Will the COVID-19 pandemic end with the Delta and Omicron variants?

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Two years after the first known outbreak of the coronavirus disease 2019 (COVID-19), the cumulative number of confirmed cases of infections has exceeded 260 million worldwide. Even more alarming, the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) and its many variants are still circulating on a massive scale in the world population. Here, we present a brief analysis on the most widely spread SARS-CoV-2 variant, known as the ‘Delta variant’, with particular emphases on environmental transmission, knowledge gaps, hypotheses, and urgent questions.

A new situation

Has the long-sought relief finally arrived 18 months after the COVID-19 was declared a pandemic? Not really. Recent surges of new infections painted a dire picture. In the week ending on July 18, 2021, 4 weeks since the onset of the latest wave of the COVID-19 outbreak in Europe, there were nearly 300,000 newly confirmed cases in the United Kingdom and about one million newly confirmed cases in total across Europe (WHO 2021a). In the following week, the number of newly confirmed cases in the United States reached 370,000 after steadily dropping to about 80,000 per week levels since it peaked at the beginning of January 2021 (WHO 2021a). In China, where the new weekly cases of domestic COVID-19 infections had been kept under 500 since February 2021, about 2500 newly confirmed cases were reported in the week ending on May 23, effectively ending the quasi-safe status of domestic COVID-19 infections in the country (WHO 2021a). Since then, weekly new confirmed cases of COVID-19 have steadily increased around the globe, from about 2.6 million in mid-June to the peak of 4.6 million in late August and now rising to 4.0

million again, triggering a massive wave of new infections. The eradication of COVID-19 looks like a distant goal in the coming months near the end of 2021 (Fig. 1).

A super-spreading variant

There is active surveillance on the emergence of new SARS-CoV-2 variants. The phylogenetic assignment of named global outbreak network (PANGO) and the global initiative on sharing all influenza data (GISAID) referred to the B.1.617.2 and all AY.* as the ‘Delta variant’, which constitutes a class of mutant strains of the SARS-CoV-2, the causation agent of the COVID-19 pandemic (GISAID 2021; PN 2021). Since it was first discovered in October 2020, the Delta variant has spread to most countries around the globe and become the predominant circulating SARS-CoV-2 variant in newly confirmed cases of COVID-19 (Yadav et al. 2021a) (Fig. 2). In India, where the Delta variant was first detected, it was identified as the main causation agent for the massive COVID-19 outbreak in the country between March and May 2021, a period with record numbers of infections and overlapping with the Kumbh Mela pilgrimage and festival (THS 2021). According to the US centers for disease control and prevention (CDC), the B.1.617.2 variant was responsible for 99.9% of total confirmed cases between September 18 and 25 in the United States (CDC 2021a). Similar situations were reported in the United Kingdom and China where the Delta variant accounted for 100% of the newly confirmed cases of COVID-19 in the 4 weeks ending on October 20 (GISAID 2021). As of December 1, 2021, a total of 176 countries and regions have verified cases of infections by the Delta (B.1.617.2) variant (CDC 2021b).

What makes the Delta variant so dangerous?

The most representative variant, B.1.617.2, is the predominant and the initial pango lineage of the Delta variant (CDC 2021a). At present, there is no proof that the

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Fig. 1 The Delta variant (B.1.617.2 and AY. *) of the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) has triggered a massive wave of new infections and re-emergent outbreaks around

the globe, making the eradication of the coronavirus disease 2019 (COVID-19) a more distant goal and adding significant uncertainty to the future of mankind

transmission routes of the B.1.617.2 variant are significantly different from those of the original SARS-CoV-2, although there is strong evidence that the transmissibility of B.1.617.2 is much higher than the original SARS-CoV-2.

Compared with the original virus, B.1.617.2 is characterized by seven mutations on its spike proteins, namely, the T19R, Δ 157–158, L452R, T478K, D614G, P681R, and D950N (ECDC 2021). There are five connected amino acids, proline, arginine, arginine, alanine, and arginine, located at the junction of the spike protein subunits on the original SARS-CoV-2, where they form an amino acid chain known as the furin cleavage site. As it mutates into the B.1.617.2 variant, the proline on the furin cleavage site is replaced by arginine (P681R), which reduces the acidity of this sequence (Planas et al. 2021). The result is that the furin host enzymes can more effectively recognize and cut the spike proteins on replicated viruses before they leave the host cell, which enables more spike proteins to invade human cells and facilitates the fusion between the virus envelope and the host cell membrane, thereby increasing the probability of infection in the new host (Scudellari 2021). To put it into context, about 50% of the spike proteins on SARS-CoV-2 are available for invading human cells, whereas on B.1.617.2 more than 75% of the spike proteins are capable of effectuating such actions (Scudellari 2021). Moreover, a recent study reported that L452R is also a contributor to the enhanced infectivity of B.1.617.2 by promoting interactions between

the spike protein and the angiotensin-converting enzyme 2 (ACE2) receptor (Kimura et al. 2021).

These may be the key factors of the higher viral loads found in Delta variant-infected individuals and the higher transmissibility of this particular variant compared with the original SARS-CoV-2 (Choi et al. 2021a; Young et al. 2018) (Fig. 3). Further, some of these spike protein mutations may affect human immune responses directed toward the key antigenic regions of the receptor-binding protein (452 and 478) and the deletion of part of the N-terminal domain, which may explain the reduced effectiveness rates of current vaccines toward this variant (Bernal et al. 2021). In conclusion, the B.1.617.2 variant poses a more dangerous threat than the original SARS-CoV-2.

Knowledge gaps concerning the environmental transmission of B.1.617.2 variant

There are important differences between the original SARS-CoV-2 and the B.1.617.2 variant. Table 1 lists the current findings and highlights the knowledge gaps on the latter in the current literature. Li et al. (2021a) reported that the mean oropharyngeal swab viral load of B.1.617.2-infected individuals was about 1260 times higher than that of the cases infected by the original SARS-CoV-2. Notably, Zhang et al. (2021) reported that the transmissibility of the B.1.617.2

Fig. 2 Transmissions of the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) Delta variant around the globe (top). Phylogeny of the Delta variant of 3948 genomes collected between January 2021 and November 2021 (bottom). Source: global initiative on

sharing all influenza data (GISAID 2021). GISAID is the largest open-access portal, hosting the genome sequences and related epidemiological and clinical data of more than 5.6 million SARS-CoV-2 strains. All data were last updated on 30 November 2021

variant was substantially higher than the latter, which is consistent with the earlier findings by Bjorkman et al. (2021), who showed that viral load is positively correlated to transmissibility of SARS-CoV-2.

In Japan, the minimum social distance for mitigating human-to-human transmission of the B.1.617.2 variant was determined as 2.5 m based on simulations by the *Fuyue* supercomputer, compared with the earlier recommendation of 1.0 and 1.8 m social distancing for the original SARS-CoV-2 (CCTV 2021; CDC 2021c; WHO 2021b). It should be noted that all these recommended social distances—which are widely implemented by public health authorities for the infection prevention and control of COVID-19—are based on virus transmission by respiratory droplets. In reality, SARS-CoV-2 can survive on

aerosols for 3–16 h under the room temperature and travel long distances in air (van Doremalen et al. 2020; Fears et al. 2020). Using computational fluid dynamics simulations, Rosti et al. (2020) showed that dry aerosols carrying SARS-CoV-2 could travel to 7.5 m in 20 min without the influence of ambient airflows. Indeed, airborne transmission has been recognized as an important route for the spread of COVID-19, especially in enclosed public spaces with poor ventilation (CDC 2021d; Chen et al. 2021; Choi et al. 2021b; He and Han 2021a; Morawska and Milton 2020; Sun et al. 2021). However, given the fact that there are no scientific data published to date on the persistence of the B.1.617.2 variant on aerosols, it is difficult to estimate the level of risks regarding the airborne transmission of the B.1.617.2 variant, which represents a major

Fig. 3 The Delta variant has higher transmissibility compared with the original severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), and has become the dominating causation agent of newly confirmed infections in the global population, as of 30 November 2021

knowledge gap concerning the environmental transmission of the Delta variant.

Wearing face masks has been widely adopted as a mandate in public settings to contain the virus spread. There are currently no data on the effectiveness of protection against the B.1.617.2 variant by wearing face masks, although it is almost certain that due to the much higher viral loads in the respiratory tract of B.1.617.2-infected individuals, risks are likely to be substantially higher for those who do not wear masks in public places. Further, as imperfect fitting on wearers often leads to leakages from face masks, it would be more difficult to achieve the same level of protection against the B.1.617.2 variant for mask-wearers under similar situations. Previous studies showed that the nose and mouth of mask-wearers could inhale aerosols containing influenza viruses from the interspace between the face and the mask (Cowling et al. 2010; He et al. 2013). A recent study showed that more than half of the small respiratory droplets (0.5–20 μm) ejected from a talking person wearing a standard face mask would be leaked from the top, with 15% leaked from the side and another 9% from the bottom of the mask (Cappa et al. 2021).

The fecal–oral route has been recognized as a potential route of transmission for SARS-CoV-2 (Han and He 2021; Sun and Han 2021a, 2021b). No data have been reported on the viral load of the B.1.617.2 variant in the feces of infected individuals. Recent studies on the original SARS-CoV-2 have found that there were generally high viral loads of the virus in the feces of COVID-19 patients, posing risks of fecal–oral transmission (Gu et al. 2020; Jeong et al. 2020; Olusola-Makinde and Reuben 2020; Sharma et al. 2021; Singh et al. 2021; Xiao et al. 2020). Since SARS-CoV-2

can replicate in gastrointestinal environments by binding to ACE2 receptors, and that the P681R and L452R provide more binding sites with enhanced fusion between the virus envelope and the host cell membrane, it is reasonable to anticipate that the viral load of B.1.617.2 is likely to be substantially higher in the feces of infected individuals, similar to findings in the respiratory tract and increasing the likelihood of virus transmission via fecal–oral routes. These knowledge gaps present urgent questions to the research community. Clinical and experimental data—both must be rigorously designed and executed—are needed to address these gaps and to inform public health authorities and the public for implementing more effective prevention and control measures on the Delta variant.

Effectiveness of current vaccines on the Delta variant

Do current vaccines provide meaningful protection against the Delta variant? Since there is currently no specific treatment for COVID-19, vaccination is the most effective means to prevent the transmission of SARS-CoV-2, including its variants (Dai et al. 2021). There were speculations that all current vaccines may only have limited effectiveness to protect people against infections by the Delta variant (BFA 2021). Indeed, post-vaccination infections by the Delta variant have been reported in some individuals, raising concerns on the efficacy of the current vaccines (Grant et al. 2021; Li et al. 2021b). Nonetheless, clinical and laboratory testing data published to date are generally positive showing their considerable effectiveness against

Table 1 Data pertinent to the environmental transmission of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) and the Delta (B.1.617.2) variant with knowledge gaps highlighted on the latter

Characteristic	SARS-CoV-2 (original)	B.1.617.2 (Delta)	Reference
Transmissibility	GT = 5.7 d $R_0 = 2.2$	GT = 2.9 d $R_0 = 3.2$	Zhang et al. (2021)
Oropharyngeal swab viral load	$n = 63$ $C_t = 34.3$	$n = 62$ $C_t = 24.00$ Mean viral load was 1,260 times higher than those in SARS-CoV-2 infections	Li et al. (2021a)
Viral load in patient's feces	$1.17 \pm 0.32 \log_{10}$ copies/mL (recovery stage) $2.18 \pm 0.11 \log_{10}$ copies/mL (acute stage) $2.01 \pm 0.28 \log_{10}$ copies/mL (recovery stage)	No data at present	Jeong et al. (2020)
Mean incubation period	5.2 d	4.4 d	Zhang et al. (2021)
Environmental persistence (aerosols)	At 23 °C and 53% relative humidity, SARS-CoV-2 on aerosols maintained the ability to replicate after 16 h At 21–23 °C and 40% relative humidity, SARS-CoV-2 survived on aerosols for 3 h with a moderate reduction in infection titer	No data at present	van Doremalen et al. (2020) Fears et al. (2020)
Environmental persistence (on surfaces)	SARS-CoV-2 survived for 2 h–9 d on various types of common surfaces	No data at present	WHO (2020a)
Environmental persistence (in water & wastewater)	At 20 °C, 10% of the initial viral titer (3.16×10^4 TCID ₅₀ /mL) remained after 1.9–2.9 d in river water and 1.0–1.3 d in seawater At 20 °C, almost no initial viral titer (10^3 TCID ₅₀ /mL) remained after 3.2–6.5 d in municipal wastewater and 3.6–4.4 d in tap water	No data at present	Buonerba et al. (2021) Sala-Comorera et al. (2021)
Environmental transmission	Inhalation of respiratory droplets ejected from the nose or mouth of an infected person Inhalation of aerosols (e.g., airborne particulates, droplet nuclei) carrying viruses Touching eyes, nose or mouth by hand contacted with virus-laden surfaces or objects ('fomites') Fecal–oral transmission possible	No data at present	Choi (2021c) Han and He (2021) WHO (2020b)
Protection by face mask (surgical)	When the spreader and the receiver models were separated by 50 cm and both wore surgical masks, 71% of the viral titer and 76% of the viral RNA from the spreader were blocked by the masks, respectively	No data at present	Ueki et al. (2020)
Social distancing requirement	≥ 1.0 m (WHO) ≥ 1.8 m (6 feet) (CDC)	≥ 2.5 m	CCTV (2021) CDC (2021c) WHO (2021b)

Abbreviations (in the order of appearance in the table): mean generation time (GT); basic reproductive number (R_0); sample size (n), number of cycles when amplification reaches a certain load in polymerase chain reaction (C_t , lower C_t value indicates higher viral load of infection); median tissue culture infective dose (TCID₅₀)

Table 2 Effectiveness of current vaccines against the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) and the Delta (B.1.617.2) variant

Vaccine type	SARS-CoV-2 (original)	B.1.617.2 (Delta variant)	References
BNT162b2 (Pfizer)	<i>n</i> = 43,448 Effectiveness rate ^a : 95%	<i>n</i> = 15,749 Effectiveness rate ^a : 88%	Bernal et al. (2021) Pfizer (2020)
		<i>n</i> = 12,330 (0–13 d after two dose) Effectiveness rate ^a : 82% ^b	Pouwels et al. (2021)
		<i>n</i> = 215,577 (≥ 14 d after two doses) Effectiveness rate ^a : 80% ^b	
		<i>n</i> = 1,043,289 (≥ 7 d after two doses) Effectiveness rate ^a : 93% (within the first month after two doses) Effectiveness rate ^a : 53% (≥ 4 months after two doses)	Tartof et al. (2021)
	<i>n</i> = 25 Geometric mean neutralization titer ^c : 1,105	<i>n</i> = 25 Geometric mean neutralization titer ^c : 442	Liu et al. (2021a)
AZD1222 (ChAdOx1 nCoV-19)	<i>n</i> = 19 Geometric mean neutralization titer ^c : 246.8	<i>n</i> = 19 Geometric mean neutralization titer ^c : 106.7 (delta-S ₁), 123.4 (delta-S ₂)	Lustig et al. (2021)
	<i>n</i> = 32,451 Effectiveness rate ^a : 74%	<i>n</i> = 8244 Effectiveness rate ^a : 67%	Bernal et al. (2021) Falsey et al. (2021)
		<i>n</i> = 49,308 (0–13 d after two dose) Effectiveness rate ^a : 71% ^b	Pouwels et al. (2021)
		<i>n</i> = 330,677 (≥ 14 d after two doses) Effectiveness rate ^a : 67% ^b	
	<i>n</i> = 49 Geometric mean neutralization titer ^c : 599.4	<i>n</i> = 49 Geometric mean neutralization titer ^c : 88.4	Thiruvengadam et al. (2021)
CoronaVac	<i>n</i> = 25 Geometric mean neutralization titer ^c : 306	<i>n</i> = 25 Geometric mean neutralization titer ^c : 71	Liu et al. (2021a)
	<i>n</i> = 1,322 Effectiveness rate ^a : 91.25%	<i>n</i> = 89 Effectiveness rate ^a : 59% (included both CoronaVac and CNBG vaccines, and most participants were vaccinated with the former)	Li et al. (2021b) SINOVAR (2020)
China National Biotech Group (CNBG)	<i>n</i> is unknown Effectiveness rate ^a : 79.34%		CNBG (2020)

(a) Effectiveness rates were determined by whether participants, all vaccinated with two doses of the designated vaccine, had COVID-19 infection. (b) Effectiveness rates in B.1.617.2-dominant periods in the United Kingdom. (c) Geometric mean neutralization titers were determined in sera from participants vaccinated with two doses of the designated vaccine

the B.1.617.2 variant. Table 2 lists the testing results of four COVID-19 vaccines, namely, the BNT162b2 vaccine developed by Pfizer, the AZD1222 (ChAdOx1 nCoV-19) vaccine by AstraZeneca, the CoronaVac vaccine by Sinovac, and the China National Biotech Group (CNBG) vaccine, on the original SARS-CoV-2 and the B.1.617.2 variant, respectively. Results from phase III clinical trials of the four COVID-19 vaccines showed that they were moderately to highly effective in preventing infections by SARS-CoV-2 after receiving two doses of vaccination.

Bernal et al. (2021) recently evaluated the effectiveness of the BNT162b2 and AZD1222 vaccines against the B.1.617.2 variant. Their results showed an overall effectiveness rate of 88% among 15,749 vaccinated participants receiving two doses of the former, and an effectiveness rate of 67% in 8244 participants vaccinated by the latter, also receiving two doses. Liu et al. (2021a) studied the neutralization ability of serum samples collected from 50 participants who had been vaccinated with two doses of the BNT162b2 or AZD1222 vaccine. The study showed that the geometric

mean neutralization titer of the B.1.617.2 variant decreased by 2.5 to 4.3-fold in sera from participants ($n=25$) vaccinated with two doses of either vaccine, compared with that of the original SARS-CoV-2. Similar results were reported by Lustig et al. (2021), where the geometric mean neutralization titer of delta-S₁ and delta-S₂ (S₁ and S₂ are two branches of the B.1.617.2 lineage) decreased by 2.6 and 2.1-fold in sera from participants vaccinated with two doses of the BNT162b2 vaccine, respectively. Li et al. (2021b) studied the effectiveness of two inactivated SARS-CoV-2 vaccines against the Delta variant, the CoronaVac and the China National Biotech Group (CNBG), in a recent outbreak in Guangzhou, China. The study showed an overall effectiveness rate of 59% among 89 vaccinated participants receiving two doses of any of the two vaccines or a mix of both, although most participants were vaccinated with the former. It was concluded that, although their effectiveness rates decreased to some extent, the current vaccines developed for SARS-CoV-2 still provide considerable protection against the Delta variant.

What next after the Delta variant?

As of November 30, 2021, the Delta variant is the only SARS-CoV-2 variant being categorized as ‘Variant of Concern’ by the U.S. Centers for Disease Control and Prevention (CDC), based on evidence on its increased transmissibility and potential reduction in neutralization by some Emergency Use Authorization monoclonal antibody treatments and post-vaccination sera (CDC 2021e). The Delta variant has caused massive infections around the globe, including areas with high vaccination rates. In January 2021, Zvulun (2021) reported that Israel could become the first country

in the world to achieve mass immunization by COVID-19 vaccines. As of March 22, 2021, more than half of the Israeli population (53.1%) had been vaccinated with two doses of the BNT162b2 (Pfizer) vaccine (TN 2021a). The Israeli government subsequently abolished the mask order on June 15, 2021 (XH 2021). Shortly after, new COVID-19 infections began to rebound in Israel, and the Delta variant spread rapidly in the country (TN 2021b; WHO 2021c). On September 7, 2021, new daily confirmed cases in Israel set a record of 5000 since the onset of the COVID-19 pandemic, despite the fact that more than 60% of its population had been fully vaccinated (WHO 2021c).

Like other RNA viruses, SARS-CoV-2 has very high mutation rates (Akter et al. 2021; Dai et al. 2020; Duffy 2018; Wu et al. 2021). To date, a total of 407 pango lineages of SARS-CoV-2 variants have been identified (Nextstrain 2021). Of those, the B.1.617.2.1 (AY.1) and Lambda (C.37) variants—both have been identified with cases reported in different countries—have stronger immune escape ability than the B.1.617.2 variant, meaning that current vaccines are likely to be even less effective on these strains (Kimura et al. 2021; Liu et al. 2021b; Newsweek 2021; Yadav et al. 2021b). Recently, the AY.4.2 variant, known as the ‘Delta Plus’, has spread in the United Kingdom, which would be 10% more transmissible than its parent lineage, the B.1.617.2 (Newsweek 2021). It is of concern that, at present, both the original SARS-CoV-2 and its various variants are still being transmitted on a large scale between different hosts and species, as global newly confirmed cases have been maintained at about three million per week or above since the beginning of July 2021 (He et al. 2021; WHO 2021a). Morales et al. (2021) estimated that the true underlying mutation rate of SARS-CoV-2 is about 50% higher than previous estimates. If the transmission is not effectively contained, what is bound

Fig. 4 Mutations of the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) with its main variants identified to date. The Delta variant, which includes the B.1.617.2 and AY.* pango lineages, has become the dominant causation agent of coronavirus disease 2019 (COVID-19) infections reported around the globe. As of 30 November 2021, a total of 407 pango lineages have emerged since the onset of the COVID-19 pandemic. The continuing massive scale of transmission of SARS-CoV-2 and its variants may lead to the emergence of potentially more dangerous ‘super-variants’ in the future

to happen is that the novel coronavirus, including SARS-CoV-2 and its variants, will continue to evolve into newer variants that are potentially more contagious and difficult to control (Fig. 4). As the virus continues to mutate, public health authority has warned of the possibility that eventually, some new SARS-CoV-2 variants will emerge which may render all current vaccines ineffective (SAGE 2021). There may also be new or under-investigated environmental transmission routes of these newer SARS-CoV-2 variants emerging in the future (Propper 2020).

A new ‘super variant’ of SARS-CoV-2—named as the ‘Omicron’ variant (B.1.1.529) which was first discovered in South Africa on 9 November 2021—has been reported and designated as a ‘Variant of Concern’ by the World Health Organization (WHO 2021d). Preliminary findings on the new variant immediately raised widespread concerns due to its unusually high number of mutations, which could make it more transmissible and result in immune evasion with increased risks of reinfection (Callaway 2021). The Omicron variant has 32 mutated sites on its spike proteins, with some associated with the transmissibility and immune escape ability of the virus. While studies are still being carried out to assess its threats and the efficacy of current vaccines on the Omicron variant, researchers have warned that the immune escape ability of the Omicron variant may exceed all previous SARS-CoV-2 variants, including the dominant Delta variant. In that sense, the Omicron variant may be the first ‘super-variant’ of SARS-CoV-2. Governments and public health authorities have responded swiftly by implementing travel bans and surveillance systems, providing booster shots, and informing the public of the current situation on the Omicron variant (CDC 2021f; NYT 2021; WHO 2021d). If the Omicron variant proves to be a more transmissible or deadly SARS-CoV-2 variant, scientists and public health authorities will face the urgent tasks of re-assessing its environmental transmission modes, environmental persistence, and prioritizing future infection prevention and control efforts. Meanwhile, the WHO reiterated that the Delta variant is still the major current cause of the pandemic, despite the recent concerns on the new Omicron variant (Choudhury 2021).

In light of the current knowledge gaps and urgent situations, we put forward the following recommendations and urgent questions. First, we recommend that face masks should continue to be worn in addition to social distancing requirements in areas with active COVID-19 transmission. This is a lesson from Israel's recent re-emergent outbreaks of COVID-19 infections. Secondly, we appeal to people all over the world to be fully vaccinated as soon as possible. Although not 100% effective, current vaccines provide considerable protection against the dominant viral strains that are currently circulating. Meanwhile, more testing data are needed to evaluate the effectiveness of current

vaccines on Delta and other variants, and public health authorities should inform the public by making these data available (Dai et al. 2020). Thirdly, the research, development, and production of new COVID-19 vaccines should accelerate to increase preparedness for new SARS-CoV-2 variants and their possible long existence and recurring outbreaks in our communities and animal reservoirs, much like the influenza viruses (He et al. 2021; He and Han 2021b). Last but not the least, researchers should investigate whether the transmission routes of new SARS-CoV-2 variants have indeed changed and particularly, whether there are existing or new environmental transmission routes that have been overlooked or underappreciated in previous dealing with the SARS-CoV-2 (Chen et al. 2021; Han et al. 2021; Han and Zhang 2020; Propper 2020; Wang et al. 2020).

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Declarations

Conflict of interest The authors declare no conflict of interest in this work.

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