Family matters for coronavirus disease and vaccines

David J. Bean, Manish Sagar

*J Clin Invest.* 2021;131(24):e155615. [https://doi.org/10.1172/JCI155615](https://doi.org/10.1172/JCI155615).

Commentary

The increasing frequency of pathogenic coronaviruses in the human population has raised public health concerns about possible future pandemics. It is critical to understand whether immune responses to the current circulating coronaviruses provide protection against related viruses or those that may emerge in the future. In this issue of the *JCI*, Dangi, Palacio, and co-authors detail the extent of coronavirus cross-protection following both vaccination and natural infection and ultimately used murine models to highlight the mechanism behind this heterotypic immunity. This study provides insight into the possibility of a pan-coronavirus vaccine that could protect humans against future coronavirus outbreaks.

Find the latest version:

[https://jci.me/155615/pdf](https://jci.me/155615/pdf)
Family matters for coronavirus disease and vaccines

David J. Bean1 and Manish Sagar1,2

1Department of Microbiology, and 2Department of Medicine, Boston University School of Medicine, Boston, Massachusetts, USA.

The Journal of Clinical Investigation

Diverse coronaviruses

The repeated emergence of different pathogenic human coronaviruses over the past 20 years has highlighted the impact of these viruses on public health and the need for a vaccine that can protect against future outbreaks. Animals, such as bats, harbor a wide variety of coronaviruses, and zoonotic spillovers are the likely source of both the current coronavirus infections and potentially of future viral outbreaks in humans (1). Currently, the known human coronaviruses cause a range of disease outcomes, from the four endemic coronaviruses (eCoVs) that are often the etiologic agent for the common cold, to the more pathogenic coronaviruses that can cause severe disease and even death for some individuals (2). Severe acute respiratory syndrome coronavirus 1 (SARS-CoV-1) emerged in 2003, and infections were associated with a mortality rate of approximately 10% (3). Fortunately, transmission chains faded fairly quickly as a result of effective containment measures. Middle East respiratory syndrome coronavirus 1 (SARS-CoV-1) emerged in 2012, resulting in severe pneumonia and mortality rates reaching nearly 40% (4). Transmission of MERS-CoV remains mostly geographically restricted, although cases still appear to this day. SARS-CoV-2, which causes coronavirus disease 2019 (COVID-19), quickly became a worldwide pandemic after March 2020, primarily because of the high transmissibility of the virus and the relatively late implementation of public health measures (5–7). The SARS-CoV-2 disease course varies from asymptomatic to death and depends on a variety of factors including age and preexisting medical conditions. Despite the range in disease outcomes, these diverse coronaviruses have the same genotypic architecture, share conserved gene sequences, and often use similar proteins and cellular processes to infect and replicate in host cells (8, 9). Given these relationships, it has always been an intriguing possibility that a previous infection with one or more of the human coronaviruses may provide heterotypic immunity that protects against subsequent infection and ameliorates disease outcomes for the other members of this extended coronavirus family.

Heterotypic immunity among coronaviruses

Preexisting heterotypic immunity may provide a partial explanation for the varying outcomes observed in SARS-CoV-2–infected individuals, yet this concept remains highly controversial (10, 11). Some, but not all, investigations have demonstrated that individuals with prior eCoV infection may be protected against SARS-CoV-2 acquisition and may have substantially lower mortality rates and less severe COVID-19 after SARS-CoV-2 infection (12–14). These discrepant results are not necessarily unexpected or surprising and may be explained by a range of factors. Nearly all humans have been infected by one or more of the eCoVs sometime during their lifetime, eliciting humoral and cellular immune memory against the infecting coronavirus. However, immune memory against coronaviruses is generally believed to be relatively short-lived, and individuals are repeatedly infected with the various circulating eCoVs (15, 16). The magnitude, quality, and breadth of this immunological footprint against other coronavirus family members likely depends on numerous variables, such as recency, severity, frequency, and sequence similarity. Only examination of large cohort data and routine longitudinal sampling would be potentially adequately powered to account for these diverse factors that affect heterotypic immunity among the various human coronaviruses.

In this issue of the JCI, Dangi, Palacio, and colleagues examined human samples and used murine models to understand heterotypic immunity among coronaviruses (17). Similar to previous studies, they show that SARS-CoV-2–infected and –vaccinated individuals possessed cross-reactive antibodies against some other coronaviruses (18). Importantly, subsequent mouse studies by Dangi, Palacio, and co-authors overcame some of the highlighted confounding variables present in natural history studies in humans, such as the type, timing, severity, and number of previous coronavirus infections. In their mouse model, the researchers demonstrate that diverse SARS-CoV-1 or SARS-CoV-2 vaccines, similar to the ones being used and in development

Conflict of interest: The authors have declared that no conflict of interest exists.

Copyright: © 2021, American Society for Clinical Investigation.


Related Article: https://doi.org/10.1172/JCI151969
The greatest limitation in the mouse studies by Dangi, Palacio, and co-authors and the most important variable in the context of human infections is time. In the murine studies, immune responses were examined, or mice were challenged, within a few weeks of vaccination or infection (17). The durability and long-term protective efficacy of heterotypic immunity against other virus family members remains uncertain. For coronavirus infections, even homotypic immunity is relatively short, and humans are repeatedly infected with the other human coronaviruses because of waning immunity. This decline in immunity has also been observed with SARS-CoV-2, as reinfections after a primary infection and breakthrough infection are common (16).
Acknowledgments
This work was supported by K24-AI145661 and P30-AI042853, DJB was supported by NIH grant T32-5T32AI00730928. The funders had no role in the decision to submit this article for publication.

Address correspondence to: Manish Sagar, Boston University, 650 Albany Street, Room 647, Boston, Massachusetts 02118, USA. Phone: 617.414.5239; Email: msagar@bu.edu.