References

1. Harms A, Dehio C. Intruders below the radar: molecular pathogenesis of *Bartonella* spp. Clin Microbiol Rev. 2012;25:42–78. https://doi.org/10.1128/CMR.05009-11
2. McKee CD, Bai Y, Webb CT, Kosoy MY. Bats are key hosts in the radiation of mammal-associated *Bartonella* bacteria. Infect Genet Evol. 2021;89:104719. https://doi.org/10.1016/j.meegid.2021.104719
3. Stuckey MJ, Chomel BB, de Fleurieu EC, Aguilar-Setién A, Boulouis HJ, Chang CC. *Bartonella*, bats and bugs: a review. Comp Immunol Microbiol Infect Dis. 2017;55:20–9.
4. York HA, Rodríguez-Herrera B, LaVal RK, Timm RM, Lindsay KE. Field key to the bats of Costa Rica and Nicaragua. J Mammal. 2019;100:1726–49. https://doi.org/10.1093/jmammal/gyz150
5. Wenzel RL. The streblid batflies of Venezuela (Diptera: Streblidae). Brigham Young Univ Sci Bull. 1976;20:1–177.
6. Wenzel RL, Tipton VJ. Ectoparasites of Panama. In: Chicago, Field Museum of Natural History. Chicago: University of Illinois Urbana-Champaign; 1966. p. 882.
7. Billeter SA, Hayman DTS, Peel AJ, Baker K, Wood JLN, Cunningham A, et al. *Bartonella* species in bat flies (Diptera: Nycteribiidae) from western Africa. Parasitology. 2012;139:324–9. https://doi.org/10.1017/S0031182011002113
8. Judson SD, Frank HK, Hadly EA. *Bartonellae* are prevalent and diverse in Costa Rican bats and bat flies. Zoonoses Public Health. 2015;62:609–17. https://doi.org/10.1111/zph.12188
9. Bai Y, Kosoy M, Recuenco S, Alvarez D, Moran D, Turmelle A, et al. *Bartonella* spp. in bats, Guatemala. Emerg Infect Dis. 2011;17:1269–72. https://doi.org/10.3201/eid1707.101867

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COMMENT LETTERS

Predictors of Nonseroconversion after SARS-CoV-2 Infection

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To the Editor: Recently, Liu et al. (*1*) described the predictors of nonseroconversion after severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) infection (36.1% of cases), where nonresponders had significant higher cycle threshold (C_t) and were younger. Although a recent study showed that 1 dose of mRNA vaccine is sufficiently effective in previously infected persons (*2*), Reynolds et al. reported a previously infected vaccinee who never seroconverted (*3*). We report the case of a previously infected vaccinee who did not seroconvert and was subsequently reinfected.

In April 2020, a 55-year-old female nursing manager had mild SARS-CoV-2 pneumonia diagnosed that did not require admission, confirmed by weakly positive genes E and RNA-dependent RNA polymerase PCR testing (both C_t >33, near the limit of detection using homemade techniques). Concomitantly, her husband experienced symptoms and also tested positive, supporting that the woman's case was not a false-positive. One month later, SARS-CoV-2 serology revealed no detectable antibodies to nucleocapsid or spike (S) proteins.

Despite a low risk for SARS-CoV-2 reinfection in a healthcare worker without underlying conditions (*4*) and having been vaccinated with 1 dose of mRNA BNT162b2 (Pfizer-BioNTech, https://www.pfizer.com) in April 2021, as recommended for previously infected persons, the woman was reinfected in September 2021 by the Delta variant. She had mild symptoms and a high estimated viral load (C_t 26 for genes E and N2). Serologic testing at the time of the first detection of reinfection revealed a relatively low titer of 20 binding antibody units/mL of S antibodies, which then increased to 243 BAU/mL 1 month after reinfection. Testing to rule out immune deficiency (serum protein electrophoresis, quantitative immunoglobulin assay, and assessment for complement deficiency) detected no abnormalities.

Our findings support a 2-dose vaccine policy for previously infected persons, as applied in the United States. This cautious approach is even more relevant because neutralizing antibody titers are substantially reduced in patients infected with the Delta variant (*5*) and in light of efforts to promote a third dose of vaccine, to ensure a stable antibody level over time in

persons at high risk of being hospitalized for severe coronavirus disease.

B.D., C.L., K.J., and E.G. conceptualized and designed the manuscript; coordinated and drafted the initial manuscript; and reviewed the manuscript. P.D.T., D.A., and B.D. reviewed and revised the manuscript. All authors approved the final manuscript as submitted and agree to be accountable for all aspects of the work in ensuring that questions related to the accuracy or integrity of any part of the work are appropriately investigated and resolved.

References

1. Liu W, Russell RM, Bibollet-Ruche F, Skelly AN, Sherrill-Mix S, Freeman DA, et al. Predictors of nonseroconversion after SARS-CoV-2 infection. Emerg Infect Dis. 2021;27:2454–8. https://doi.org/10.3201/eid2709.211042
2. Hirotsu Y, Amemiya K, Sugiura H, Shinohara M, Takatori M, Mochizuki H, et al. Robust antibody responses to the BNT162b2 mRNA vaccine occur within a week after the first dose in previously infected individuals and after the second dose in uninfected individuals. Front Immunol. 2021;12:722766. https://doi.org/10.3389/fimmu.2021.722766
3. Reynolds CJ, Pade C, Gibbons JM, Butler DK, Otter AD, Menacho K, et al.; UK COVIDsortium Immune Correlates Network. UK COVIDsortium Investigators. Prior SARS-CoV-2 infection rescues B and T cell responses to variants after first vaccine dose. Science. 2021;372:1418–23. https://doi.org/10.1126/science.abh1282
4. Davido B, De Truchis P, Lawrence C, Annane D, Domart-Rancon M, Gault E, et al. SARS-CoV-2 reinfections among hospital staff in the greater Paris area. Travel Med. 2021;28:taab058. https://doi.org/10.1093/jtm/taab058
5. Planas D, Veyer D, Baidaliuk A, Staropoli I, Guivel-Benhassine F, Rajah MM, et al. Reduced sensitivity of SARS-CoV-2 variant Delta to antibody neutralization. Nature. 2021;596:276–80. https://doi.org/10.1038/s41586-021-03777-9

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High Infection Attack Rate after SARS-CoV-2 Delta Surge, Chattogram, Bangladesh

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To the Editor: After an initial serosurvey (*1*) to understand the prevalence of total antibodies to severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) in residents of the Sitakunda subdistrict was completed, a large epidemic wave hit the area, and nearly all publicly available samples genotyped via GISAID (https://www.gisaid.org) were the SARS-CoV-2 Delta variant (*2*,*3*). Of the total confirmed infections during the entire pandemic from the Chattogram District, 48.4% (48,253) were reported June 14–August 31, 2021. During September 21–October 9, 2021, we revisited all enrolled households and collected blood from 84% (1,938/2,307) of those tested in our initial serosurvey (Appendix Figure, https://wwwnc.cdc.gov/EID/article/28/2/21-2417-App1.pdf).

We tested 721 of the initially seronegative participants who agreed to a second blood draw using the same Wantai total Ab receptor-binding domain assay and found that 68% (492/721) had seroconverted in the approximately 3-month period between survey rounds (Appendix Table 1). Participation in the second round was not associated with serostatus in the first round. Among seropositive participants, 87 (18%) had received ≥1 dose of SARS-CoV-2 vaccine, and 28.3% (140/492) of those who seroconverted reported having had a sud-

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