https://www.cdc.gov/west-nile-virus/index.html>

## Exploratory Graphics

### How long is the WNV genome?

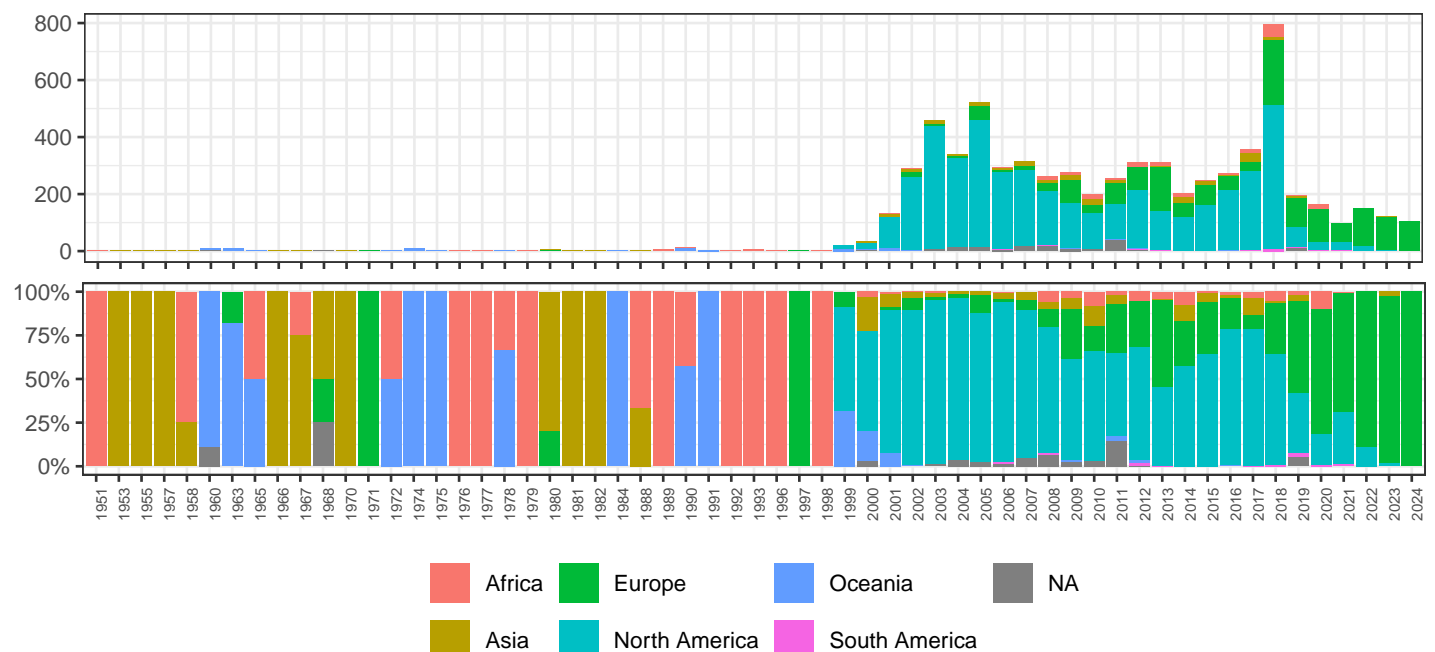
WNV is approximately 11k nt long. The samples pulled from NCBI GenBank have the following distribution of lengths. Mostly seeing two clusters—very short sequences or around the full genome length.

Diagnostic plot to estimate min-length filter for phylogenetic analysis (all data = 24197)



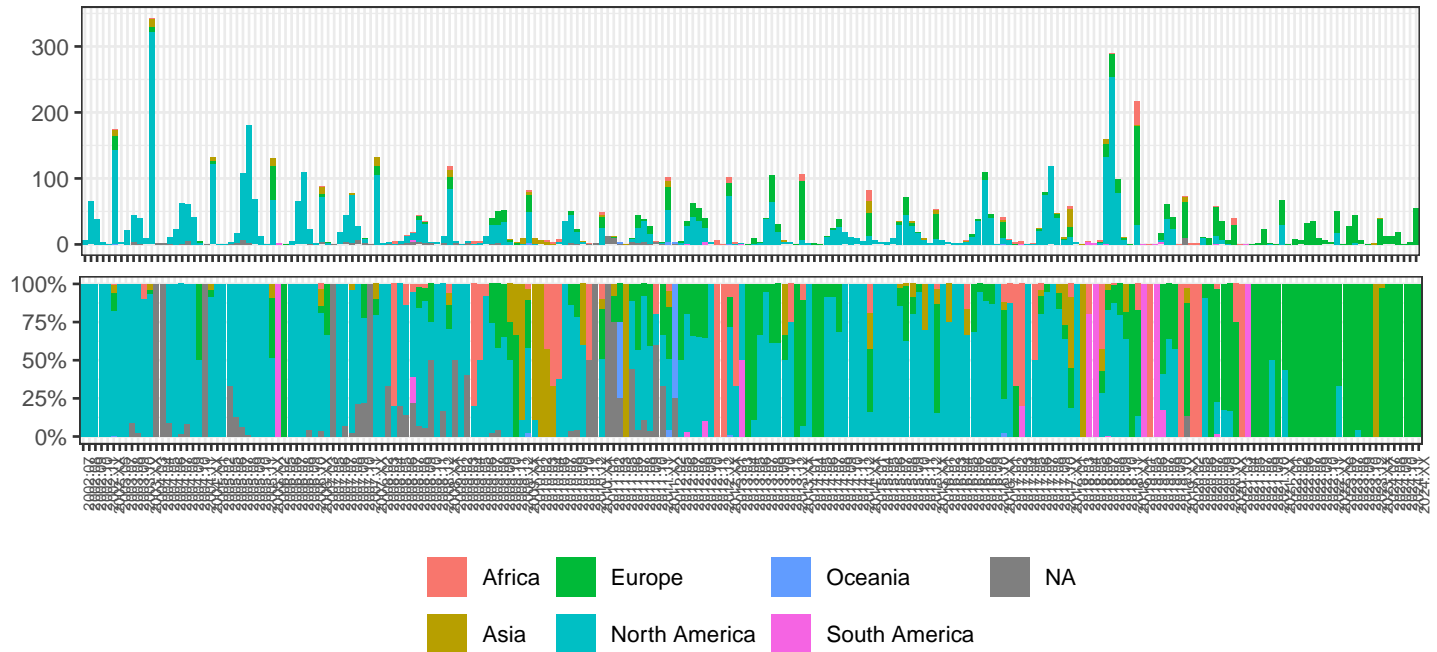
### How well sampled is WNV across time and space?

Frequency and proportion (n=6855)

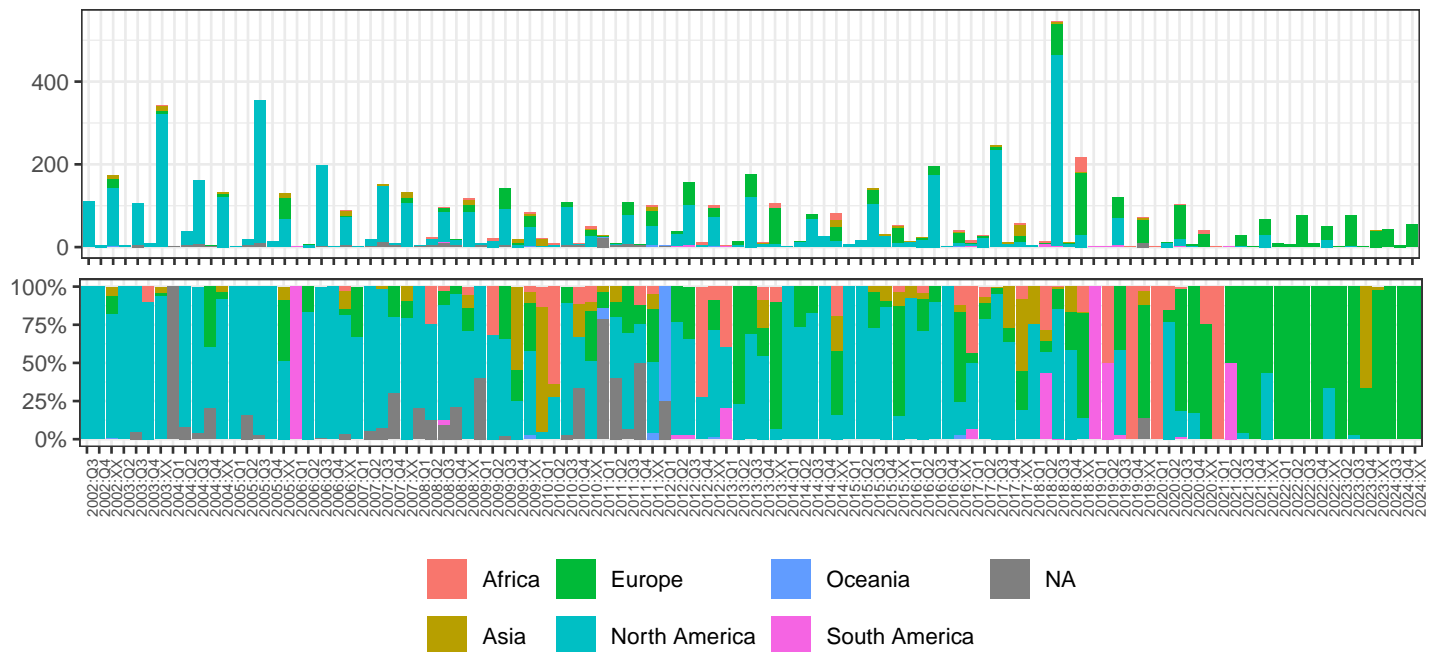


## Pick a narrow bandwidth for the frequencies plot

### Monthly counts (n=6554)



### Quarterly counts (n=6554)



The earliest samples seem to be from 1931. However, these are EF631122 and EF631123 and are supposedly collected in Illinois, USA, much earlier than the NY99 event. We might need to dig into publications that contain these GenBanks to check if this collection date is correct. Such as publication:

- Amore, G., Bertolotti, L., Hamer, G.L., Kitron, U.D., Walker, E.D., Ruiz, M.O., Brawn, J.D. and Goldberg, T.L., 2010. Multi-year evolutionary dynamics of West Nile virus in suburban Chicago, USA, 2005–2007. *Philosophical Transactions of the Royal Society B: Biological Sciences*, 365(1548), pp.1871-1878.

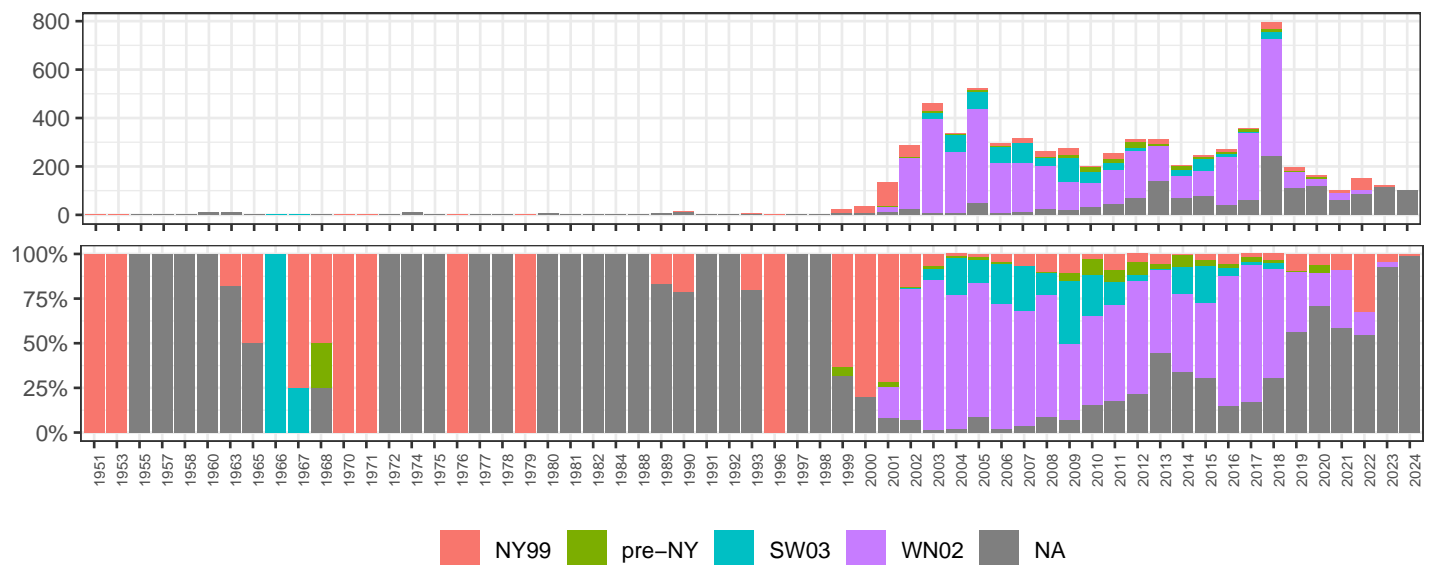
## What lineages are available for WNV?

- **Global lineage system:** Koch, R. Tobias, Diana Erazo, Arran J. Folly, Nicholas Johnson, Simon Dellicour, Nathan D. Grubaugh, and Chantal BF Vogels. "Genomic epidemiology of West Nile virus in Europe." *One Health* (2023): 100664.
- **USA-based system:** Hadfield, J., Brito, A.F., Swetnam, D.M., Vogels, C.B., Tokarz, R.E., Andersen, K.G., Smith, R.C., Bedford, T. and Grubaugh, N.D., 2019. Twenty years of West Nile virus spread and evolution in the Americas visualized by Nextstrain. *PLoS pathogens*, 15(10), p.e1008042.

### Global lineage (n=6855)



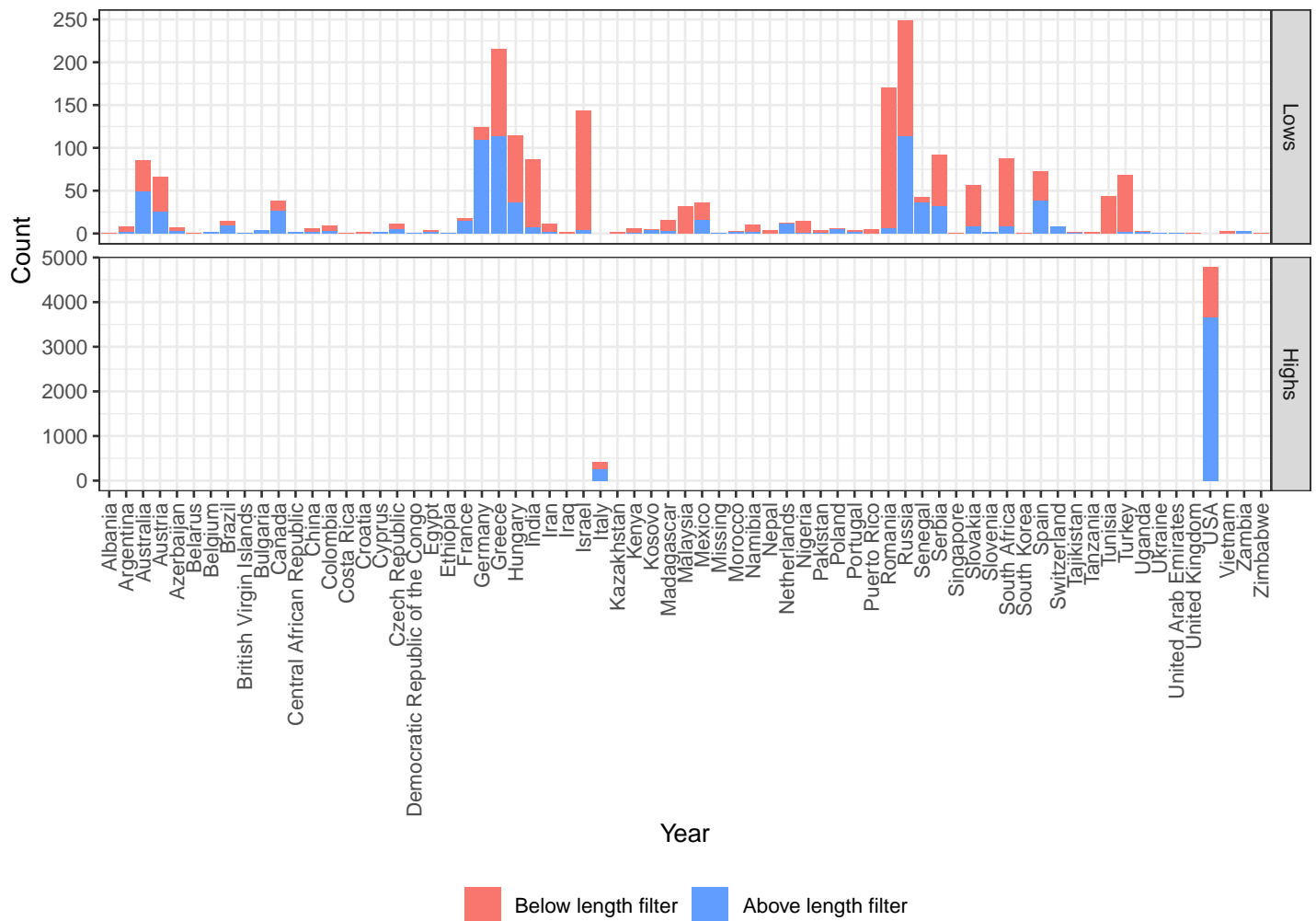
### Count of USA-based lineage samples with collection date (n=6855)



## Global subsampling

If min length is set to 80 percent, or 8800nt:

WNV entries that were above or below filter, by country (n = 4908 where min-length=8800)



- Total WNV records = 24197. Note how this includes records without collection date
- Total WNV records that passes the length filter = 4908

If this number is lower than 4k, probably don't need to sub sample further.

## Who are the main submitters of sequence data?

Table 1: Top 25 most frequent sequence submitters with their region and countries

authors	n	regions	countries
blatt et al.	15308	NA	NA
grubaugh et al.	1180	North America	USA
feriancek et al.	627	North America	USA
newman et al.	479	North America	USA
shabman et al.	458	North America	USA
linnen et al.	342	NA	NA
henn et al.	273	North America, NA	USA, NA
bertolotti et al.	208	North America	USA
herring et al.	199	North America	USA, Canada
derby et al.	171	NA	NA
dinu et al.	161	Europe	Romania
ebel et al.	141	NA, North America	NA, USA
duggal et al.	132	North America, NA	USA, NA
amore et al.	126	North America	USA
anderson et al.	126	North America	USA
phillips et al.	112	North America	USA
nagy et al.	109	Europe	Hungary, Serbia
papa et al.	109	Europe	Greece
platonov et al.	109	Europe, Asia	Russia, Azerbaijan
davis et al.	108	North America, NA	USA, NA
armstrong et al.	104	North America, NA	USA, NA
antonov et al.	92	Europe	Russia
swetnam et al.	91	North America	USA
bernardin et al.	88	North America	USA
?	87	Europe, Asia	Germany, India

## What hosts are represented?

Host samples with collection date (n=6855)

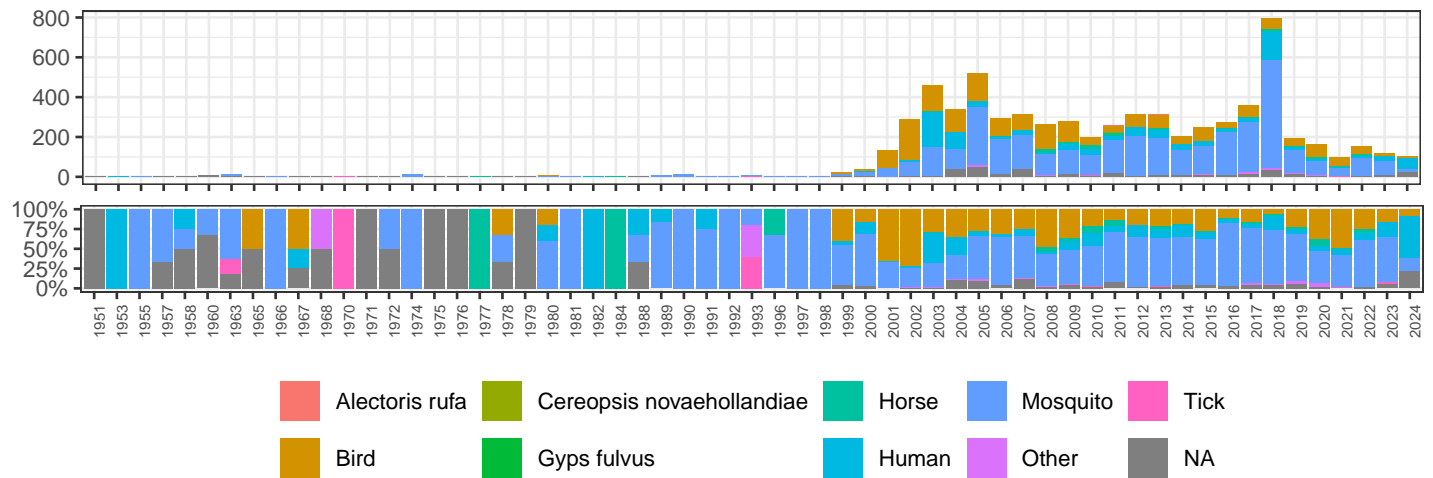


Table 2: Host counts

host_type	n
NA	17154
Mosquito	3732
Bird	2085
Human	931
Horse	157
Other	115
Tick	18
Alectoris rufa	3
Cereopsis novaehollandiae	1
Gyps fulvus	1