

Understanding SARS-CoV-2 Omicron (B.1.1.529) Lineage Dynamics in South Africa Through Epidemiological, Spatial, and Phylogenetic Analysis



Zijing (Carol) Zhou, Joshua Levy
Andersen Lab, Scripps Research



Introduction

- The B.1.1.529 (Omicron) variant of SARS-CoV-2 was first identified in South Africa and Botswana in November 2021 [1].
- Though many countries, including India, imposed a travel ban on southern African countries, Omicron (being more transmissible than previous variants) soon spread around the world, suggesting the variant was possibly widespread before identification [2].
- To understand the spread and evolution of Omicron in South Africa and help prevent future outbreaks, we analyzed epidemiological and genomic data, as well as geospatial connectivity among countries that had early Omicron outbreaks (South Africa, Botswana, and India).



Figure 1. A map of South Africa, Botswana, and India with their first detection dates of Omicron respectively.

Methods

The epidemiological data for South Africa were analyzed and graphed mainly using the Outbreak.info R package [3].

We analyzed and graphed geospatial and connectivity data across location.

A phylogenetic analysis using maximum likelihood tree inference was performed.

Results

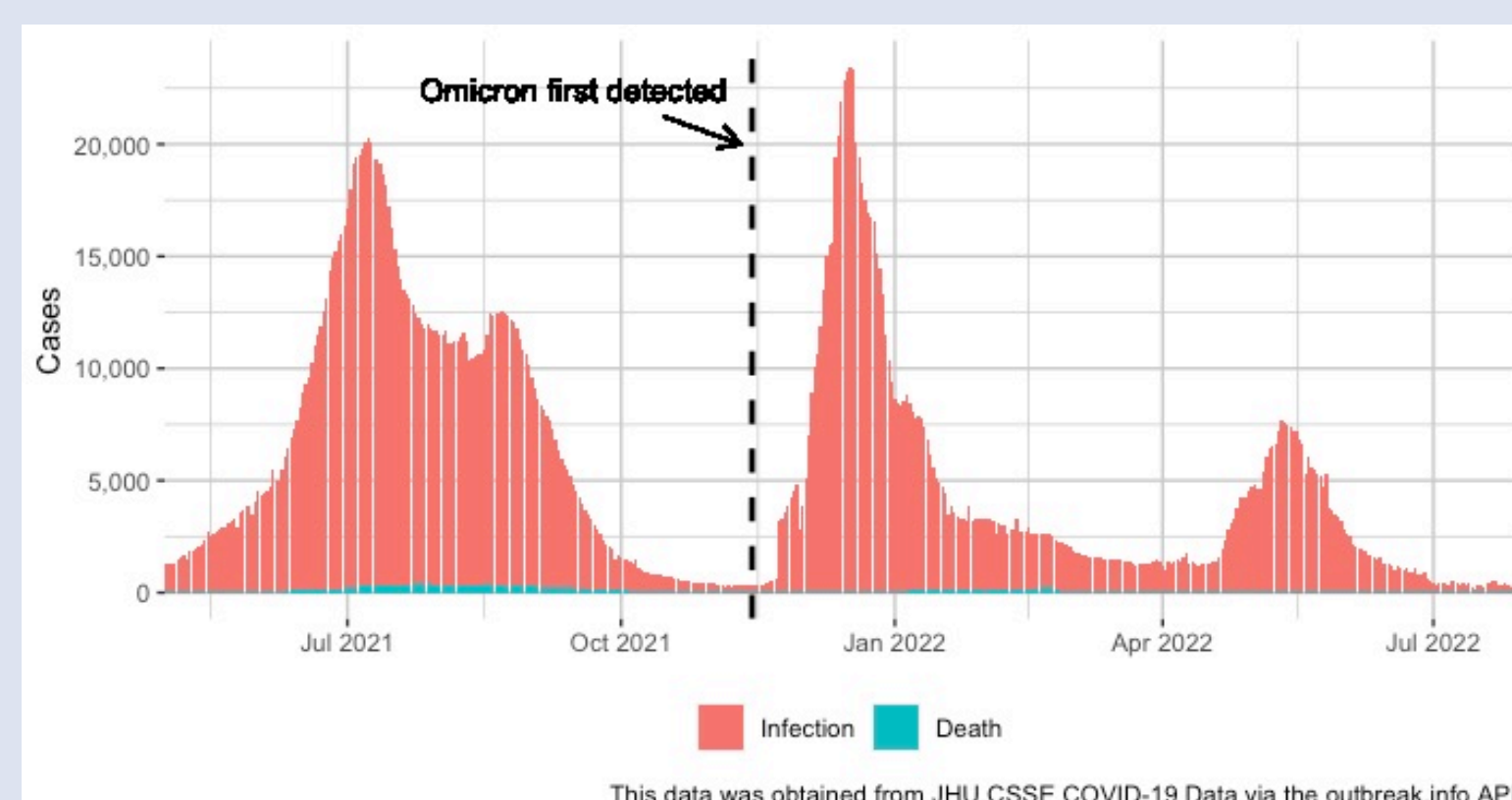


Figure 2. Daily COVID-19 cases and deaths in South Africa from May 2021 to July 2022 (7 day rolling average).

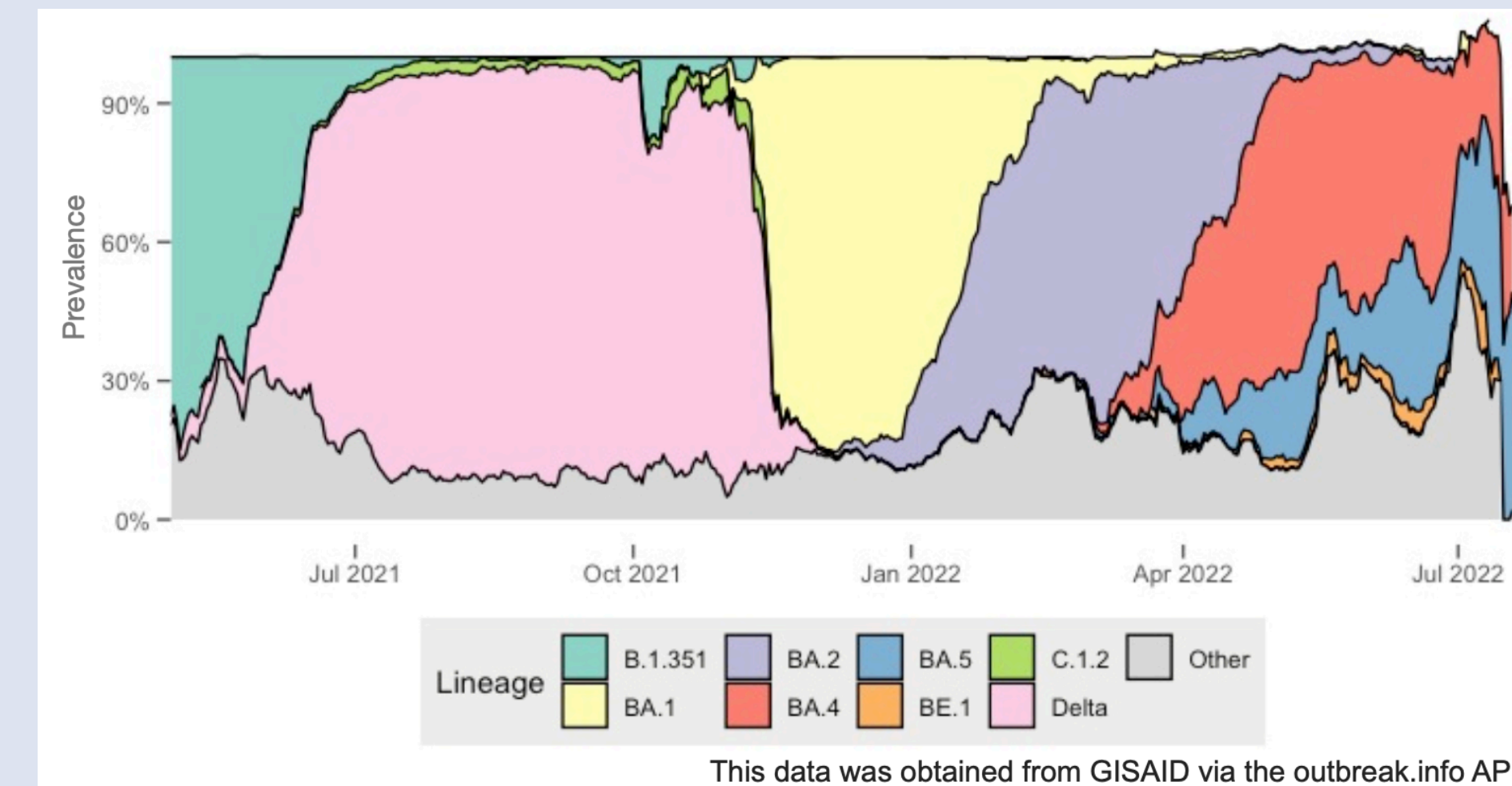


Figure 3. Daily lineage proportion for all lineages from May 2021 to July 2022 (7 day rolling average). Lineages without daily prevalence > 5% for at least 10 days in the last 456 days were grouped into "Other".

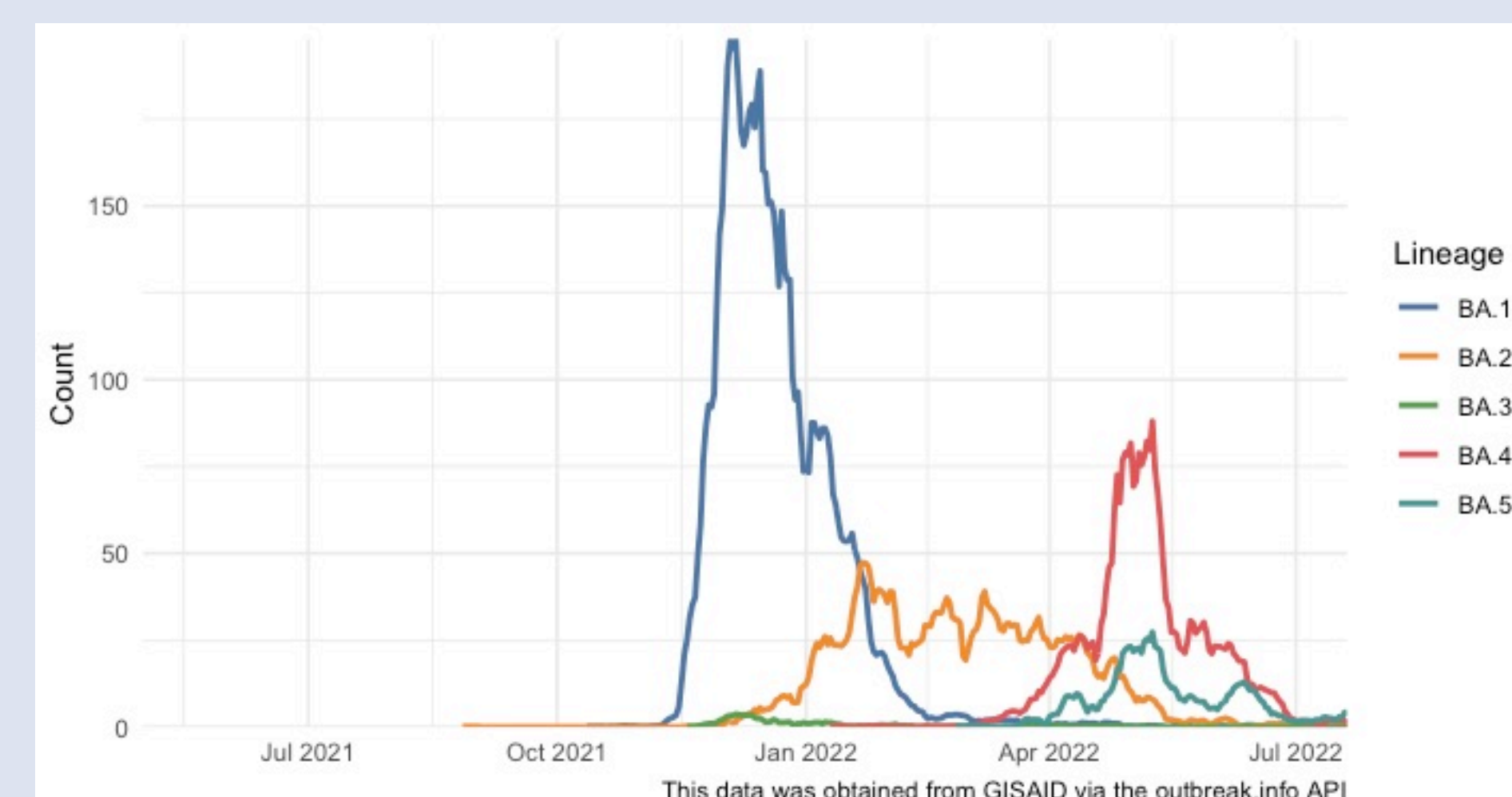


Figure 4. Daily Omicron lineage count from May 2021 to July 2022 (7 day rolling average). BA.1 and BA.2 were first detected around November 2021, while BA.4 and BA.5 were first detected around January and February 2022 respectively.

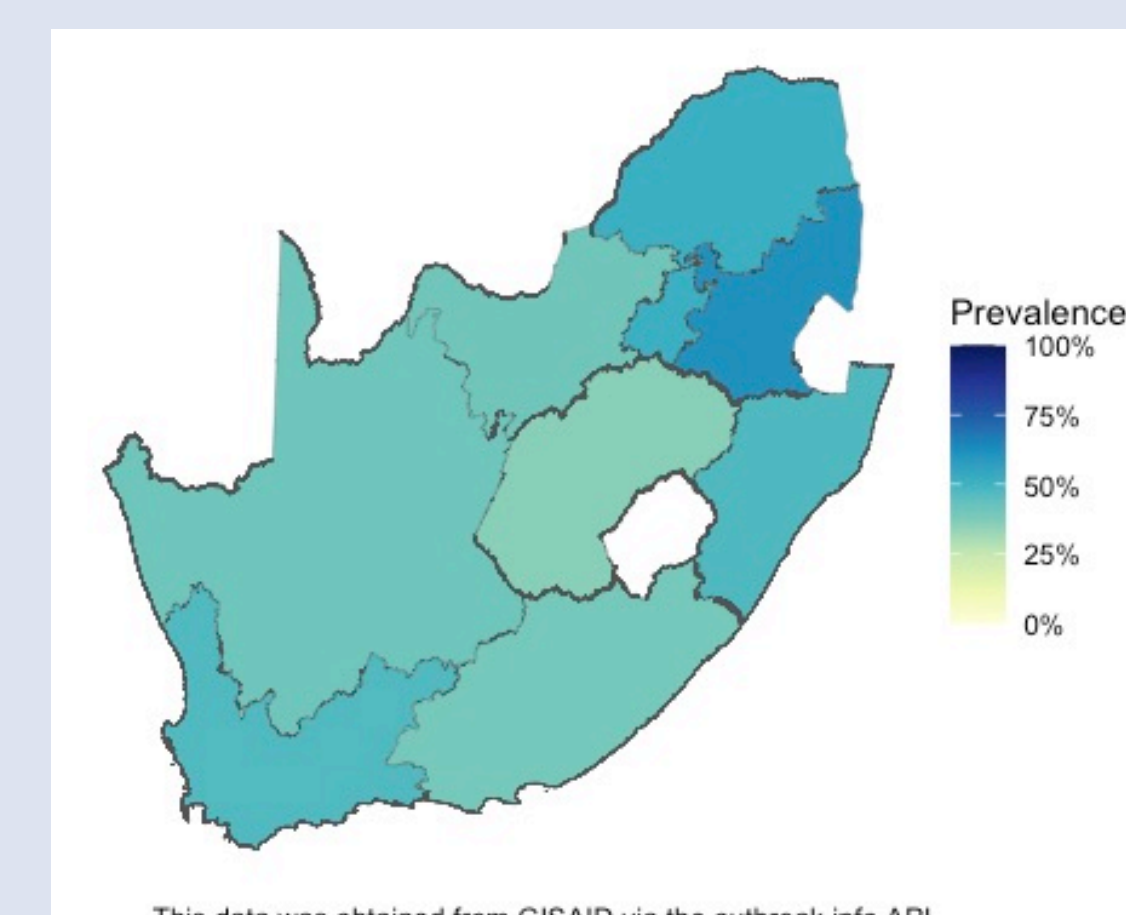


Figure 5. The estimated prevalence of Omicron lineages in each province in South Africa before July 2022. The northern states, Mpumalanga (61%), Gauteng (51%), and Limpopo (51%) have the highest prevalence.

Results

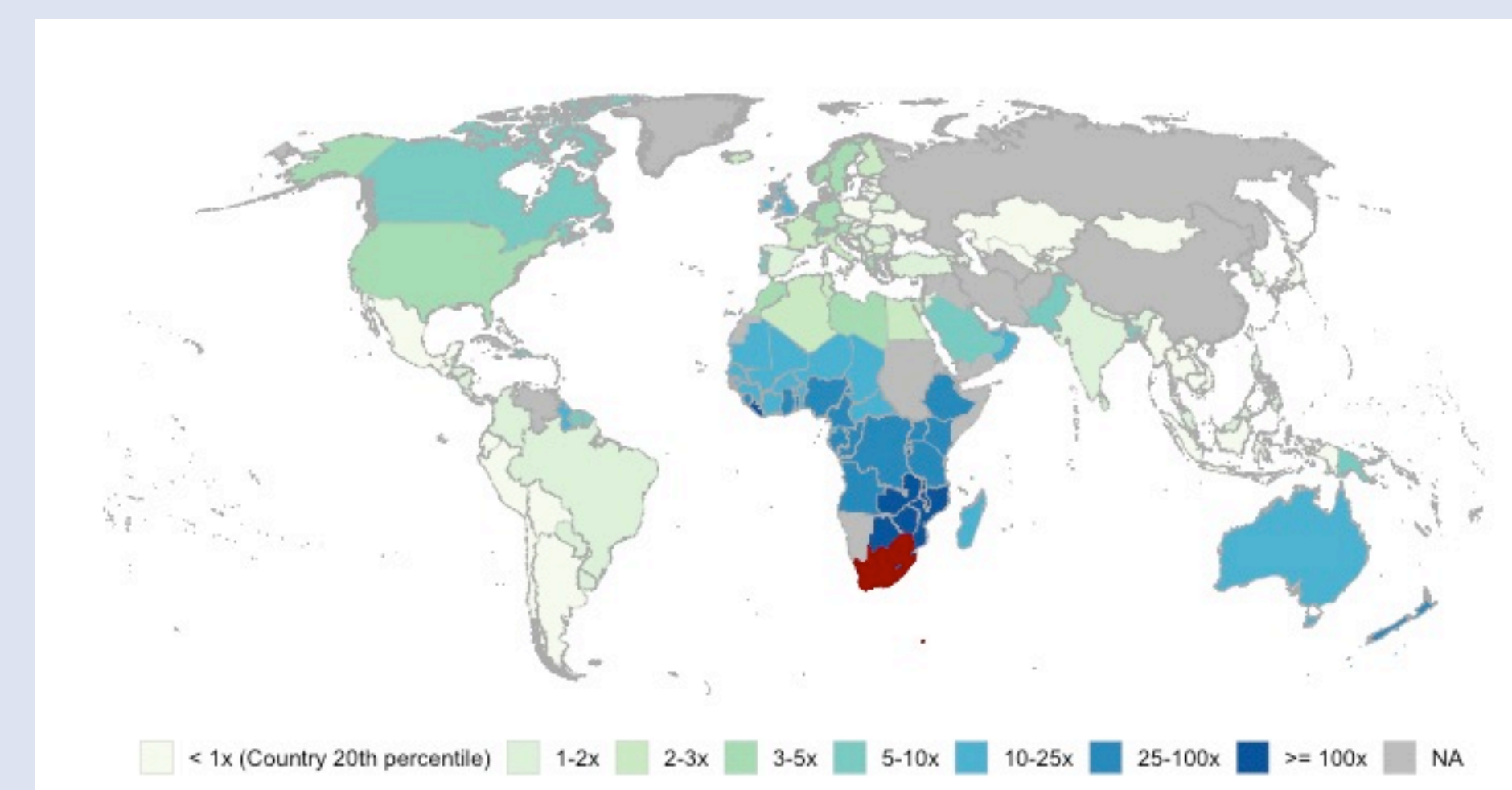


Figure 6. The Social Connectedness Index (SCI) measures the relative probability of a Facebook friendship link between South Africa and other countries scaled with a maximum value of 1,000,000,000 and a minimum of 1 [4]. SCI for Botswana is 144,021 and for India is 417.

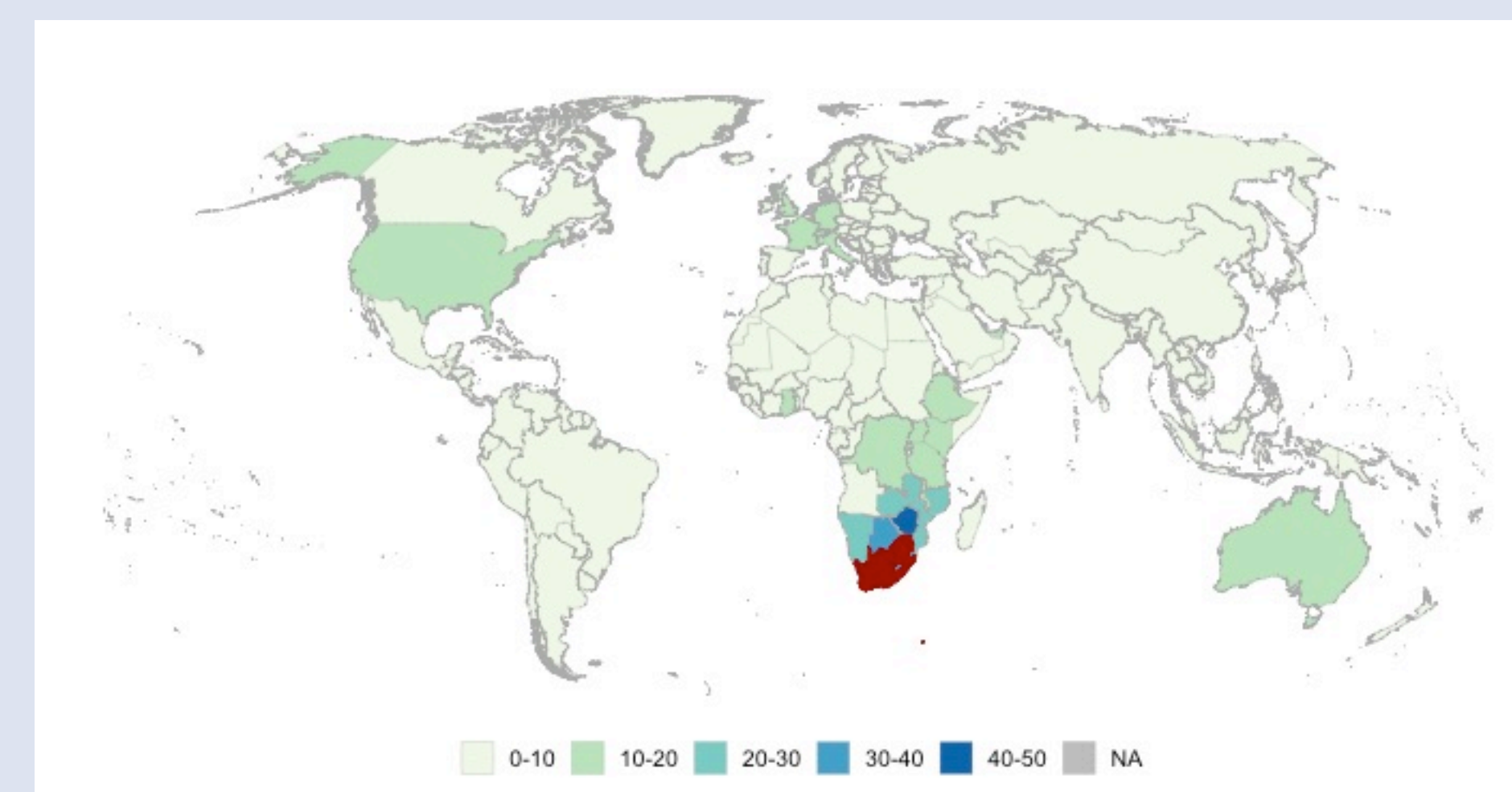


Figure 7. The Place Connectivity Index (PCI) measures the normalized number of shared unique Twitter users between South Africa and other countries in 2019 scaled with a maximum value of 1,000 and a minimum of 1 [5]. The PCI for Botswana is 37.42 and for India is 5.51.

Country	Exporter	Partner Share (%)	Importer	Partner Share (%)
South Africa	China	18.47%	China	10.73%
	Germany	9.87%	Germany	8.01%
	United States	6.57%	United States	7%
	India	4.91%	Unspecified	5.59%
	Saudi Arabia	4.15%	United Kingdom	5.24%
Botswana	South Africa	57.93%	India	21.60%
	Namibia	7.94%	Belgium	19.59%
	Canada	6.92%	United Arab Emirates	18.19%
	India	4.11%	South Africa	9.61%
	Belgium	3.29%	Israel	7.14%
India	China	14.28%	United States	16.79%
	United States	7.29%	United Arab Emirates	9.14%
	United Arab Emirates	6.33%	China	5.35%
	Saudi Arabia	5.64%	Hong Kong, China	3.55%
	Iraq	4.61%	Singapore	3.32%

Table 1. Top 5 export and import partners of South Africa, Botswana, and India in 2019.

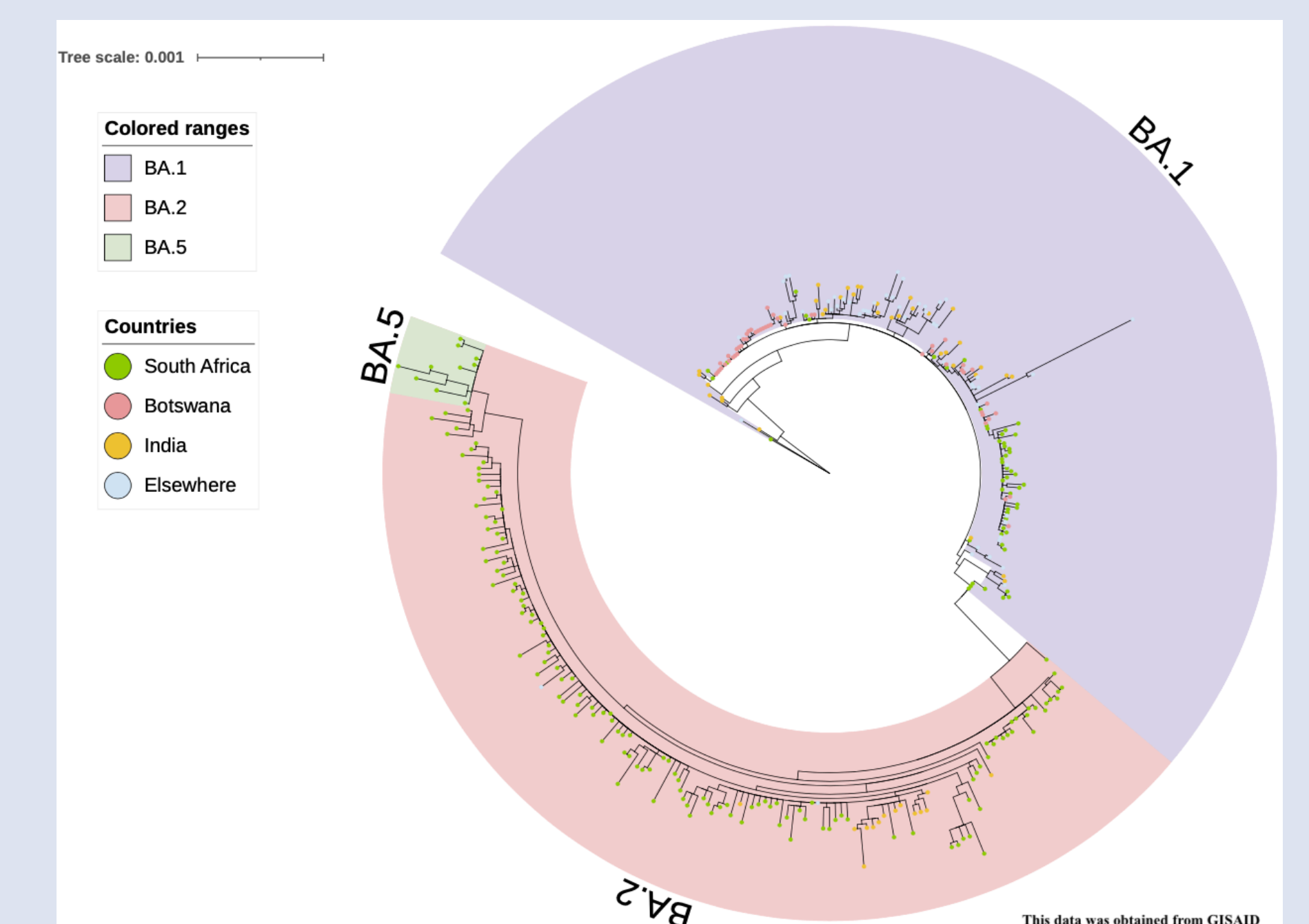


Figure 8. A maximum likelihood tree of 347 Omicron sequences sampled from South Africa (n = 197), Botswana (n = 50), India (n = 50), and elsewhere (n = 50) was constructed using the general time reversible (GTR) model.

Conclusion

- Omicron quickly swept through South Africa (Figure 4), and Mpumalanga, Gauteng, and Limpopo were primarily hit (Figure 5).
- While SCI and PCI only indicate a strong connection between South Africa and Botswana (Figures 6 and 7), Table 1 indicates close trade relationships across all three countries.
- Phylogenetic analysis suggests sequences from South Africa were ancestral to sequences from India, signifying a possible importation event via travel/trade (Figure 8). BA.5 appeared to descend from BA.2, but since there is a lot of missing evolutionary history, this may not be the true evolutionary path.

Acknowledgements

I thank the Andersen Lab. I thank the following organizations for data: JHU CSSE, GISAID Initiative, and WITS.

References

- [1] "Omicron Variant: What You Need to Know." *Centers for Disease Control and Prevention*, Centers for Disease Control and Prevention, <https://www.cdc.gov/coronavirus/2019-ncov/variants/omicron-variant.html>.
- [2] Petersen, Eskild et al. "Emergence of new SARS-CoV-2 Variant of Concern Omicron (B.1.1.529) - highlights Africa's research capabilities, but exposes major knowledge gaps, inequities of vaccine distribution, inadequacies in global COVID-19 response and control efforts." *International journal of infectious diseases : IJID : official publication of the International Society for Infectious Diseases* vol. 114 (2022): 268-272. doi:10.1016/j.ijid.2021.11.040
- [3] <https://www.biorxiv.org/content/10.1101/2022.01.20.477133v4>
- [4] Bailey, Michael, Rachel Cao, Theresa Kuchler, Johannes Stroebel, and Arlene Wong. 2018. "Social Connectedness: Measurement, Determinants, and Effects." *Journal of Economic Perspectives*, 32 (3): 259-80.
- [5] Li, Z., Huang, X., Ye, X. et al. Measuring global multi-scale place connectivity using geotagged social media data. *Sci Rep* 11, 14694 (2021). <https://doi.org/10.1038/s41598-021-94300-7>