single mutants (i.e., BA.2_L452Q and BA.2_S704L) had neutralizing-antibody escape that was similar to that of the BA.4/5 and BA.2.12.1 subvariants, with neutralizing-antibody titers that were 14.1% and 26.6% lower, respectively, than those against BA.2 (P>0.05 for both comparisons) (Fig. 1D). Notably, 2 of 30 BA.1-infected but unvaccinated patients (Patients U12 and U13) had high neutralizing-antibody titers against all the variants except BA.4/5, whereas patients who had received a booster dose had broader neutralization against all the variants examined (Fig. S3C and S3D). Overall, these results showed that infection during the BA.1 wave did not appear to offer effective protection against the newly emerged sublineages.

In this study, we characterized infection-induced immunity and vaccine-induced immunity against newly emerged omicron subvariants. Booster vaccination provided sufficient neutralizing-antibody titers against the BA.4/5 and BA.2.12.1 subvariants, albeit to a lower extent than against BA.1 and BA.2.[4,5] These findings underscore the importance of booster vaccination for protection against emerging variants.

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Detection of Marburg Virus Disease in Guinea

TO THE EDITOR: On August 2, 2021, a 46-year-old man from Temessadou M'Boké, a village in Guéckédou prefecture in Guinea, died after hemorrhaging from several natural orifices. On August 3, an initial diagnosis of Marburg virus (MARV) infection was made after real-time reverse-transcriptase–polymerase-chain-reaction testing of a postmortem buccal sample obtained from the patient was performed and revealed a cycle-threshold value of 13.4 (Fig. 1A). Field investigation teams were deployed, and the diagnostic finding was validated in two additional laboratories within a few days. In-country metagenomic next-generation sequencing allowed for full-length MARV genome recovery (99.3%), and phylogenetic analysis indicated that the new Guinea MARV strain that had been identified in the patient clustered with MARV strains isolated from bats in Sierra Leone and from humans in Angola (Fig. S1 and Table S1 in the Supplementary Appendix, available with the full text of this letter at NEJM.org). Close monitoring for a period of 21 days confirmed that all the patient's contacts had remained asymptomatic, and no additional cases were detected.

Guinean forests, along with other areas of West Africa, including Sierra Leone, are thought to be environmentally suitable for zoonotic transmission of Marburg virus disease by bats and particularly by *Rousettus aegyptiacus* (Egyptian fruit bat), which has been identified as a natural MARV reservoir host (Fig. 1B).[1-3] Among the bat

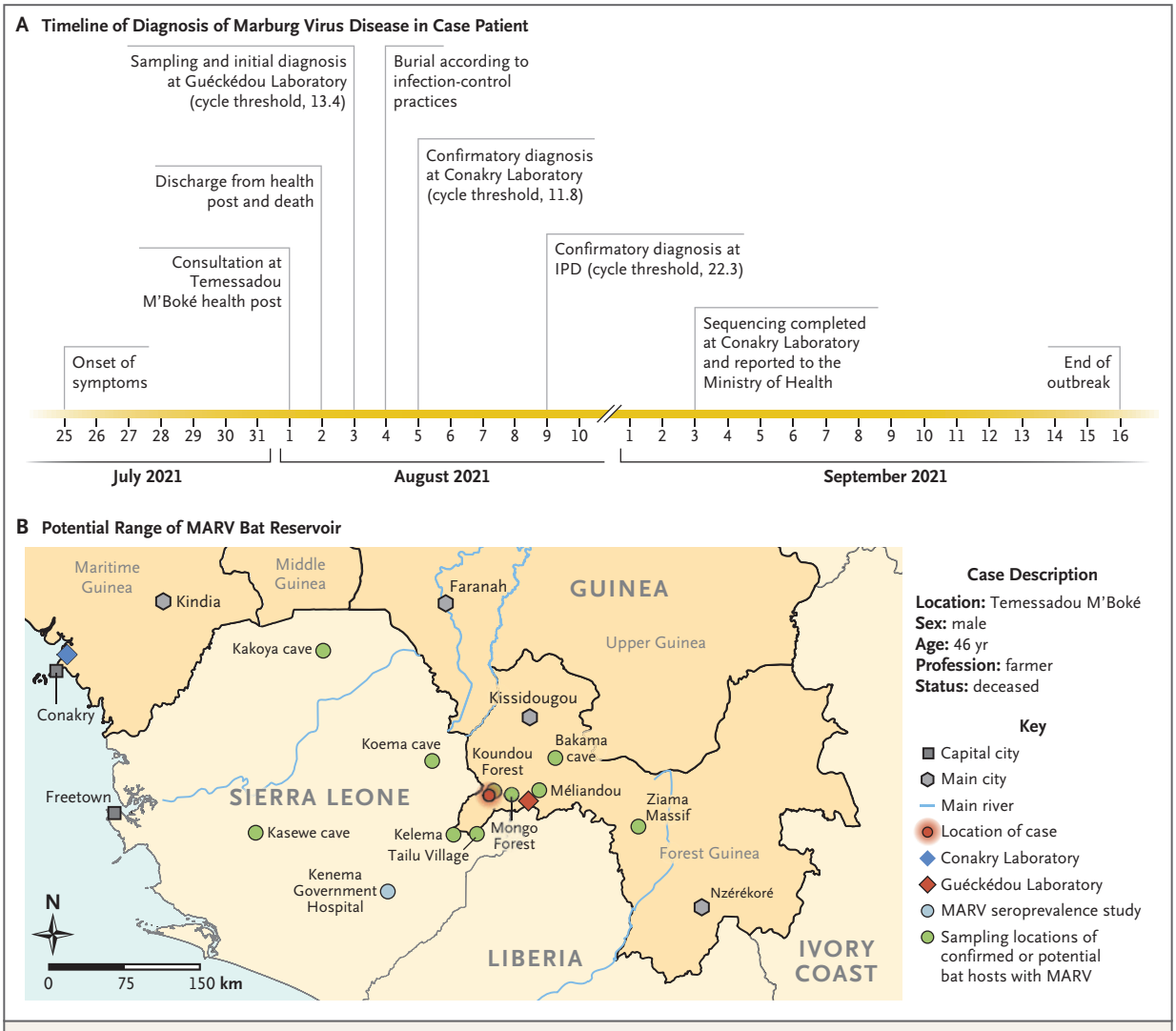

Figure 1. Timeline and Map of Marburg Virus (MARV) Infection in Guinea.

Panel A shows the timeline of events in the diagnosis of MARV infection in a 46-year-old man in Guéckédou prefecture in Guinea in August 2021. On September 3, Laboratoire des Fièvres Hémorragiques Virales de Guéckédou shared the MARV genetic sequence with the public (https://virological.org/t/marburg-virus-sequence-from-guinea-2021/755) to support the public health response as well as the development and evaluation of diagnostic tests and therapeutic agents for MARV infection. IPD denotes Institut Pasteur de Dakar. Panel B shows a map depicting portions of Guinea, Sierra Leone, Liberia, and Ivory Coast, with a focus on the Guinean forests (Forest Guinea) and the Guéckédou prefecture, where the case of MARV infection emerged. Relevant locations of sites with reported evidence of MARV circulation in bats and in humans in Sierra Leone are shown, along with sites in Guinea where bat species that are known to be potential reservoir hosts of MARV have been identified, including Méliandou (the location of the 2014–2016 Ebola virus disease outbreak), as well as Mongo Forest, Koundou Forest, Bakama cave, and Ziama Massif. Details regarding the mapping procedure are provided in the Supplementary Appendix.

reservoirs of MARV is Koundou, which is close to the location where the case emerged. The patient had limited social interactions and lived in a household of four people. There was no evidence of a travel history outside Guinea for the patient or his close contacts or of contact with returning travelers. He was a farmer living in close contact with nature and wildlife and may therefore have had repeated exposure to an environment or food contaminated with excreta of MARV-infected bats. Community surveys showed that although he may have harvested wild fruits for personal consumption, there was no suggestion that he had visited caves or been

involved in hunting activities for bushmeat, including bats. Traditional practices of bushmeat consumption or preparation (i.e., direct exposure to body fluids) cannot be fully excluded, since it is unlikely that such exposures would have been disclosed owing to the national ban on such consumption that had been enforced after the 2021 outbreak of Ebola virus disease.

The new Guinea MARV and the Angola MARV clade share a common ancestor that probably existed in 1965 (95% confidence interval, 1944 to 1981 on Bayesian molecular clock analysis). This finding indicates that approximately 55 years ago, these lineages diverged from a common ancestor, and each evolved independently in its respective reservoir host, with the presence of the Guinea MARV remaining undetected until this 2021 spillover event. This timescale of decades provided ample opportunity for the virus to be dispersed over large distances by bat migration. A parallel could be drawn with the emergence of the West African Ebola virus lineage (Makona) that diverged from a central African ancestor and independently evolved in its host until the spillover event happened.[4] In the case of MARV, the basal clustering of bat MARV in Sierra Leone suggests that even the Angola outbreak may have had its roots in West Africa.

Both the epidemiologic features and phylogenetic history argue against the possibility that the newly emerging MARV might have been imported. Overall, it seems plausible that the viral emergence in Guinea was due to a zoonotic transmission event from a bat reservoir at the end of July 2021.

The patient's isolated lifestyle probably played a role in minimizing the risk of secondary infections. Notably, a timely laboratory diagnosis was facilitated by the establishment of capacity-building programs, long-term collaborative partnerships, and decentralized laboratories with well-trained staff members. The same capacities proved to be key during the recent reemergence of Ebola virus disease in Guinea.[5]

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Association between Covid-19 Vaccination and Influenza Vaccination Rates

TO THE EDITOR: The polarizing nature of vaccination against coronavirus disease 2019 (Covid-19) within the United States threatens public health and has contributed to variable statewide vaccine uptake that ranged from 50 to 80% as of January 2022.[1] Given the divided national landscape and anecdotal evidence from our own patients, we hypothesized that low Covid-19 vaccination rates would be associated with decreases in influenza vaccination rates.

Using nationally representative data from the Centers for Disease Control and Prevention,[2] we calculated changes in influenza vaccine uptake at the state-population level during the pandemic after Covid-19 vaccines became widely available (September 2021 through January 2022) relative to before the pandemic (September 2019 through January 2020). To account for pandemic-related factors unrelated to Covid-19 vaccines that might affect changes in influenza vaccine uptake (e.g., worsening inequities in access to care[3,4] or employment), we also compared September 2020 through January 2021 (the first influenza season during the pandemic but before widespread Covid-19 vaccine availability) to before the pandemic. We stratified changes in influenza vaccine uptake according to quartile of state-level cumulative Covid-19 vaccine uptake through January 2022. We used mixed-effects linear regressions (difference-in-differences analyses) to examine whether changes in influenza vaccine uptake during influenza seasons before as compared with during the pandemic differed between states with high as compared with low Covid-19