Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID-19. The COVID-19 resource centre is hosted on Elsevier Connect, the company's public news and information website.

induced SARS-CoV-2 antibodies after vaccination with inactivated SARS-CoV-2 vaccines is critically important. In addition, more studies are needed to establish whether the inactivated SARS-CoV-2 vaccines are capable of inducing and maintaining virus-specific T-cell responses, because CD4-positive T-cell help is important for optimal antibody responses, as well as for cytotoxic CD8-positive T-cell activation, which, in turn, are crucial for viral clearance if neutralising antibody-mediated protection is incomplete.[10]

Finally, because the correlates of protection afforded by inactivated SARS-CoV-2 vaccines are yet to be identified, the results of a phase 3 trial of BBIBP-CorV vaccine (currently underway in Abu Dhabi, United Arab Emirates; ChiCTR2000034780), will provide information on whether this vaccine is safe and efficacious against SARS-CoV-2 infection, and for how long the protective effect is maintained.

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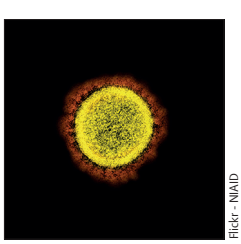
What reinfections mean for COVID-19

One of the key questions in predicting the course of the COVID-19 pandemic, caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), is how well and how long the immune responses protect the host from reinfection. For some viruses, the first infection can provide lifelong immunity; for seasonal coronaviruses, protective immunity is short-lived.[1]

In *The Lancet Infectious Diseases*, Richard L Tillett and colleagues describe the first confirmed case of SARS-CoV-2 reinfection in the USA.[2] A 25-year-old man from the US state of Nevada, who had no known immune disorders, had PCR-confirmed SARS-CoV-2 infection in April, 2020 (cycle threshold [Ct] value 35·24; specimen A). He recovered in quarantine, testing negative by RT-PCR at two consecutive timepoints thereafter. However, 48 days after the initial test, the patient tested positive again by RT-PCR (Ct value 35·31; specimen B). Viral genome sequencing showed that both specimens A and B belonged to clade 20C, a predominant clade seen in northern Nevada. However, the genome sequences of isolates from the first infection (specimen A) and reinfection (specimen B) differed significantly, making the chance of the virus being from the same infection small. What is worrisome is that SARS-CoV-2 reinfection resulted in worse disease than did the first infection, requiring oxygen support and hospitalisation. The patient had positive antibodies after the reinfection, but whether he had pre-existing antibody after the first infection is unknown (table).

This case report adds to rapidly growing evidence of COVID-19 reinfection, in which viral genomic sequences were used to confirm infections by distinct isolates of SARS-CoV-2. What do reinfection cases mean for public health and vaccination endeavors to stop the COVID-19 pandemic?

Do reinfections occur because of a scant antibody response after first infection? Of the four reinfection cases reported to date, none of the individuals had known immune deficiencies. Currently, only two individuals had serological data from the first infection and one had pre-existing antibody (IgM) against SARS-CoV-2. Because of the wide range of serological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	Sex	Age (years)	First infection (Ct)	Second infection (Ct)	Intervening period (days)	Antibody after first infection	Antibody after reinfection
Hong Kong[3]	Male	33	Mild (N/A)	Asymptomatic (27)	142	Negative	IgG+
Nevada, USA[2]	Male	25	Mild (35)	Hospitalised (35)	48	N/A	IgM+ and IgG+
Belgium[4]	Female	51	Mild (26–27)	Milder (33)	93	N/A	IgG+
Ecuador[5]	Male	46	Mild (37)	Worse (N/A)	63	IgM+ and IgG–	IgM+ and IgG+

Data were obtained Sept 14, 2020, for reinfection cases confirmed by viral genome sequences. Ct=cycle threshold. N/A=not available. SARS-CoV-2=severe acute respiratory syndrome coronavirus 2.

Table: **Characteristics associated with reinfection with SARS-CoV-2**

testing platforms used across the globe, it is impossible to compare results from one assay to another. For example, antibody reactivity to nucleocapsid protein indicates previous exposure to SARS-CoV-2 but not whether antibodies that can block infection (anti-spike) are present. Also, antibody levels are highly dependent on the timing after exposure. The key goal for the future is to ascertain the level and specificity of antibody to spike protein at the time of reinfection, to determine immune correlate of protection.

Does immunity protect an individual from disease on reinfection? The answer is not necessarily, because patients from Nevada and Ecuador had worse disease outcomes at reinfection than at first infection. It is important to keep in mind that the reinfection cases in general are being picked up because of symptoms and are biased towards detection of symptomatic cases. Due to the paucity of broad testing and surveillance, we do not know how frequently reinfection occurs among individuals who recovered from their first infection. Asymptomatic reinfection cases can only be picked up by routine community testing or at an airport, for example,[3] and we are probably severely underestimating the number of asymptomatic reinfections. Why do some reinfections result in milder disease,[3,4] whereas others are more severe?[2,5] Further investigation is needed of pre-existing immune responses before second exposure, and viral inoculum load.

Does infection by different viral isolates mean we need a vaccine for each type? While differences in the viral genome sequence of the various isolates are a great way to know if an individual is reinfected (ruling out reactivation of lingering virus infection), it does not indicate that the second infection was due to immune evasion. There is currently no evidence that a SARS-CoV-2 variant has emerged as a result of immune evasion. For now, one vaccine will be sufficient to confer protection against all circulating variants.[6] Furthermore, reinfection by a distinct viral variant from the original virus does not imply immune escape.

Does immunity prevent transmission from those who are reinfected? The Ct value of PCR correlates with viral load, and low Ct values (high viral load) might indicate infectiousness of the individual. Although Ct values can vary substantially between various tests and laboratories, in one study, samples with Ct values greater than 35 were only 8% positive for cultivable virus.[7] A good proxy for infectiousness can be obtained through viral plaque assays that measure the infectious virus. However, these assays require biosafety level 3 facilities and are labour intensive, and the assays are not routinely done in clinical laboratories. Since some reinfection cases had Ct values less than 35,[3,4] infectious virus might have been harboured in the nasal cavity. Thus, reinfection cases tell us that we cannot rely on immunity acquired by natural infection to confer herd immunity; not only is this strategy lethal for many but also it is not effective. Herd immunity requires safe and effective vaccines and robust vaccination implementation.

As more cases of reinfection surface, the scientific community will have the opportunity to understand better the correlates of protection and how frequently natural infections with SARS-CoV-2 induce that level of immunity. This information is key to understanding which vaccines are capable of crossing that threshold to confer individual and herd immunity.

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COVID-19 in malaria-endemic regions: potential consequences for malaria intervention coverage, morbidity, and mortality

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COVID-19 has had a massive impact on the populations and economies of the world. As of Sept 9, 2020, the virus has infected more than 27 million people in 216 countries and territories worldwide, and the number of deaths is approaching a million.[1] Although the spread of COVID-19 to Africa has been slow and its direct impact in Africa is below the level seen in other continents, the potential effects of COVID-19 on strategies and methods to combat other diseases such as malaria—which pose significant burdens on substantial proportions of the world and the African population, and especially children—are a cause for great concern. Thus, understanding how the COVID-19 pandemic could indirectly affect malaria control intervention strategies is urgent in all malaria-endemic regions, and especially those that are part of WHO's "high burden to high impact" initiative.[2]

Since 2010, active malaria intervention control strategies have had a positive effect on lowering malaria burden and morbidity in Africa and worldwide. These strategies include the use of long-lasting insecticide-treated nets (ITNs), indoor residual spraying,[4] and timely access to antimalarial drugs, including the use of intermittent preventive treatment aimed at killing forms of the malaria parasite in infected individuals,[5–7] in addition to the other mechanisms aimed at disrupting the transmission of malaria by exploiting the feeding behaviour and gonotrophic and reproductive cycles of mosquitoes.[8–11] However, despite the progress of the past decade, evidence suggests that the rate of reduction in malaria mortality in the WHO African Region has slowed since 2016, although total deaths due to malaria decreased overall.[3] In particular, from 2017 to 2018, among the ten African countries with the highest malaria burden, Ghana and Nigeria reported absolute increases in the number of malaria cases, while case numbers did not change substantially in seven countries and only Uganda reported a decrease.[3] Given that this deceleration could be compounded by the COVID-19 pandemic, there is an urgent need to quantify and analyse the potential impact of the pandemic on malaria control and intervention strategies.

In *The Lancet Infectious Diseases*, Daniel Weiss and colleagues[12] quantified the indirect effects of COVID-19 on the distribution of ITNs and on access to effective antimalarial drugs—two key components of malaria control in Africa. Using a range of counterfactual scenarios based on different levels of reduction in ITN and antimalarial drug coverage, the authors estimated the additional morbidity and mortality due to malaria that might be seen in the year 2020 across malaria-endemic Africa. Current data were used to generate geospatial estimates of malaria infection prevalence, clinical case incidence and mortality, *Plasmodium falciparum* parasite rates, ITN coverage, and effective treatment availability. The anticipated malaria burden in the absence of COVID-19 disruptions served as a baseline for comparison. On the basis of their estimates, Weiss and colleagues concluded that COVID-19-related disruptions to malaria control efforts in Africa could lead to significant reversals of the progress made over the past two decades in reducing malaria morbidity and mortality, with a possibility of a near doubling in mortality due to malaria under the worst case scenario (combined reductions of 75% in effective antimalarial treatment and 75% in routine ITN distribution, with no mass ITN distribution campaigns).[12]