

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.

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References

- 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>
- Parola P, Rovero C, Rolain JM, Brouqui P, Davoust B, Raoult D. *Rickettsia slovacica* and *R. raoultii* in tick-borne rickettsioses. *Emerg Infect Dis*. 2009;15:1105-8. <https://doi.org/10.3201/eid1507.081449>
- Rudolf I, Vencliková 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>
- Rózsa L, Reiczig 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](https://doi.org/10.1645/0022-3395(2000)086[0228:QPISOH]2.0.CO;2)
- 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>
- 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>
- Špitalská E, Sparagano O, Stanko M, Schwarzová K, Špitalský Z, Škultéry L, 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>
- Švehlová A, Berthová L, Sallay B, Boldiš V, Sparagano OAE, Špitalská 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>
- 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>
- 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>

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

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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 autochthonous 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 $\geq 90\%$ 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).

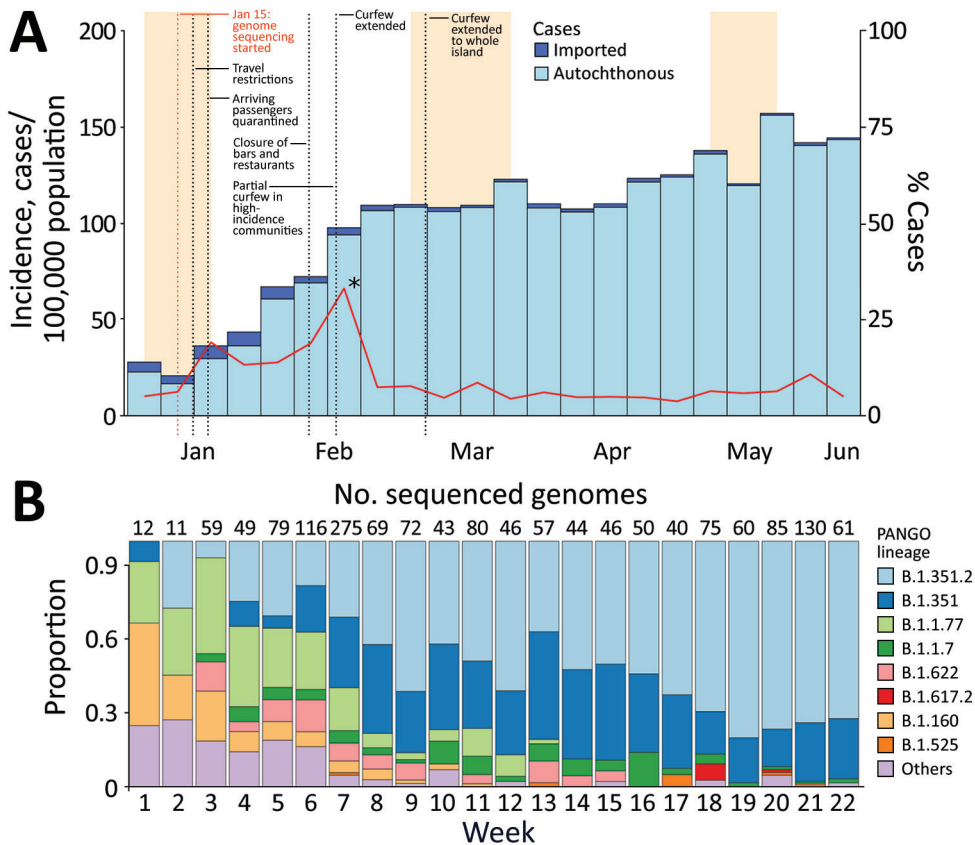


Figure. A) Epidemic curve of severe acute respiratory syndrome coronavirus 2 cases detected in Réunion, France by week of sampling, weeks 1–22, 2021. Orange bars correspond to school holidays. B) Distribution of severe acute respiratory syndrome coronavirus 2 lineages identified in Réunion, France. Weekly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

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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: geographical 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](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>

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

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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

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