SUERF
The European Money and Finance Forum

SUERF Policy Briefs
No 110, June 2021

Global vulnerabilities to the COVID-19 variant B.1.617.2*

By David Mackie
J.P. Morgan

Keywords: COVID-19, Global vulnerabilities.

- The variant first identified in India—B.1.617.2—is more transmissible than other strains, which pushes up the reproduction number and the herd immunity threshold
- Vaccines are still effective as long as individuals are fully vaccinated with two doses
- Morbidity and mortality risk look lower for B.1.617.2
- The most vulnerable individuals are the unvaccinated in Latin America, Africa, and Asia

---

Since being first detected in India at the end of last year, SARS-CoV-2 variant B.1.617.2 has spread across the world.[1] According to GISAID data,[2] it has been identified in 66 countries, most notably India, the UK, the US, Germany, Singapore, Ireland, Australia, Belgium, Japan, Canada, and Italy. Given limited capacity for genomic sequencing, the prevalence of variant B.1.617.2 could be much greater than the current data suggest.

Given recent developments in India, where a dramatic and devastating second wave of COVID-19 infections started unexpectedly in early March, it is not surprising that other countries are concerned about the spread of variant B.1.617.2 and are discussing whether to either impose new COVID-19 restrictions or to delay further steps of easing restrictions.

In this note we examine what is known about variant B.1.617.2. It does seem more transmissible than other variants, but it doesn't seem to significantly reduce the efficacy of existing vaccines as long as individuals are fully vaccinated. Also, the morbidity and mortality associated with infections with variant B.1.617.2 seem less than infections with variant B.1.1.7 (the variant first identified in Kent, England). This suggests that the most vulnerable individuals to variant B.1.617.2 are those that have not been fully vaccinated, which accounts for a significant proportion of the global population, especially in Latin America, Asia, and Africa.

Variant B.1.617.2 is more transmissible

It appears that variant B.1.617.2 is more transmissible than other strains of SARS-CoV-2, which suggests that it will continue to spread around the world. According to research by Public Health England (PHE),[3] the secondary attack rate (SAR) of variant B.1.617.2—the probability of infection given contact between an infectious individual and a susceptible individual—is around 70% higher than for the dominant strain in the UK, variant B.1.1.7 (Table 1). The SAR of variant B.1.1.7 for index cases that have not traveled is estimated by PHE to be 8.1%, while for B.1.617.2 it is estimated to be 13.5%, an increase of 66.7%. Given that variant B.1.1.7 was itself more transmissible than the original SARS-CoV-2 strain that emerged 18 months ago, this suggests that variant B.1.617.2 is significantly more transmissible than the original strain, which is probably still dominant in much of the world.

Table 1: Secondary attack rates of COVID-19 variants

	Secondary attack rate of contacts of cases that have traveled	Secondary attack rate of contacts of cases who have not traveled
B.1.1.7	1.7%	8.1%
B.1.617.2	2.9%	13.5%
% increase	70.6	66.7

Source: SARS-CoV-2 variants of concern and variants under investigation in England, Technical Briefing 13, PHE, 27 May 2021. The SAR is measured as secondary cases divided by contacts.

[1] The B.1.617.2 variant first identified in India is also known as variant Delta. The B.1.1.7 variant first identified in Kent, England is also known as variant Alpha.

[2] https://www.gisaid.org/hcov19-variants/

[3] SARS-CoV-2 variants of concern and variants under investigation in England, Technical Briefing 13, Public Health England, 27 May 2021.

In our view, the PHE estimates of the SAR are likely too large. The PHE estimates are based on contact tracing (the SAR is calculated as number of secondary cases divided by the number of contacts) and the UK contact tracing regime may not pick up all contacts, so the absolute level of the estimated SAR may be too high. Moreover, the growth increase from variant B.1.1.7 to variant B.1.617.2 is also likely too high due to the concentration of genomic sequencing at infection hotspots. Sequenced cases are not spread randomly across the country.

Table 2: Deriving the secondary attack rate (SAR) and the basic reproduction number

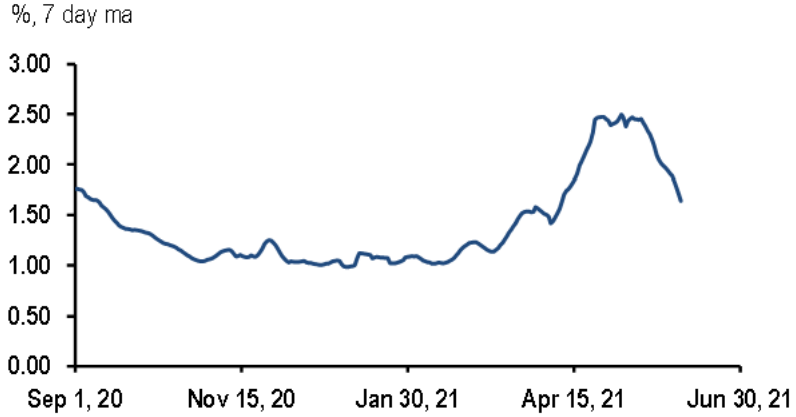
Situation	Basic reproduction number	Effective reproduction number	Actual SAR	SAR excl. NPIs and vaccinations	Vaccinations, % of population still susceptible
Original strain	3.0	2.3	2.50	2.50	100
Original strain + NPIs	3.0	0.95	1.47	2.50	100
B.1.1.7 + NPIs and vaccinations	3.9	0.87	1.60	3.22	72.9
B.1.1.7 and B.1.617.2 + NPIs and vaccinations	4.8	1.14	1.86	3.97	63.3

Source: J.P. Morgan. It is assumed that in late May, variant B.1.617.2 accounted for 70% of new infections, which means that the SAR of variant B.1.617.2 excluding the impact of NPIs and vaccinations is around 4.29%. The basic reproduction number of variant B.1.617.2 is estimated at 5.2.

Table 2 presents our estimates of the impact of the SARS-CoV-2 variants in the UK using a framework where the SAR is calibrated from the reproduction number (estimated from daily infections), the average number of daily contacts (estimated from Google mobility data), and the number of days an infected individual is infectious (assumed to be eight throughout). At the start of the epidemic in the UK in mid-March 2020, the SAR of the original SARS-CoV-2 strain, excluding the impact of non-pharmaceutical interventions (NPIs—social distancing, mask wearing, increased hygiene, and contact tracing and quarantine) and vaccinations, appeared to be around 2.5%. We have taken November 2020 as representative of a period with the original strain of SARS-CoV-2 with NPIs but before the impact of vaccinations (also with similar weather conditions to March). In November 2020 the actual SAR was around 1.47%. This suggests that NPIs reduced the SAR by 1.03%-pts, which is worth 1.2 on the reproduction number. By April 2021, the variant B.1.1.7 was dominant and the vaccination program was underway. The SAR excluding the impact of NPIs and vaccinations looks to have been around 3.22%. By the time we get to late May, variant B.1.617.2 accounted for around 70% of new infections so the SAR of this variant excluding the impact of NPIs and vaccinations looks to be around 4.29% (4.29=(3.97-(0.3*3.22))/0.7). These calculations suggest that variant B.1.1.7 is around 29% more infectious than the original strain of SARS-CoV-2, and that variant B.1.617.2 is around 33% more infectious than variant B.1.1.7. This suggests that variant B.1.617.2 is around 72% more infectious than the original strain.

These estimates of infectiousness based on UK data resonate with the reported data in India. Figure 1 shows the evolution of our estimate of the SAR in India. If we assume that the estimated SAR of 1.17% from September 2020 to January 2021 represented the original strain of SARS-CoV-2, and that the estimated SAR of 2.11% since April represents variant B.1.617.2, this suggests an increase in transmissibility of 80%, almost exactly the same as our estimate based on UK data. (Note that the estimated level of the SAR will not be the same across countries due to differences in demography, population density, and climate.)

Figure 1: India COVID-19 secondary attack rate



Source: J.P. Morgan

The impact on the herd immunity threshold

Although our estimates of infectiousness based on the UK data are lower than those of PHE, they are still worrisome because it is the SAR excluding the impact of NPIs and vaccinations that determines the basic reproduction number,[4] which determines the vaccination threshold for herd immunity.[5] Our calculations suggest that it will be hard to reach herd immunity through vaccinations alone, and that some non-pharmaceutical interventions (NPIs) and mobility restrictions will likely need to remain in place for an extended period.

The calculations in Table 2 can be used to estimate the basic reproduction numbers for SARS-CoV-2 variants. These suggest that the basic reproduction number in the UK is 3.0 for the original strain, 3.9 for variant B.1.1.7, and 5.2 for variant B.1.617.2. These estimates for the basic reproduction number look high but they align with the estimates from the UK government's academic advisors (Table 3). On average, these academic institutions put the basic reproduction number for variant B.1.1.7 at 4.4. They have not yet published an estimate for variant B.1.617.2.

The basic reproduction number is the number of secondary infections assuming no restrictions and full population susceptibility. The effective reproduction number is the number of secondary infections after restrictions and the buildup of immunity.

The herd immunity threshold is the percentage of total population who need to be vaccinated to hold the effective reproduction number at one without any other interventions or changes in behavior.

Table 3: Estimates of reproduction number excluding immunity for variant B.1.1.7

After step 4 lockdown easing with some other NPIs	
Imperial College	3.50
University of Warwick	3.51
LSHTM	3.05
After step 4 lockdown easing with no other NPIs	
Imperial College	4.50
University of Warwick	4.69
LSHTM	4.11

Source: Gov.UK SAGE, Imperial college, University of Warwick, LSHTM, J.P. Morgan

[4] The basic reproduction number is the number of secondary infections assuming no restrictions and full population susceptibility. The effective reproduction number is the number of secondary infections after restrictions and the buildup of immunity.

[5] The herd immunity threshold is the percentage of total population who need to be vaccinated to hold the effective reproduction number at one without any other interventions or changes in behavior.

Table 4 illustrates what the journey to herd immunity looks like if the basic reproduction number of variant B.1.617.2 is 5.2. The second column shows the reproduction number after the impact of vaccinations but without any NPIs or mobility restrictions. With a fully susceptible population and no NPIs, the reproduction number is 5.2 (equal to the basic reproduction number). Without NPIs, herd immunity is reached when 90% of the total population has been fully vaccinated (assuminging vaccine efficacy of 90%).

At this level of vaccination, no NPIs are needed and daily contacts can return to the pre-COVID-19 average of 15. The third column shows the reproduction number after the additional impact of NPIs, which are assumed to reduce the reproduction number by 1.2. If the current level of NPIs is maintained, then herd immunity is achieved once 65% of the total population is vaccinated. The final column shows what daily contacts have to do to get the reproduction number to one, given the impact of vaccinations and NPIs. With no vaccination effect but NPIs in place, daily contacts would need to be 3.8 (25% of the pre-COVID-19 average of 15) to hold the reproduction number at one. This broadly describes the UK in April 2020, when NPIs and daily contacts of 3.7 held the reproduction number at 1.1 (although the basic reproduction number at the time was 3.0).

Table 4 helps to understand the current situation in India. In early May, with very little protection afforded by the vaccine, the Indian reproduction number was brought down to one by a decline in daily contacts to 5.3. This is almost exactly what Table 4 would suggest, given our estimates for the basic reproduction number and the impact of NPIs.

Table 4: The journey to herd immunity with variant B.1.617.2

% of total population fully vaccinated	Reproduction number after vaccinations	Reproduction number after vaccinations and NPIs	Daily contacts to keep reproduction number at one
0	5.2	4.0	3.8
10	4.7	3.5	4.4
25	4.0	2.8	5.6
50	2.9	1.7	9.0
65	2.2	1.0	15.0
75	1.7	0.5	15.0
90	1.0	0.0	15.0

Source: J.P. Morgan. These calculations assume the following: that the basic reproduction number of variant B.1.617.2 is 5.2; that vaccine efficacy is 90%; that NPIs depress the reproduction number by 1.2; and that the pre-COVID-19 average number of daily contacts was 15.0.

Variant B.1.617.2 and vaccine efficacy

In a PHE study of vaccine efficacy against symptomatic disease, variant B.1.617.2 did significantly diminish the efficacy of the first dose of both the Pfizer-BioNTech and the Oxford-AstraZeneca vaccines, but not the efficacy of the second dose.[6] After the first dose of the Pfizer-BioNTech vaccine, symptomatic infections were reduced by only 33.2% with the B.1.617.2 variant, while they were reduced by 49.2% with the B.1.1.7 variant. But after the second dose of the Pfizer-BioNTech vaccine, symptomatic infections were reduced by 87.9% with the B.1.617.2 variant, compared with a reduction of 93.4% with the B.1.1.7 variant (Table 5). A similar pattern is evident with the Oxford-AstraZeneca vaccine. These results explain why, after extending the gap between first and second doses to 12 weeks to make the limited supply go further, the UK government is now shortening the gap to provide more protection against variant B.1.617.2.

Table 5: Public Health England study of vaccine efficacy against COVID-19 variants

Efficacy against symptomatic disease, %

		Variant B.1.1.7	Variant B.1.617.2
Pfizer	First dose	49.2	33.2
	Second dose	93.4	87.9
AstraZeneca	First dose	51.4	32.9
	Second dose	66.1	59.8

Source: Public Health England, Effectiveness of COVID-19 vaccines against the B.1.617.2 variant, J. Bernal et al.

Vaccine efficacy is normally measured against symptomatic infections. But, that is not the only thing that matters. Vaccines can also affect the morbidity and mortality of symptomatic infections. Table 6 shows the results of a PHE study that looked at all sequenced cases between February 1 and May 25.[7] Identified cases of infections with variant B.1.617.2 had a much lower hospital admissions rate and case fatality rate than infections with variant B.1.1.7.

A more detailed PHE study of vaccinations and variant B.1.617.2 presents a more nuanced picture (Table 7).[8] Vacc Vaccinated individuals are much less likely to become infected with variant B.1.617.2, especially if two doses have been administered. But when it comes to hospitalizations and deaths, it looks as if vaccinated individuals are more likely to be hospitalized and more likely to die than unvaccinated individuals (combining those with one and two doses). This seems implausible to us, given the other evidence, and most likely reflects the very small sample sizes. Only 12 vaccinated individuals were hospitalized and only 4 died.

[6] Effectiveness of COVID-19 against the B.1.617.2 variant, J. Lopez Bernal.

[7] SARS-CoV-2 variants of concern and variants under investigation in England, Technical Briefing 13, PHE, 27 May 2021.

[8] SARS-CoV-2 variants of concern and variants under investigation in England, Technical Briefing 13, PHE, 27 May 2021.

Table 6: The severity of COVID-19 variant infections

1 February to 25 May, 2021

Variant	Number of infections	Hospital admissions	Admissions rate %	Deaths	Case fatality rate %
B.1.1.7	136,048	2079	1.5	1703	1.3
B.1.617.2	5599	43	0.8	12	0.2

Source: SARS-CoV-2 variants of concern and variants under investigation in England, Technical Briefing 13, PHE, 27 May 2021. These data refer to all sequenced cases rather than all cases. During this period there were 673,000 reported cases, which means that 21% of all cases were sequenced.

Table 7: Vaccinations and B.1.617.2 infections

	Total	Unvaccinated	Vaccinated	
			One dose	Two doses
B.1.617.2 infections	5599	3367	1093	177
Hospital admissions	43	29	11	1
Admissions rate, %	0.77	0.86	1.01	0.56
Deaths	12	8	2	2
Case fatality rate, %	0.21	0.24	0.18	1.13

Source: SARS-CoV-2 variants of concern and variants under investigation in England, Technical Briefing 13, PHE, 27 May 2021. These data refers to all sequenced cases between February 1 and May 25, 2021.

Global vulnerabilities to SARS-CoV-2 variant B.1.617.2

Our reading of the evidence suggests that variant B.1.617.2 is much more transmissible than either the original SARS-CoV-2 strain or variant B.1.1.7, but fully vaccinated individuals are well protected. This means that infections will spread very rapidly through a susceptible population, as has happened in India in recent months. And even though the hospitalization and case fatality rates might be lower with variant B.1.617.2 infections, a higher number of cases will still deliver an increase in the pressure on healthcare systems and more deaths. There is good reason for the world to be concerned about variant B.1.617.2. What matters is the proportion of the total population that has been vaccinated, especially the proportion that has been fully vaccinated. Across Developed Markets only Japan, Australia, and New Zealand look especially vulnerable with vaccination rates still relatively low. But the real concern is across Emerging Markets. In Latin America, vaccination rates are low everywhere except in Chile. In Africa, every country looks very vulnerable with very low vaccination rates across the whole continent. In Emerging Asia, everyone looks very vulnerable except for China and Singapore. Finally, in Emerging Europe the most vulnerable countries are Russia and Turkey. EU member states in Emerging Europe have benefited from the regional vaccine distribution scheme, while Israel is the least vulnerable country in the world with 60% of its total population fully vaccinated. India's experience in recent months illustrates what can happen when SARS-CoV-2 variant B.1.617.2 runs through a susceptible population. This argues strongly not only for faster vaccine production but also a more equal distribution. Of the 2.1 billion doses of vaccine administered thus far, 30% has gone to DM countries, even though they account for only 12% of the world's population.

About the author

David Mackie is a Managing Director and Senior Advisor for European and Global Thematic Research. He has been at JPMorgan for 30 years, analyzing a number of different European economies and various regional and global issues. From 2000 to 2018 he was the Head of Economic Research for Western Europe, managing a small group of economists, but he is now in a new role focusing on thematic research. Prior to joining JPMorgan he spent 5 years at the Bank of England, both as an economist and as a manager of the official foreign exchange reserves. David completed his undergraduate studies at Cambridge University in 1981 and his postgraduate studies at Oxford University in 1984.

SUERF Publications

Find more **SUERF Policy Briefs** and **Policy Notes** at www.suerf.org/policynotes

SUERF
The European Money and Finance Forum

SUERF is a network association of central bankers and regulators, academics, and practitioners in the financial sector. The focus of the association is on the analysis, discussion and understanding of financial markets and institutions, the monetary economy, the conduct of regulation, supervision and monetary policy.

SUERF's events and publications provide a unique European network for the analysis and discussion of these and related issues.

SUERF Policy Briefs (SPBs) serve to promote SUERF Members' economic views and research findings as well as economic policy-oriented analyses. They address topical issues and propose solutions to current economic and financial challenges. SPBs serve to increase the international visibility of SUERF Members' analyses and research.

The views expressed are those of the author(s) and not necessarily those of the institution(s) the author(s) is/are affiliated with.

SUERF Secretariat
c/o OeNB
Otto-Wagner-Platz 3
A-1090 Vienna, Austria
Phone: +43-1-40420-7206
www.suerf.org • suerf@oenb.at