SARS-CoV-2 Omicron BA.5 Infections in Vaccinated Persons, Rural Uganda

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DOI: http://doi.org/10.3201/eid2901.220981

We describe a cluster of COVID-19 breakthrough infections after vaccination in Kyamulibwa, Kalungu District, Uganda. All but 1 infection were from SARS-CoV-2 Omicron strain BA.5.2.1. We identified 6 distinct genotypes by genome sequencing. Infections were mild, suggesting vaccination is not protective against infection but may limit disease severity.

The SARS-CoV-2 Omicron variant BA.5 was initially reported in South Africa in late February 2022 (*1*). The BA.5 variant, and especially the subvariant BA.5.2.1, has now spread to at least 104 countries globally; 197,425 genomes had been reported in GISAID (http://www.gisaid.org) as of September 16, 2022. The BA.5 spike protein shares substitutions with earlier Omicron variants but includes some of the Delta variant immune evasion changes. The BA.4/BA.5 viruses are reported to escape earlier Omicron immune responses, and vaccination does not fully block infection but may limit severity of disease (*2*–*5*). Infection of vaccinated persons (breakthrough infections) with SARS-CoV-2 strains is known, and such infections were reported recently among a highly vaccinated community within the US Embassy in Uganda (*6*). The frequency and outcomes of BA.5 vaccine breakthrough infections, both in Uganda and globally, are yet to be determined.

The Medical Research Council Unit in Uganda maintains a rural population cohort in Kyamulibwa, Kalungu District, southwestern Uganda (*7*). Unit staff were vaccinated as soon as vaccines were available in the country (March 2021), and most received at least 2 doses of COVID-19 vaccine by June 2021, with ongoing efforts for booster vaccination rolling out in the country. Staff members who had any symptoms indicating respiratory infections, including COVID-19, were routinely tested using Abbott's Panbio COVID-19 antigen rapid tests (Abbott, https://www.abbott.com). If cases of COVID-19 were detected, all staff were tested to detect asymptomatic cases. During such routine testing of staff members, a cluster of SARS-CoV-2 infections among vaccinated staff was detected. Test positivity during this period of infection was 18.5% (12 positive from 65 staff members tested), which was in the range of previous infection waves (January 3–10, 2022: 11.7%; June 6–14, 2021: 32.5%; November 30−December 1, 2020: 19.3%). Most infected staff members had mild symptoms, and all cases were quickly resolved (Appendix Table, https://wwwnc.cdc.gov/EID/article/29/1/22-0981-App1.pdf).

We performed sequencing by methods previously described (*8*). Nine cases yielded full genome SARS-CoV-2 sequences that we lineage-typed using Nextclade (*9*) and Pangolin (*10*) software; 8 of the 9 genomes were from the BA.5 lineage and 1 was BA.2.31, all variants within the Omicron variant-of-concern lineage. Although all 9 genomes belonged to the Omicron lineage, we detected 6 distinct subvariants (Figure). Genomes from cases 1, 2, 7, and 10 (all BA.5.2.1) were identical, suggesting a common infection source for these 4 cases. However, genomes for cases 4, 6, 11, and 12 genomes (also BA.5.2.1) were distinct from cases 1, 2, 7, and 10 and from each other, differing by 2–5 nt changes. The case 5 genome (BA.2.31) represents a 6th virus source for the cluster of breakthrough infections.

The detection of 5 distinct BA.5.2.1 sublineages found in Kalungu District in a short time period indicates multiple BA.5 sublineages were already circulating in other parts of Uganda and demonstrates the speed of movement of SARS-CoV-2. Uganda reported an increase in COVID-19 cases during this period, and both BA.5.2.1 and BA.2.31 virus strains potentially contributed to this increase in infections. Of note, 9 of the 12 COVID-19–positive staff members in this report routinely traveled on shared unit vehicles to and from Masaka or Kampala, which might account for the virus spread. In addition, the unit travel records show shared vehicle usage, suggesting a likely but not confirmed source of infection for cases 2, 7, and 10. The 3 infected staff members whose testing results did not yield sufficient PCR products for sequencing were asymptomatic, suggesting low viral loads (Appendix Table).

Many countries have reported increasing COVID-19 cases with BA.4 or BA.5 and derivatives as a major identified lineage. The global trend toward relaxed travel and quarantine restrictions and the mild

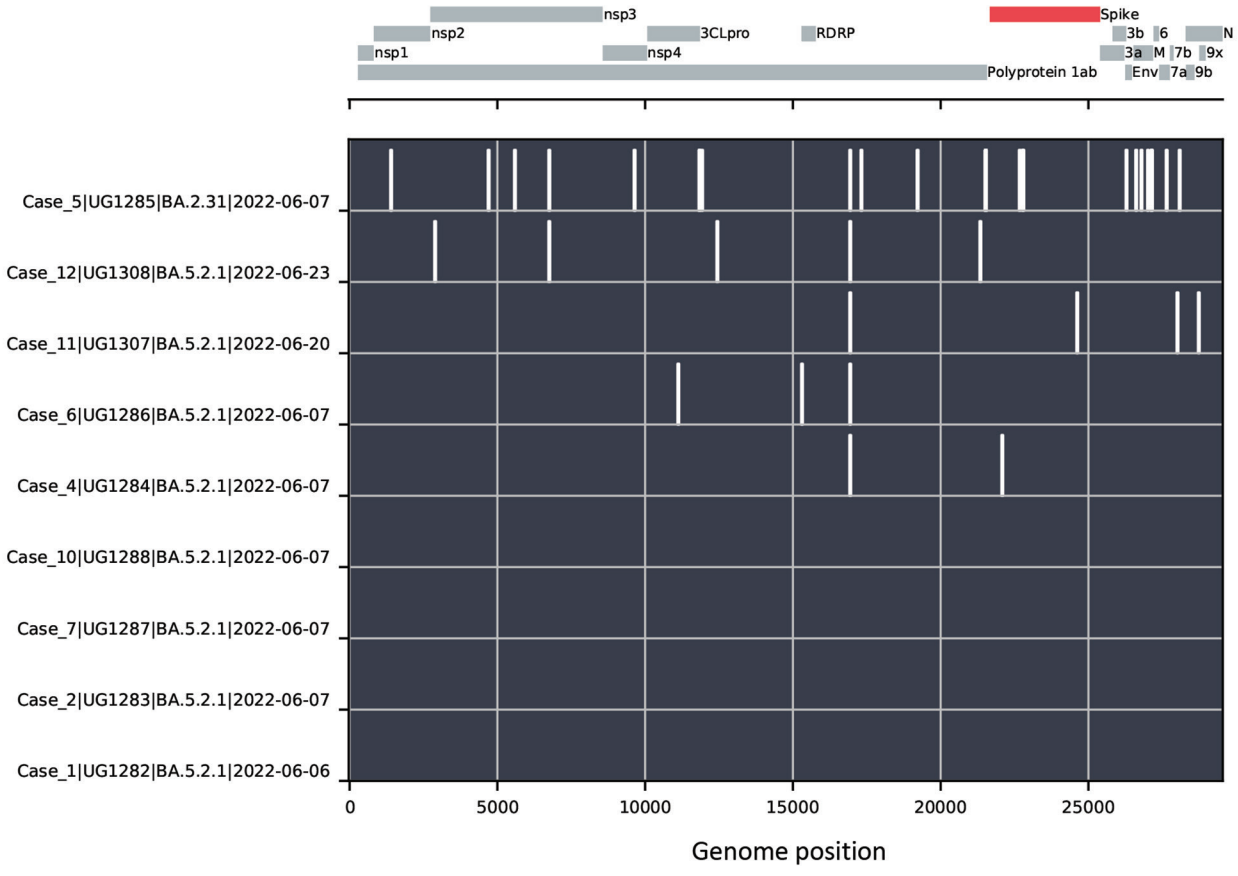

Figure. Nucleotide changes between SARS-CoV-2 genomes from a cluster of COVID-19–positive persons in Kyamulibwa, Kalungu District, rural Uganda. The lower portion of the chart shows nucleotide differences from the case 1 genome, plotted as white bars. The absence of bars in the BA.5.2.1 genomes from cases 1, 2, 7, and 10 indicates identical sequences. Case 5 was determined to be lineage BA.2.31, and cases 4, 6, 11, and 12 genomes demonstrated virus variants of lineage BA.5.2.1 distinct from the genomes from cases 1, 2, 7, and 10. A schematic of the SARS-CoV-2 genome is shown in the top portion of the chart, with protein coding regions marked.

infections in vaccinated and previously infected individuals might help enable global movement of these variants. This probably is evidenced by the timing of BA.5 appearance in rural Uganda within weeks of the variant being initially reported in other parts of the world (South Africa in late February 2022, Germany in mid-March 2022, the United States in late March 2022, Portugal in early April 2022, and Uganda in early June 2022).

In conclusion, the detection of 6 distinct sublineages of SARS-CoV-2 (5 of BA.5.2.1 and 1 of BA.2.31) in Kyamulibwa, Kalungu District, Uganda, within a short period indicates substantial diversity of and rapid movement of these viruses into and within Uganda. Combined with recent increases in reported SARS-CoV-2 infections throughout the country, our findings emphasize the need for vigilance, surveillance, and continued testing in this rural community and throughout the country. The mild nature of symptoms in these 12 cases, and in many vaccinated persons, reinforces the importance of community vaccination efforts.

Acknowledgments

We thank the staff and technicians working at the Kyamulibwa, Kalungu District field station that help make this work possible.

This work was supported by the UK Medical Research Council (MRC/UK Research and Innovation) and the UK Department for International Development under the MRC/DFID Concordat agreement (grant agreement no. MC_PC_20010) and Wellcome Trust, UK FCDO—Wellcome Epidemic Preparedness—Coronavirus (grant agreement no. 220977/Z/20/Z). The COVID-19 surveillance project in Kalungu District was supported with additional funding from the UK MRC (grant agreement no. MC_PC_20011).

This study was approved by the Uganda Virus Research Institute-Research and Ethics Committee (UVRI-REC Federalwide Assurance [FWA] FWA No. 00001354, study reference GC/127/20/04/771). Sequences described here are available from GISAID under accession numbers EPI_ISL_13332769–75, 15005215 and 15005216.

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Dr Mugisha is a medical scientist working at the Uganda Research Unit of the Medical Research Council/Uganda Virus Research Institute and London School of Hygiene & Tropical Medicine. During COVID-19, he has led surveillance activity in the unit's General Population Cohort in southwestern Uganda. His research interests are primarily on the health and social issues affecting older people in low- and middle-income countries.

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Rapid SARS-CoV-2 Seroprevalence Survey in Central and Western Divisions of Fiji, 2021

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DOI: https://doi.org/10.3201/eid2901.221514

During November–December 2021, we performed a SARS-CoV-2 seroprevalence survey in Central and Western Divisions of Fiji. A total of 539 participants 8–70 years of age were 95.5% (95% CI 93.4%–97.1%) seropositive, indicating high community levels of immunity. Seroprevalence studies can inform public health responses to emerging SARS-CoV-2 variants.

In Fiji, the SARS-CoV-2 Delta variant wave occurred in a largely unvaccinated and nonimmune population during April–November 2021 (*1*). A risk-based COVID-19 vaccine rollout strategy commenced in March 2021, and, by late November 2021, a total of 90.6% of persons ≥18 years of age had received 2 vaccine doses and 97.3% had received 1 dose (*1*). Because of the high vaccination coverage, the government of Fiji had planned to reopen international borders by early December 2021.

Serosurveillance is a fundamental component of public health response to disease. Estimating disease epidemiology, including population immunity, by using serosurveillance can inform government policy. In November 2021, no serosurveillance data were available from any Pacific Island country or territory, and data from this region remain sparse (*2*). To inform public health decisions on the safe opening

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Article DOI: http://doi.org/10.3201/eid2901.220981

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Appendix Table. Epidemiologic, demographic, and genomics features from a cluster of COVID-19–positive US Embassy staff members in Kyamulibwa, rural Uganda.

Case no.	Age, y	Gender	Vaccination dose 1	Vaccination dose 2	Vaccine booster	Previous SARS-CoV-2 infections	Travel history (eg, contact with Kampala)	Used Unit bus to Kampala	Shared Unit car to Masaka	Other epi links	Date of disease onset	Symptoms	Outcome	Co-morbidities	Sample collection date	Genome lineage
1	31	F	Mar-21	Jun-21	No	No	Internal travel to Masaka	No	Yes		04-Jun-22	Cough, runny nose, sore throat, chills	Recovered	None	06-Jun-22	BA.5.2.1
2	30	F	Mar-21	Jun-21	No	No	Internal travel to Kampala	Yes	No	Shared office with case 6	06-Jun-22	Runny nose, sore throat, red eyes	Recovered	None	07-Jun-22	BA.5.2.1
3	29	F	Jul-21	Sep-21	No	No	Internal travel to Masaka	No	Yes	Shared office with case 5	Asympt	Asympt	Recovered	None	07-Jun-22	Insufficient material to sequence
4	54	M	Mar-21	Jun-21	No	No	Local travel within Kyamulibwa	No	No		05-Jun-22	Runny nose, fever, chills	Recovered	None	07-Jun-22	BA.5.2.1
5	29	F	Jun-21	Sep-21	No	No	Internal travel to Kampala	Yes	No	Shared office with case 3	06-Jun-22	Cough, runny nose	Recovered	None	07-Jun-22	BA.2.31
6	53	M	Mar-21	Jun-21	No	No	Local travel within Kyamulibwa	No	No	Shared office with case 2	04-Jun-22	Cough, runny nose	Recovered	None	07-Jun-22	BA.5.2.1
7	43	M	Mar-21	Jun-21	No	Yes	Internal travel to Kampala	Yes	No		04-Jun-22	Cough, runny nose, fever, headache	Recovered	Severe allergies	07-Jun-22	BA.5.2.1
8	34	F	Mar-21	Jun-21	No	No	Internal travel to Kampala	Yes	No		Asympt	Asympt	Recovered	None	07-Jun-22	Insufficient material to sequence
9	42	F	Jun-21	No	No	Yes	Local travel within Kyamulibwa	No	No	Cooked and served lunch to station staff.	Asympt	Asympt	Recovered	None	07-Jun-22	Insufficient material to sequence
10	52	M	Mar-21	Jun-21	No	No	Internal travel to Kampala	Yes	No		30-May-22	Cough, runny nose, general weakness, chills	Recovered	None	07-Jun-22	BA.5.2.1
11	29	F	Mar-21	Jun-21	No	Yes	Internal travel to Kampala	Yes	No		19-Jun-22	Flu-like symptoms, malaise	Recovered	None	20-Jun-22	BA.5.2.1
12	42	F	May-21	Jul-21	No	No	Internal travel to Masaka	No	Yes		21-Jun-22	Flu-like symptoms, malaise	Recovered	None	23-Jun-22	BA.5.2.1

Vaccination was with the AstraZeneca COVID-19 vaccine (https://www.astrazeneca.com). Genome lineage determined from near complete genome sequence using Nextclade (*1*) and Pangolin (*2*). Asympt, asymptomatic.

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