case, orf virus infection was suspected because of the patient's occupational exposure and clinical compatible skin lesions (e.g., single pustular lesion and erythema multiforme aspect on the rest of the body and the absence of systemic symptoms) (*9*); infection was diagnosed with positive parapoxvirus PCR test (*3*). However, an unusual recent case in Portugal involved monkeypox infection after a needle stick injury (*10*). The patient had a solitary pustular lesion of the finger, similar to our patient, but that lesion was painful, and the clinical picture was completed with the appearance of diffuse vesicles and systemic symptoms.

This case highlights the importance of collecting a careful history at the time of patient care, including collection of exposures to possible zoonoses. Those measures are warranted to avoid unnecessary isolation and treatment and to enable appropriate infection control measures.

C.C. and S.Z. were the major contributors in writing the manuscript and performing the literature review. A.S.D. provided the pictures and the legend. A.F.R. and O.F. conducted the microbiologic study. T.K. revised the manuscript. Both lead authors have read and agreed to the published version of the manuscript. The data presented in this case study are available on request from the corresponding author.

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About the Author

Dr. Zayet is a specialist in the Infectious Diseases Department of Nord Franche-Comte Hospital, Trevenans, France. His primary research interests focus on hepatitis and tuberculosis, especially in HIV-infected patients and COVID-19 patients.

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Address for correspondence: Souheil Zayet, Department of Infectious Disease, Nord Franche-Comté Hospital, 100 Route de Moval, 90400 Trevenans, France; email: souhail.zayet@gmail.com or souheil.zayet@hnfc.fr

SARS-CoV-2 Molecular Evolutionary Dynamics in the Greater Accra Region, Ghana

Bright Adu,[1] Joseph H.K. Bonney,[1] Beverly Egyir, Isaac Darko Otchere, Prince Asare, Francis E. Dennis, Evelyn Yayra Bonney, Richard Akuffo, Ivy A. Asante, Evangeline Obodai, Selassie Kumordjie, Joyce Appiah-Kubi, Quaneeta Mohktar, Hilda Opoku Frempong, Franklin Asiedu-Bekoe, Mildred A. Adusei-Poku, James O. Aboagye, Bright Agbodzi, Clara Yeboah, Seyram B. Agbenyo, Peace O. Uche, Keren O. Attiku, Bernice Twenewaa Sekyere, Dennis Laryea, Kwame Buabeng, Helena Lamptey, Anita Ghansah, Dorothy Yeboah-Manu, Abraham K. Anang, William K. Ampofo, George B. Kyei, John K. Odoom

[1]These authors contributed equally to this article.

Author affiliations: Noguchi Memorial Institute for Medical Research, University of Ghana College of Health Sciences, Legon, Ghana (B. Adu, J.H.K. Bonney, B. Egyir, I.D. Otchere, P. Asare, F.E. Dennis, E.Y. Bonney, R. Akuffo, I.A. Asante, E. Obodai, S. Kumordjie, J. Appiah-Kubi, Q. Mohktar, H. Opoku Frempong, J.O. Aboagye, B. Agbodzi, C. Yeboah, S.B. Agbenyo, P.O. Uche, K.O. Attiku, B.Twenewaa Sekyere, D. Laryea, K. Buabeng, H. Lamptey, A. Ghansah, D. Yeboah-Manu, A.K. Anang, W.K. Ampofo, G.B. Kyei, J.K. Odoom); Ghana Health Service, Accra, Ghana (F. Asiedu-Bekoe); University of Ghana Medical School, Accra (M.A. Adusei-Poku); University of Ghana Medical Centre, Legon (G.B. Kyei)

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To assess dynamics of SARS-CoV-2 in Greater Accra Region, Ghana, we analyzed SARS-CoV-2 genomic sequences from persons in the community and returning from international travel. The Accra Metropolitan District was a major origin of virus spread to other districts and should be a primary focus for interventions against future infectious disease outbreaks.

The emergence of SARS-CoV-2 variants with superior transmissibility or immune evasion advantages may cause outbreaks and dominate transmission in a population (*1*). Thus, keeping track of the dynamics of variant transmissions in a population is crucial for developing timely and appropriate responses to outbreaks.

In Ghana, whereas the entire population experienced the COVID-19 pandemic, most infections were primarily recorded in the Greater Accra Region (GAR), the most densely populated region in Ghana with the smallest landmass (*2*). The genetic diversity of SARS-CoV-2 infections in Ghana during early (*3*) and recent (*4*) transmissions showed initial transmission driven by multiple lineages of the virus, after which the Alpha, Delta, and Omicron variants dominated. To gain information about the dynamics of SARS-CoV-2 spread within the GAR, the epicenter of the COVID-19 outbreak in Ghana, we performed a detailed analysis of variants.

We analyzed 1,163 SARS-CoV-2 genomic sequences from 834 community samples collected from 14 of the 21 districts in the GAR and 329 from returning international travelers (Table) during March 2020–February 2022. We extracted RNA from oro/nasopharyngeal swab samples of patients by using a QIAamp Viral RNA Mini Kit (QIAGEN, https://www.qiagen.com).

We prepared complementary DNA by using the LunaScript RT Super Mix Kit (New England BioLabs, https://www.neb.com). For amplicon generation, we used either the ARTIC nCoV-2019 version 3 primers (Artic Network, https://artic.network) (batch 1 samples, collected before July 2021) or the Midnight RT PCR Expansion kit (Oxford Nanopore Technologies, https://www.nanoporetech.com) (batch 2 samples, collected after July 2021). We sequenced batch 1 samples on Illumina MiSeq after library preparation with an Illumina DNA prep kit (https://www.illumina.com) and batch 2 samples on GridION after library preparation with SQK-RBK110.96 kit (Oxford Nanopore Technologies).

Table. Distribution of SARS-CoV-2 sequences analyzed by district of Ghana and origin of international travelers

Origin of travelers	Sequences, no. (%)
Ghana, n = 834	
Accra Metropolitan District	421 (50.5)
Ashaiman Municipal	1 (0.1)
Adenta Municipal	41 (4.9)
Ga East	19 (2.3)
Ga Central	8 (1.0)
Ga South	6 (0.7)
Ga West	21 (2.5)
Kpone Katamanso	1 (0.1)
La-Dade Kotopon	21 (2.5)
La-Nkwantanang Madina	9 (1.1)
Ledzokuku Krowor	6 (0.7)
Ningo Prampram	1 (0.1)
Shai Osudoku	12 (1.4)
Tema Municipal	25 (3.0)
Unnamed district*	242 (29.0)
World, n = 329	
Africa	159 (48.3)
Asia	85 (25.8)
Europe	57 (17.3)
North America	28 (8.5)

*Samples from within the Greater Accra Region but with no clear indication of the specific district.

For both batches of samples, we analyzed reads by using the ARTIC version 1.2 field bioinformatics pipeline (https://github.com/artic-network/fieldbioinformatics). We assigned Lineages by using Pangolin version 4.1.3 with pangolin-data version 1.17 (*5*).

For the phylogenetic analysis, we first aligned sequences in MAFFT version 7.490 (*6*). We inferred the maximum-likelihood tree topology of the variable positions with 1,000 bootstraps by using IQ-TREE version 2.0.7 (*7*) with the general time reversible nucleotide substitution model. We populated the maximum-likelihood tree with sampling dates by using TreeTime version 0.8.6 (*8*) and assuming a mean constant nucleotide substitutions per site per year rate of 8.0×10^{-4} (*9*) after excluding outlier sequences. We then rerooted the final dated tree with 936 sequences to the initial wild-type SARS-CoV-2 strain (GenBank accession no. NC_045512.2) and visualized in R version 4.1.2 (https://www.r-project.org) by using ggtree version 3.2.1 and ggtreeExtra version 1.4.2 packages (*10*). For the import–export analysis, we labeled the internal nodes and external

leaves of the dated phylogeny with the location/district of sample origin by using TreeTime. We inferred the number of state changes from one location/district to another and time of event by using a python script developed by Wilkinson Lab (https://github.com/CERI-KRISP/africa-covid19-genomics/tree/main/python_scripts).

Of the 152,896 SARS-CoV-2 infections reported in Ghana by February 28, 2022, the GAR alone contributed 90,267 (59.04%) (Appendix Table 1, https://wwwnc.cdc.gov/EID/article/29/4/22-1410-App1.pdf). Of the 21 districts in the GAR, the Accra Metropolitan District (AMD) consistently contributed ≈50% of reported SARS-CoV-2 infections in the region since the outbreak began in Ghana (https://ghs.gov.gh/covid19/archive.php). This finding mirrors our finding of 50.5% of sequences from the region being from the AMD (Table). Although all analyzed sequences (Appendix Table 2) came from the GAR, representative metadata for some samples were not indicated by all districts. Those districts were grouped as "Unnamed District" and accounted for 29% of the sequences, most of which were the Alpha variant (Appendix Figure 1).

Because different lineages have dominated SARS-CoV-2 transmission in Ghana at different periods, we categorized the data into the main SARS-CoV-2 variants (Alpha, Beta, Delta, Eta, Omicron, and others). From the phylogenetic analysis, the SARS-CoV-2 variants circulating in the districts of the GAR and those from returning international travelers resolved into 5 major clusters corresponding to defined categories (Appendix Figure 2, panel A). Sequences from the returning international travelers colocalized with the GAR samples, suggesting minimal divergence. We found that an estimated 77 SARS-CoV-2 variant introduction events occurred in the AMD, mainly from other parts of Africa and other districts (Appendix Figure 2, panel B). In contrast, there were an estimated 185 SARS-CoV-2 variant exportation events from the AMD, mainly to the other districts of the GAR and to relatively fewer to countries outside Ghana (Appendix Figure 2, panels C, D). Of those variant exportation events, 153 were to other districts in the GAR, making the AMD a prime district for targeted interventions aimed at reducing the spread of SARS-CoV-2 and other infectious pathogens.

In conclusion, SARS-CoV-2 genomic surveillance in the GAR of Ghana revealed the pattern of spread of variants among districts of the region, demonstrating the role of the AMD in the spread of SARS-CoV-2 in the GAR. We propose that the AMD should be a primary focus in public health interventions aimed at controlling SARS-CoV-2 and other future infectious disease outbreaks in the GAR.

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About the Author

Dr. Adu is a senior research fellow at the Noguchi Memorial Institute for Medical Research of the University of Ghana and the coordinator for the Next Generation Sequencing Core Facility of the Institute. His research interests include pathogen genomics and immunology.

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Address for correspondence: Bright Adu, Department of Immunology, Noguchi Memorial Institute for Medical Research, College of Health Sciences, University of Ghana, PO Box LG 581, Legon, Ghana; email: badu@noguchi.ug.edu.gh

Genomic Characterization of Respiratory Syncytial Virus during 2022–23 Outbreak, Washington, USA

Stephanie Goya, Jaydee Sereewit, Daniel Pfalmer, Tien V. Nguyen, Shah A.K. Mohamed Bakhash, Elizabeth B. Sobolik, Alexander L. Greninger

Author affiliations: University of Washington, Seattle, Washington, USA (S. Goya, J. Sereewit, D. Pfalmer, T.V. Nguyen, S.A.K. Mohamed Bakhash, E.B. Sobolik, A.L. Greninger); Fred Hutchinson Cancer Research Center, Seattle (A.L. Greninger)

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We sequenced 54 respiratory syncytial virus (RSV) genomes collected during 2021–22 and 2022–23 outbreaks in Washington, USA, to determine the origin of increased RSV cases. Detected RSV strains have been spreading for >10 years, suggesting a role for diminished population immunity from low RSV exposure during the COVID-19 pandemic.

Annual seasonality of respiratory syncytial virus (RSV) in Washington, USA, has been limited primarily to late autumn and winter (*1*). However, an RSV outbreak was not detected during the 2020–21 season because of the COVID-19 pandemic. After lockdowns were relaxed in the summer of 2021, an early RSV season began in August (Figure, panel A). The 2022–23 outbreak also began earlier, but the number of RSV cases was unexpectedly higher than in 2021, alarming public health authorities and the general community (*2*).

Increased severity of the 2022–23 RSV outbreak might have been caused by diminished protective immunity in the population from prolonged low exposure to this virus (*3*). Furthermore, selective pressure because of low transmission in 2020 might have caused emergence of new viral strains with improved fitness. We evaluated whether RSV causing the 2022–23 outbreak had genomic characteristics different from strains from previous seasons.

We performed hybridization capture-based, metagenomic next-generation sequencing of 54 RSV genomes (14 RSV strains from 2021–22 and 40 from 2022–23) isolated during outbreaks in King County, Washington. In brief, we extracted virus RNA from excess nasal or nasopharyngeal swab specimens collected from persons seeking care at University of Washington Medicine COVID-19 collection sites, clinics, emergency rooms, and inpatient facilities who tested positive for RSV by PCR with a cycle threshold <30 (Table) (*4*). All persons were outpatients except for 2 hospitalized patients from 2021. For phylogenetic analyses, we downloaded complete genomes of RSV-A and RSV-B subtypes from GenBank and GISAID (https://www.gisaid.org) databases. We performed genome alignments by using MAFFT software (https://mafft.cbrc.jp/alignment/software) and constructed phylogenetic trees by using IQ-TREE (*5*) (Appendix, https://wwwnc.cdc.gov/EID/article/29/4/22-1834-App1.pdf).

Among sequenced specimens, we detected 1 RSV-A and 13 RSV-B subtypes from 2021–22 and 30 RSV-A and 10 RSV-B subtypes from 2022–23 (Table). We did not detect co-infections with other respiratory viruses (Appendix) or differences in subtype predominance by patient age group or sex during the 2022–23 outbreak ($p>0.1$ by Fisher exact test). We genotyped the RSV *G* gene and found that 7 RSV-A sequences were GA2.3.5 and 24 were GA2.3.6b genotypes (both comprising ON1 strains), and all RSV-B sequences were the GB5.0.5.a genotype (BA strains) (*6*) (Appendix). We found that Washington RSV (WA-RSV) sequences were closely related to contemporary viruses by