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# Genomic Evidence of In-Flight SARS-CoV-2 Transmission, India to Australia, April 2021

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Epidemiologic and genomic investigation of SARS-CoV-2 infections associated with 2 repatriation flights from Australia to India in April 2021 indicated that 4 passengers transmitted SARS-CoV-2 to ≥11 other passengers. Results suggest transmission despite mandatory mask use and predeparture testing. For subsequent flights, predeparture quarantine and expanded predeparture testing were implemented.

During the first epidemic wave of SARS-CoV-2, Australia closed its borders; during March 28, 2020–November 1, 2021, international arriving passengers were required to undergo mandatory supervised quarantine (*1*). This initial response contributed to the end of the first pandemic wave in June 2020 and resulted in periods of COVID-19 control throughout the country (*2*).

Beginning October 23, 2020, a quarantine facility in Darwin, Northern Territory, Australia, received persons who arrived via government-assisted repatriation flights. On April 15 and 17, 2021, two repatriation flights (flights 1 and 2) carrying pas-

**Table.** Detailed information of case-patients belonging to SARS-CoV-2 genomic clusters detected after 2 flights from India to Darwin, Northern Territory, Australia, on April 15 and April 17, 2021*

| Cluster and case-patient | Age group, y/sex | Family group | Virus Pango lineage | Cycle threshold | Symptom onset date | Date tested positive | Vaccinated | Seat no. |
|---|---|---|---|---|---|---|---|---|
| 1 | | | | | | | | |
| A | 30–39/M | None | B.1.617.2 | 14.3 | Asymptomatic | Apr 15 | N | 56B |
| B | 40–49/M | I | B.1.617.2 | 15.6 | Asymptomatic | Apr 15 | N | 43D |
| C | 20–29/F | I | B.1.617.2 | 11.6 | Apr 20 | Apr 20 | N | 43E |
| D | 1–5/F | I | B.1.617.2 | 11.6 | Asymptomatic | Apr 20 | N | 43F |
| E | <1/M | I | B.1.617.2 | 12.2 | Asymptomatic | Apr 20 | N | 43D |
| F | 30–39/M | II | B.1.617.2 | 22.6 | Apr 20 | Apr 20 | N | 43K |
| G | 10–19/F | II | B.1.617.2 | 18 | Apr 20 | Apr 20 | N | 43H |
| H | 1–5/M | II | B.1.617.2 | 26.5 | Asymptomatic | Apr 20 | N | 43J |
| I | <1/F | II | B.1.617.2 | 19 | Asymptomatic | Apr 20 | N | 43K |
| 2 | | | | | | | | |
| J | 20–29/F | None | B.1.617.1 | 12.4 | Apr 16 | Apr 15 | N | 42A |
| K | 50–59/M | None | B.1.617.1 | 16.6 | Apr 17 | Apr 20 | N | 51H |
| L | 1–5/M | III | B.1.617.1 | 22 | Asymptomatic | Apr 22 | N | 42B |
| M | 1–5/M | III | B.1.617.1 | 18.1 | Apr 22 | Apr 22 | N | 43B |
| N | 30–39/F | III | B.1.617.1 | 20 | Asymptomatic | Apr 22 | N | 43B |
| 3 | | | | | | | | |
| O | 50–59/F | IV | B.1.617.2 | 14.9 | Asymptomatic | Apr 15 | Y | 3E |
| P | 60–69/M | IV | B.1.617.2 | 14.9 | Apr 15 | Apr 16 | Y | 3F |
| Q | 10–19/F | None | B.1.617.2 | 11.4 | Asymptomatic | Apr 17 | N | 4E |
| 4 | | | | | | | | |
| R | 50–59/M | V | B.1.617.2 | 14.9 | Asymptomatic | Apr 22 | N | 55A |
| S | 60–69/F | V | B.1.617.2 | 14.9 | Apr 22 | Apr 23 | N | 55B |
| 5 | | | | | | | | |
| T | 10–19/M | | B.1.617.2 | 11.7 | Apr 17 | Apr 18 | N | 48C |
| U | 30–39/M | VI | B.1.617.2 | 16.1 | Asymptomatic | Apr 24 | N | 48B |
| V | 30–39/F | VI | B.1.617.2 | 12.8 | Not available | Apr 24 | N | 48A |
| W | 1–5/M | | B.1.617.2 | 24.5 | Asymptomatic | Apr 24 | N | 48J |
| 6 | | | | | | | | |
| X | 30–39/M | VII | B.1.1.7 | 10.9 | Asymptomatic | Apr 17 | N | 43F |
| Y | 40–49/M | VII | B.1.1.7 | 13.1 | Asymptomatic | Apr 17 | N | 43E |

sengers from 2 regions of India experiencing major COVID-19 outbreaks landed in Darwin. The percentages of passengers positive for COVID-19 were substantially greater for these 2 flights (24/164 [15%] and 23/181 [13%]) than for all previous repatriation flights to Darwin (225/9,651 [2%] during October 2020–April 2021).

In the 48 hours before flying, all passengers on the 2 flights had tested negative for SARS-CoV-2 by quantitative reverse transcription PCR (qRT-PCR). All passengers except infants and children were required to wear masks (*3*). COVID-19 vaccination coverage among passengers was low; 24/345 (7%) passengers had received ≥1 dose, and only 14 had received 2 doses of the same vaccine ≥14 days apart. At arrival, passengers entered quarantine, where they were tested for SARS-CoV-2 by qRT-PCR on days 0, 7, and 12, in addition to testing if symptomatic (Appendix 1, https://wwwnc.cdc.gov/EID/article/28/7/21-2466-App1.pdf).

Of the 47 passengers with positive results, 21 tested positive at arrival (arrival case-patients) and 26 tested positive ≥1 day after arriving in quarantine (quarantine case-patients) (Appendix 1 Figures 1, 2). Of the 21 arrival case-patients (Table), 18 were asymptomatic. qRT-PCR cycle threshold values were available for 18/21 (86%) arrival case-patients; median was 15.2 (range 8.4–34.1) cycles. For quarantine case-patients, median time of symptom onset was 5 (range 0–8) days after arrival, and the median number of days from arrival to a positive test result was 4 (range 1–7) days.

Among 41 (87%) of 47 SARS-CoV-2 genome sequences generated from case-patients on flights and 1 and 2, variant types were Delta (B.1.617.2) for 27 (57%), Kappa (B.1.617.1) for 10 (21%), Alpha (B.1.1.7) for 3 (6%), and A.23.1 sublineage for 1 (2%). Of 41 sequences, 25 (59%) belonged to 1 of 6 genomic clusters (Table; Figure; Appendix 1 Figure 3).

To determine whether infections were likely to have been acquired during flight, we analyzed case interviews, flight manifests, and genomic sequencing. Of the 21 arrival case-patients, 4 (19%) (identified as B, J, O, and T) on both flights were likely to have transmitted SARS-CoV-2 to ≥11 other passengers (F–I, L–N, Q, and U–W) who had sequences that belonged to the same SARS-CoV-2 genomic clusters, who did not belong to the same family group of an arrival case-patient, and who had been seated within 2 rows of an arrival case-patient. Using this

information, we calculated secondary attack rates of 6% (8/143) for flight 1 and 2% (3/168) for flight 2. Five case-patients (C–E, P, and Y) with genomically linked virus belonged to arrival case family groups for which transmission possibly occurred before, during, or after the flight. One case-patient (K) with virus belonging to a genomic cluster was seated >2 rows from an arrival case-patient with genomically linked virus. Virus from 2 quarantine case-patients (R and S) genomically linked them to each other but not to an arrival case-patient (Table; Figure; Appendix 1). Only 5 quarantine case-patients from the flights had sequences that did not belong to a SARS-CoV-2 genomic cluster (Appendix 1 Figures 1, 2). Genomics refuted transmission to 6 quarantine case-patients seated within 2 rows of an arrival case-patient, linking 3 to a different cluster.

Soon after the 2 repatriation flights reported here, other repatriation flights from India were suspended, but flights resumed on May 15, 2021, when mandatory 72-hour preflight quarantine of passengers within India was instituted and testing of passengers was expanded to include rapid antigen testing on entry to preflight quarantine, qRT-PCR testing 48 hours before departure, and rapid antigen testing on the day of departure (*4*). During May 15–October 14, 2021, SARS-CoV-2 test results were positive for 13 (0.29%) of 4,543 passengers on repatriation flights from India and 30 (0.28%) of 10,679 passengers on repatriation flights to Darwin. Probable contributors to reduced repatriation cases were increasing vaccination rates and abatement of the Delta wave in India and globally (*5*).

At the time of this study, COVID-19 vaccination rates in Australia were low, most jurisdictions had little or no community transmission of SARS-CoV-2, and quarantine was key to reducing international incursions. We could not exclude transmission in the departure lounge and during boarding; however, spatial proximity of case-patients who did not belong to the same family groups but had genomically linked virus supported in-flight transmission. Previous studies that reported in-flight transmission of SARS-CoV-2 (*6–10*) did not include preflight testing, whereas our study included complete preflight and postflight testing and genomic sequencing. In conclusion, our investigation revealed evidence of flight-associated SARS-CoV-2 transmission on 2 repatriation flights from India to Australia during the Delta variant wave in April 2021.


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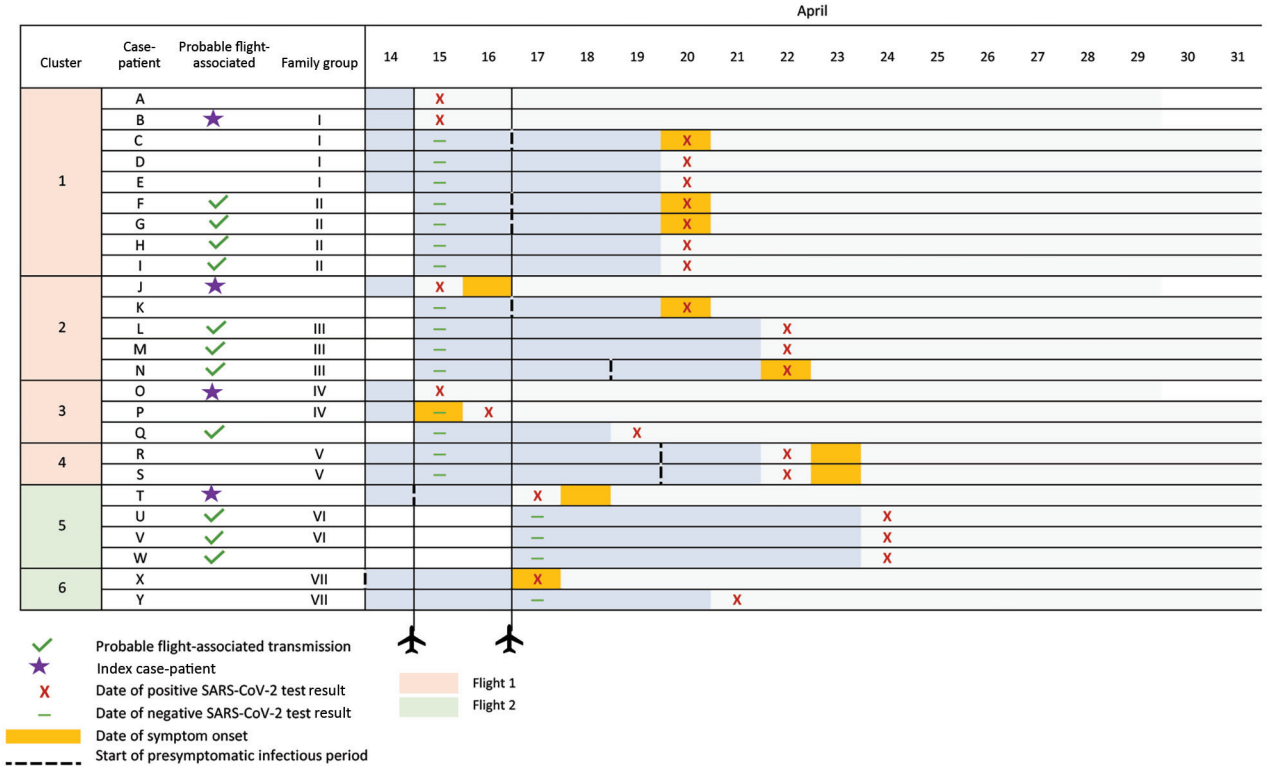


**Figure.** Schematic showing genomic clusters and in-flight transmission of SARS-CoV-2 on 2 flights from India to Australia, April 2021.

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# *Strongyloides* Hyperinfection Syndrome among COVID-19 Patients Treated with Corticosteroids

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Widespread use of corticosteroids for COVID-19 treatment has led to *Strongyloides* reactivation and severe disease in patients from endemic areas. We describe a US patient with COVID-19 and *Strongyloides* hyperinfection syndrome and review other reported cases. Our findings highlight the need for *Strongyloides* screening and treatment in high-risk populations.

Strongyloidiasis is caused by the soil-transmitted helminth *Strongyloides stercoralis* and affects ≈613.8 million persons worldwide (*1*). *S. stercoralis* infections can be asymptomatic or chronic or can cause life-threatening larva dissemination, especially in immunocompromised patients (*2*).

Among COVID-19 patients, dexamethasone is the standard treatment for persons requiring supplemental oxygen, but among persons from *Strongyloides*-