the high observed prevalence in the study locations remained consistent over a long time period.

Our data suggest an overall high prevalence of *R. raoultii* and its possible long-term stability in *D. reticulatus* tick populations in the studied region, highlighting the enduring high risk of acquiring this rickettsial infection. Besides veterinary consequences (*1*), this risk should be considered by medical personnel and public health authorities because the incidence of tick-borne lymphadenopathy might increase with the reported (*1*) expansion of the vector into new areas and its growing abundance in Central Europe.

Acknowledgement

We thank Michaela Kubelová, Markéta Rybářová, and Vojtech Baláž, who helped with collection and DNA isolations of part of the samples. Studied ticks originated from the collections of the authors.

This work was supported by project IGA 218/2020/FVHE UVPS Brno and by the grant In the light of evolution: theories and solutions (GINOP-2.3.2-15-2016-00057).

About the Author

Dr. Balážová is a junior scientist at Veterinary University in Brno, Czech Republic. Her research is aimed at vector-borne zoonotic diseases and the development of new molecular methods for pathogen detection.

References

1. Földvári G, Široký P, Szekeres S, Majoros G, Sprong H. *Dermacentor reticulatus*: a vector on the rise. Parasit Vectors. 2016;9:314. https://doi.org/10.1186/s13071-016-1599-x
2. Parola P, Rovery C, Rolain JM, Brouqui P, Davoust B, Raoult D. *Rickettsia slovaca* and *R. raoultii* in tick-borne rickettsioses. Emerg Infect Dis. 2009;15:1105–8. https://doi.org/10.3201/eid1507.081449
3. Rudolf I, Venclíková K, Blažejová H, Betášová L, Mendel J, Hubálek Z, et al. First report of *Rickettsia raoultii* and *Rickettsia helvetica* in *Dermacentor reticulatus* ticks from the Czech Republic. Ticks Tick Borne Dis. 2016;7:1222–4. https://doi.org/10.1016/j.ttbdis.2016.07.011
4. Rózsa L, Reiczigel J, Majoros G. Quantifying parasites in samples of hosts. J Parasitol. 2000;86:228–32. https://doi.org/10.1645/0022-3395(2000)086[0228:QPISOH]2.0.CO;2
5. Wölfel R, Essbauer S, Dobler G. Diagnostics of tick-borne rickettsioses in Germany: a modern concept for a neglected disease. Int J Med Microbiol. 2008;298:368–74. https://doi.org/10.1016/j.ijmm.2007.11.009
6. Szekeres S, Docters van Leeuwen A, Rigó K, Jablonszky M, Majoros G, Sprong H, et al. Prevalence and diversity of human pathogenic rickettsiae in urban versus rural habitats, Hungary. Exp Appl Acarol. 2016;68:223–6. https://doi.org/10.1007/s10493-015-9989-x
7. Špitalská E, Sparagano O, Stanko M, Schwarzová K, Špitalský Z, Škultéty Ľ, et al. Diversity of *Coxiella*-like and *Francisella*-like endosymbionts, and *Rickettsia* spp., *Coxiella burnetii* as pathogens in the tick populations of Slovakia, Central Europe. Ticks Tick Borne Dis. 2018;9:1207–11. https://doi.org/10.1016/j.ttbdis.2018.05.002
8. Švehlová A, Berthová L, Sallay B, Boldiš V, Sparagano OAE, Spitalská E. Sympatric occurrence of *Ixodes ricinus, Dermacentor reticulatus* and *Haemaphysalis concinna* ticks and *Rickettsia* and *Babesia* species in Slovakia. Ticks Tick Borne Dis. 2014;5:600–5. https://doi.org/10.1016/j.ttbdis.2014.04.010
9. Duscher GG, Hodžić A, Weiler M, Vaux AGC, Rudolf I, Sixl W, et al. First report of *Rickettsia raoultii* in field collected *Dermacentor reticulatus* ticks from Austria. Ticks Tick Borne Dis. 2016;7:720–2. https://doi.org/10.1016/j.ttbdis.2016.02.022
10. Hornok S, Meli ML, Gönczi E, Hofmann-Lehmann R. Seasonally biased or single-habitat sampling is not informative on the real prevalence of *Dermacentor reticulatus*-borne rickettsiae—a pilot study. Acta Vet Hung. 2017;65:81–8. https://doi.org/10.1556/004.2017.008

Address for correspondence: Pavel Široký, Department of Biology and Wildlife Diseases, Faculty of Veterinary Hygiene and Ecology, University of Veterinary Sciences Brno, Palackého 1946/1, 61242 Brno, Czech Republic; email: sirokyp@vfu.cz

Spread of SARS-CoV-2 Variants on Réunion Island, France, 2021

Alizé Mercier, David A. Wilkinson, Camille Lebarbenchon, Patrick Mavingui, Luce Yemadje-Menudier

Author affiliations: Santé Publique France, Saint-Denis, France (A. Mercier, L. Yemadje-Menudier); Université de La Réunion, Centre National de la Recherche Scientifique, Institut National de la Santé et de la Recherche Médicale, Institut de Recherche pour le Développement, Sainte-Clotilde, France (D.A. Wilkinson, C. Lebarbenchon, P. Mavingui); Plateforme Technologique du Cyclotron Réunion Océan Indien (CYROI), Sainte-Clotilde (D.A. Wilkinson)

DOI: https://doi.org/10.3201/eid2804.212243

In January 2021, after detection of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) variants, genomic surveillance was established on Réunion Island to track the introduction and spread of SARS-CoV-2 lineages and variants of concern. This system identified 22 SARS-CoV-2 lineages, 71% of which were attributed to the Beta variant

Coronavirus disease (COVID-19) is a respiratory illness caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). On Réunion Island, an overseas department of France located in the Indian Ocean, the first cases of COVID-19 were detected on March 11, 2020, in a group of travelers (D.A. Wilkinson et al., unpub. data, https://doi.org/10.1101/2021.01.21.21249623). In response, a regional epidemiologic surveillance focusing on contact tracing and early detection of clusters was conducted. After several months of imported cases and sporadic autochtonous cases, a sharp increase in locally acquired infections was recorded in August 2020, after the return of many Réunion Island residents from travel abroad, primarily mainland France, where the incidence rate was high. The virus subsequently spread throughout the island.

In January 2021, after SARS-CoV-2 variants were detected, genomic surveillance was established to track the introduction and spread of SARS-CoV-2 lineages on the island. During January–June 2021, we generated a total of 1,528 genome sequences with ≥90% coverage using the ARTIC protocol (https://artic.network/ncov-2019/ncov2019-bioinformatics-sop.html) and nanopore technology (MinION; Oxford Nanopore Technologies, https://nanoporetech.com). This collection represents 8.3% of all COVID-19 cases on Réunion Island during that period (n = 18,409). Sample selection was pseudo-random; a small proportion of cases was prioritized for sequencing because of atypical epidemiologic or clinical characteristics. Pangolin lineages were assigned to all genomes using Pangolin version 1.2.88 (https://github.com/cov-lineages/pango-designation/releases/tag/v1.2.88).

We present the main findings of genomic surveillance from weeks 1–22, 2021 (January 4–June 6, 2021). We focused on the evolution of the weekly proportions of the 8 most frequent SARS-CoV-2 variants and examined the correlation between the weekly number of confirmed cases and the proportion of sequences identified as Beta variant (B.1.351). We extracted lineage distributions in other islands of the Indian Ocean and South Africa from the GISAID database (http://www.gisaid.org) to investigate the origins of the Beta variant sublineages.

We identified 22 SARS-CoV-2 lineages, 71% of which were attributed to the Beta variant (sublineages B.1.351 and B.1.351.2) (Table). On the basis of available data in the GISAID database, lineage B.1.622 seems to be specific to Réunion Island; no other sequence had been reported elsewhere.

Table. Observed lineages of severe acute respiratory syndrome coronavirus 2, Réunion, France, 2021

Pangolin lineage	No. genomes
B.1.351.2 (Beta, sub-lineage 2)	716
B.1.351 (Beta, sub-lineage 0)	361
B.1.177	154
B.1.622	71
B.1.1.7 (Alpha)	65
B.1.160	55
B.1.160.18	36
B.1.1.353	18
B.1.617.2 (Delta)	14
B.1.438.2	10
B.1.525 (Eta)	8
B.1.416.1	5
B.1.177.24	3
B.1	3
B.1.177.37	2
B.1.1	1
B.1.1.241	1
B.1.160.27	1
B.1.177.81	1
B.1.221	1
B.1.428.2	1
P.2	1
Total	1,528

The Beta variant was first detected on Réunion Island during the first week of January 2021, although it may have been introduced before its detection by full-genome sequencing. During the first 6 weeks of 2021, lineages known to have high levels of circulation in Europe (e.g., B.1.160, B.1.177) represented most sequenced genomes (Figure). This finding highlights the strong effect of air travel on COVID-19 dynamics on an island such as Réunion (*1*; D.A. Wilkinson et al., unpub. data).

Since mid-February 2021 (week 7 of 2021), the Beta variant has become dominant on Réunion Island, despite low-level circulation of the Alpha variant, another variant of concern that was dominant in mainland France and other countries in Europe at that time. We detected a correlation (Spearman $\rho = 8.4 \times 10^{-4}$; $p<0.001$) between the number of COVID-19 cases in January–February 2021 and the number of sequences attributed to the Beta variant, which has been shown to have increased transmissibility (C.A. Pearson et al., unpub. data, https://cmmid.github.io/topics/covid19/sa-novel-variant.html). Several additional factors could explain the dominance of Beta variant; genetic and epidemiologic factors may have contributed to a founder effect, a higher frequency of virus introductions resulting from holiday travels, possible superspreading events, and local and regional contexts (*2*). Indeed, geographic proximity and population movements with Mayotte, another overseas department of France, and Comoros link Réunion Island to South Africa, where Beta variant was first reported (*3*).

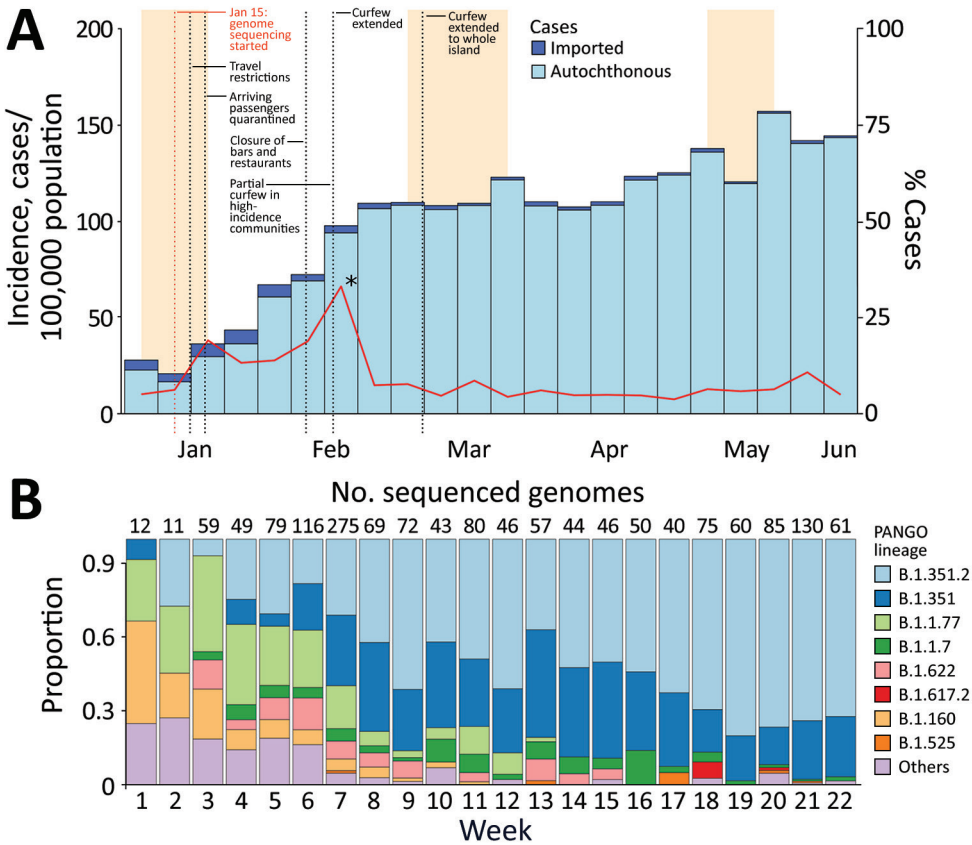


Figure. A) Epidemic curve of severe acute respiratory syndrome coronavirus 2cases detected in Réunion, France by week of sampling, weeks 1–22, 2021. Orange bars correspond to school holidays. B) Distribution of severe acute respiratory syndrome coronavirus 2 lineages identified in Réunion, France. Weekly number of sequenced genomes appears above the relevant bar.

We detected 2 sublineages of Beta variant, B.1.351 and B.1.351.2. Sublineage B.1.351.2 accounted for 3-fold more cases than B.1.351. It was detected concurrently in Mayotte, Comoros, and Réunion Island. This finding, coupled with information from GISAID, suggests that lineage B.1.351.2 was imported to Comoros and Mayotte from South Africa and could have been introduced to Réunion Island from Mayotte (*4*) (Appendix 1, https://wwwnc.cdc.gov/EID/article/28/4/21-2243-App1.pdf). This possible introduction from Mayotte is supported by the flow of travelers between the 2 departments and the notable peak in COVID-19 cases that occurred in Mayotte during weeks 1–11, mainly caused by the Beta variant (*5*). However, analysis of the origin of lineages is strongly affected by each location's capacity to sequence and report genomes in GISAID, which renders comparison between different locations difficult (*4*).

Our study provides valuable insights into the interactions between SARS-CoV-2 lineages on Réunion Island, which represents a closed system with controlled entries, especially when travel restrictions are in place. Additional research on genomic epidemiology and the effect of air travel can further improve understanding of why some variants become dominant over others, particularly in insular contexts. The future of genomic surveillance on Réunion Island will focus on mutation screening to increase reactivity, combined with real-time sequencing, as a robust approach to track the spread of emerging SARS-CoV-2 variants of concern and to inform public health actions (*6*,*7*).

Acknowledgments

We thank all the partners involved in the surveillance of COVID-19 in the Regional Health Agency and the Regional Health Insurance Fund. We acknowledge the key role of the network of sampling laboratories on Réunion Island (CHU, CHOR, Laboratoire de Saint-Benoit, Bioaustral, Réunilab, Cerballiance). We also acknowledge and thank the members of the EMERGEN consortium, as well as Laetitia Ali Oicheih, Elsa Balleydier, Adeline Feri, Javier Castro Alvarez, Sibylle Bernard-Stoecklin, Anna Maisa, Justine Schaeffer, Bruno Coignard, Guillaume Spaccaferri, Bruno Lina, Marie-Alice Simbi, Magali Turpin, Christian Mériau, and Maya Cesari. We are also grateful to the originating and submitting laboratories of the sequences from GISAID database (Appendix 2, https://wwwnc.cdc.gov/EID/article/28/4/21-2243-App1.xlsx). All data submitters may be contacted via the GISAID website (https://www.gisaid.org).

About the Author

Dr. Mercier is an epidemiologist at Santé publique France, based in the regional office of Réunion. She has a PhD in epidemiology specialized in epidemic intelligence. Her research interests include infectious disease epidemiology, epidemic intelligence, and modeling.

References

1. O'Toole Á, Hill V, Pybus OG, Watts A, Bogoch II, Khan K, et al. Tracking the international spread of SARS-CoV-2 lineages B. 1.1. 7 and B. 1.351/501Y-V2. Wellcome Open Research. 2021;6. https://doi.org/10.12688/wellcomeopenres.16661.1
2. Díez-Fuertes F, Iglesias-Caballero M, García-Pérez J, Monzón S, Jiménez P, Varona S, et al. A founder effect led early SARS-COV-2 transmission in Spain. J Virol. 2021;95:e01583–20. https://doi.org/10.1128/JVI.01583-20
3. Taglioni F. La Réunion; Mayotte; Union des Comores. In: Simon G., dir. Dictionary of international migration: geohistorical approach [in French]. Paris: Armand Colin; 2015.
4. Latif AA, Mullen JL, Alkuzweny M, Tsueng G, Cano M, Haag E, et al.; Center for Viral Systems Biology. B.1.351.2 lineage report [cited 2021 Oct 28]. https://outbreak.info/situation-reports?pango=B.1.351.2
5. Santé publique France. COVID-19: weekly report from Mayotte as of 1 April 2021 [in French]. 2021 [cited 2021 Oct 28]. https://www.santepubliquefrance.fr/regions/ocean-indien/documents/bulletin-regional/2021/covid-19-point-epidemiologique-a-mayotte-du-1er-avril-2021
6. Meredith LW, Hamilton WL, Warne B, Houldcroft CJ, Hosmillo M, Jahun AS, et al. Rapid implementation of SARS-CoV-2 sequencing to investigate cases of health-care associated COVID-19: a prospective genomic surveillance study. Lancet Infect Dis. 2020;20:1263–71. https://doi.org/10.1016/S1473-3099(20)30562-4
7. Wang H, Jean S, Eltringham R, Madison J, Snyder P, Tu H, et al. Mutation-specific SARS-CoV-2 PCR screen: rapid and accurate detection of variants of concern and the identification of a newly emerging variant with spike L452R mutation. J Clin Microbiol. 2021;59:e0092621. https://doi.org/10.1128/JCM.00926-21

Address for correspondence: Luce Yemadje-Menudier, Santé Publique France—Réunion Island, 2 bis avenue Georges Brassens, 97408 Saint-Denis CEDEX 9, La Réunion, France; email: luce.menudier@santepubliquefrance.fr

Community Transmission of SARS-CoV-2 Omicron Variant, South Korea, 2021

Eun-Young Kim,[1] Young June Choe,[1] Hanul Park, Hyoseon Jeong, Jae-Hwa Chung, Jeonghee Yu, Hwa-Pyeong Ko, Hyun Jeong Ahn, Mi-Young Go, Ju-Hyung Lee, Won Ick Kim, Bu Sim Lee, Sooyeon Kim, Mi Yu, Jia Kim, Hye Ryeon Lee, Eun Jung Jang, Ji Joo Lee, Hye Young Lee, Jong Mu Kim, Ji Hyun Choi, Sang Eun Lee, Il-Hwan Kim, Ae Kyung Park, Jee Eun Rhee, Eun-Jin Kim, Sangwon Lee, Young-Joon Park

Author affiliations: Honam Regional Center for Disease Control and Prevention, Gwangju, South Korea (E.-Y. Kim, H. Jeong, J.-H. Chung, J. Yu); Korea University Anam Hospital, Seoul, South Korea (Y.J. Choe); Korea Disease Control and Prevention Agency, Cheongju, South Korea (H. Park, M. Yu, J. Kim, H.R. Lee, E.J. Jang, J.J. Lee, H.Y. Lee, J.M. Kim, J.H. Choi, S.E. Lee, I.-.H. Kim, A.K. Park, J.E. Rhee, E.-J. Kim, S. Lee, Y.-J. Park); Gwangju Metropolitan Government, Gwangju (H.-P. Ko); Jeollabuk-do Government, Jeonju, South Korea (H.J. Ahn, M.-Y. Go); Jeollabuk-do Center for Infectious Disease Control and Prevention, Jeonju, South Korea (J.-H. Lee); Jeollanam-do Government, Muan, South Korea (W.I. Kim, B.S. Lee); Jeollanam-do Communicable Disease Management Support Team, Muan (S. Kim)

DOI: https://doi.org/10.3201/eid2804.220006

In South Korea, a November 2021 outbreak caused by severe acute respiratory syndrome coronavirus 2 Omicron variant originated from 1 person with an imported case and spread to households, kindergartens, workplaces, restaurants, and hospitals, resulting in 11 clusters within 3 weeks. An epidemiologic curve indicated rapid community transmission of the Omicron variant.

The severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) B.1.1.529 (Omicron) variant of concern has been suggested to be more transmissible than previous variants of concern (*1*). We describe an outbreak caused by the Omicron variant that originated from 1 person with an imported case and rapidly spread within 3 weeks to the community in South Korea.

Details of the surveillance and quarantine system in South Korea have been described (*2*). Public health officers interviewed case-patients, and to identify links between clusters, we created epidemic curves

[1]These authors contributed equally to this article.

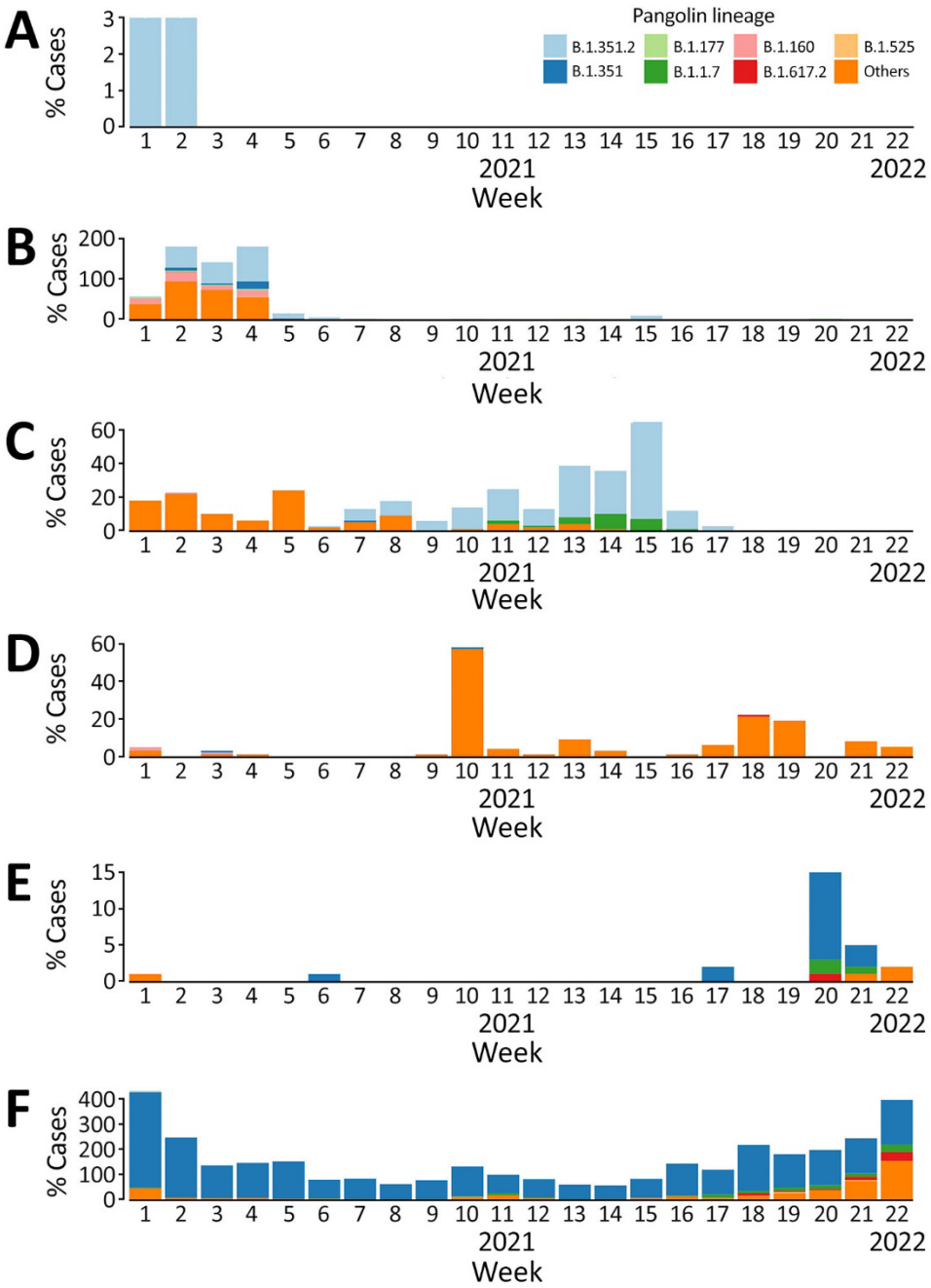
Article DOI: https://doi.org/10.3201/eid2804.212243

Spread of SARS-CoV-2 Variants on Réunion Island, France, 2021

Appendix 1

GISAID Sequences

We searched in the GISAID database for sequences collected over the same time period as our study (January 4–June 6, 2021). The amount of sequencing data available from the different countries in the region was highly variable. We obtained 705 sequences from Mayotte, where B.1.351.2 accounted for 49% of all submitted sequences and was more frequent than B.1.351. Only 6 sequences were available from the neighboring islands of the Comoros archipelago, of which all were B.1.351.2. There were 27 sequences available from the Seychelles, most of which were B.1.351. Réunion's closest neighboring island, Mauritius, had 153 sequences deposited over the same study period; none were from lineage B.1.351.2. Three isolates were associated with the Beta variant, which suggested that Mauritius and Réunion have highly contrasting epidemiologic circulation of SARS-CoV-2 variants. The amount of data from Madagascar was also limited considering its size and population; 569 sequences were available for the study period. B.1.351.2 lineage only became prevalent among GISAID-deposited genomes from Madagascar in week 07-2021, after its emergence and circulation in other islands of the southwestern Indian Ocean.



Appendix Figure. Circulation of SARS-CoV-2 lineages in islands of the southwestern Indian Ocean and South Africa, weeks 01–22, 2021. A) Comoros. B) Mayotte. C) Madagascar. D) Mauritius. E) Seychelles, F) South Africa.