



COVID-19 Global Trends and Analyses

Mutations
of SARS-CoV-2,
Superspreading

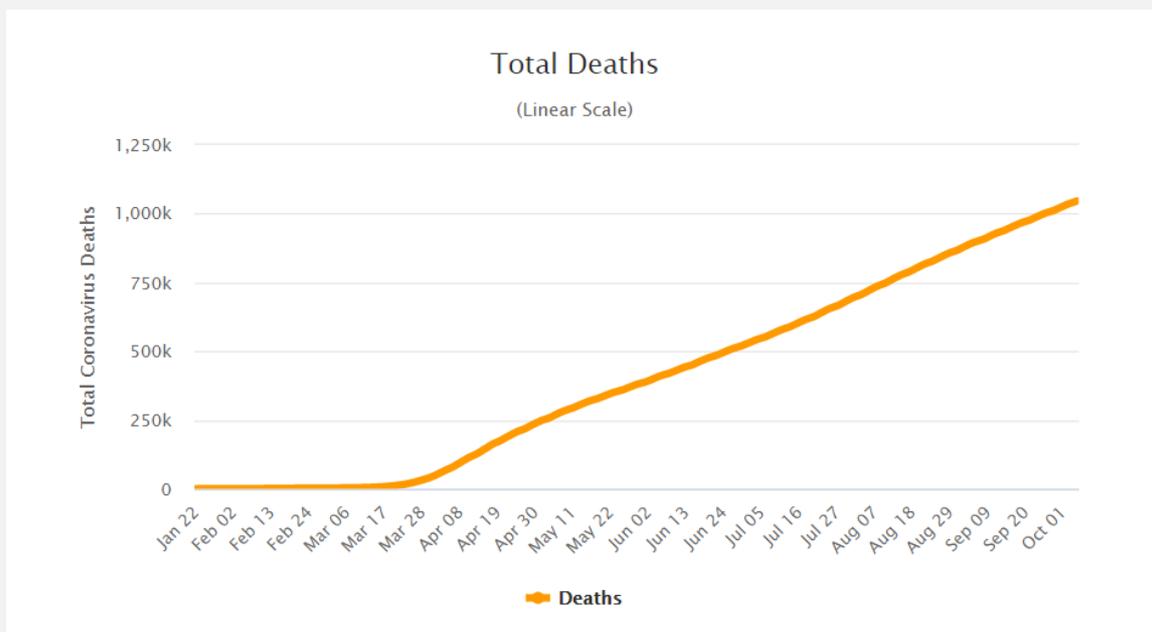
October 2020 | Update 1

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SUMMARY

COVID-19 GLOBAL TRENDS AND ANALYSES | 23 Sept - 6 Oct 2020

- The **global number of deaths** reached a grim milestone of one million on 28 September.



- The **global** total number of reported cases has surpassed 35.7 million as of 5 October. At least 73 countries are now experiencing surges in infections.
- The situation in **Europe** is worsening, as many countries are seeing resurgences in COVID-19 cases. The **UK, France** and **Spain** have reported record numbers of daily new cases.
- In the **United States**, the number of cases has surpassed 7 million and the death toll has surpassed 214,000. Over the past two weeks, 27 of the 50 states have reported upswings in new daily cases.
- India's** epidemic has continued to grow at an alarming rate. The country has recorded over 7 million cases just 12 days after it reached 6 million.
- Indonesia's** case numbers have shown no signs of slowing down and continue to grow, reporting more than 4,800 new cases for the first time on 25 September.
- Myanmar** has reported 18,781 cases and 444 deaths, reporting an all-time high of 1,291 new cases on 4 October. The outbreaks are centred in a number of townships in Yangon.
- Since the last update, **Victorian** daily case numbers have continued to decline. The number of active cases was 241 on 6 October. Of those cases, 29 (12%) are healthcare workers and 77 (32%) are aged care facility residents.
- To trigger the next stage of release from lockdown, metro **Melbourne** must continue to average fewer than five cases over a period of 14 days. On 6 October that number was 10.6. A further metric is zero cases of unknown source of infection. In the past 14 days there have been 13 such cases in Melbourne.

Viral Mutations

- The D614G mutation of SARS-CoV-2, which probably originated in China, spread rapidly around the world and had almost become the universal form of the virus by June.
- There is still no consensus on whether this mutation made the virus more transmissible but some laboratory studies and population-based genetic epidemiology studies in the US and UK suggest that it may be more infectious than its predecessor.
- There is general agreement that this mutation has not made the virus more clinically virulent. It also appears that the D614G mutation has not affected the immune system's ability to recognise the virus. Therefore, it is unlikely to reduce the efficacy of vaccines under development, but it may impair some potential therapeutic agents.

Overdispersion of the Virus (Superspreading)

- COVID-19, like other diseases caused by coronaviruses, such as SARS and MERS, tends to cluster rather than spread linearly like influenza. COVID-19 is also subject to large superspreading events where one person may infect dozens or hundreds of others. Thus, the metric R_0 does not reflect the reality of SARS-CoV-2 transmission.
- On the other hand, the dispersion factor k is a better metric to characterise transmission. The lower the value of k the fewer people are causing most spread of the virus. This value has been estimated as 0.12 for SARS and 0.25 for MERS while estimates for COVID-19 are as low as 0.1 meaning that just 10% of infected cases are infecting more than 80% of people.
- Superspreading events have been associated with large indoor gatherings in poorly ventilated spaces and where people may be singing (choir practices and church services) or speaking loudly (nightclubs and bars). It is likely that in this environment an individual with a high viral load in their pharynx has introduced the virus into an environment where it spreads rapidly.
- The concept of over-dispersion has implications for contact tracing. Rather than focusing only on 'forward' tracing, namely finding people that have been in contact since the person was infected, there should also be efforts to see who first infected the subject. This may reveal previously unidentified infected individuals within the cluster.

GLOBAL EPIDEMIOLOGY AND TRENDS

The **global** total number of reported cases has reached 35.7 million with more than one million deaths recorded as of 6 October¹. At least 73 countries are reporting surges of new infections. Only six countries in the world have so far effectively controlled significant second waves of infections – Vietnam, South Korea, Hong Kong, New Zealand, Serbia and Australia.

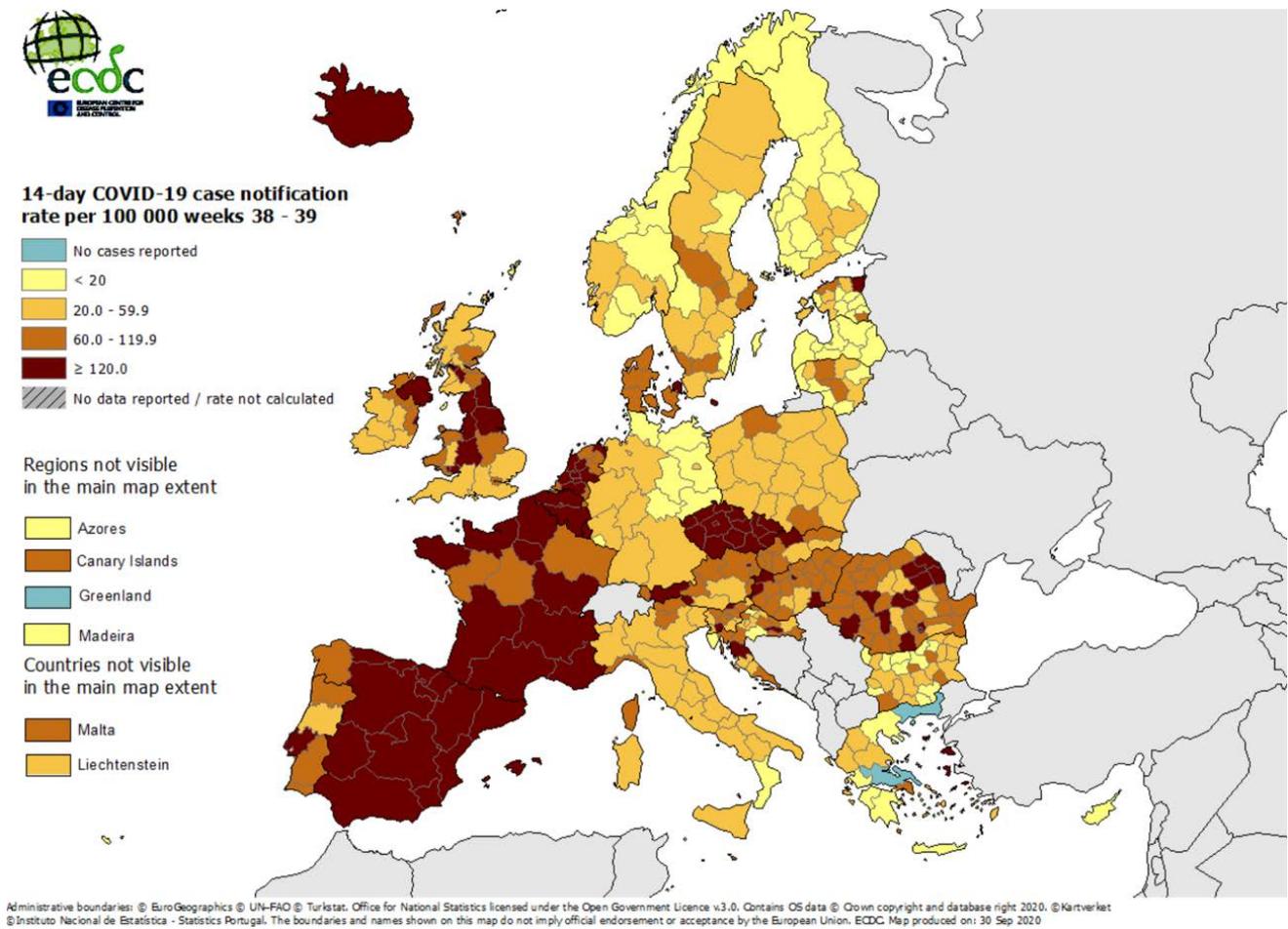
European Region

- Countries across **Europe** are seeing resurgences in COVID-19 cases after successfully slowing outbreaks early in the year. Many countries — such as Albania, Bulgaria, Croatia, Czech Republic, Denmark, France, Greece, Hungary, Montenegro, the Netherlands, North Macedonia, Poland, Romania, Spain, Slovakia and the UK — are seeing much higher case numbers in September than they did earlier in the year².
 - The **UK** reported an all-time high of 12,594 cases on 5 October.
 - The number of patients in ICU in **France** has surpassed 1,400 for the first time since April.
 - **Madrid, Paris** and **Liverpool** have reintroduced lockdowns.
- Other countries, like **Belgium** and **Austria** are experiencing second waves equal in scale to their first waves. All are re-introducing various forms of restrictions, including mandating face masks in public and closing bars and restaurants in some regions.
- A few countries, such as **Portugal, Norway, Finland, Belarus, Germany, Ireland, Italy, Estonia, Iceland** and **Sweden** have reported modest surges in new cases. Although Sweden's second wave began later than most other European countries, it is now reporting more than 600 new cases daily.
- In **Ukraine**, daily new cases have steadily been increasing ever since April and they show no sign of abating.
- **Serbia** appears to be the only country in Europe that has effectively managed a second wave.

¹ <https://www.worldometers.info/coronavirus/#countries>

² <https://www.euronews.com/2020/09/28/is-europe-having-a-covid-19-second-wave-country-by-country-breakdown>

Figure 1: 14-Day Incidence of New COVID-19 Cases in EU/UK Countries



Source: European Centre for Disease Control, <https://www.ecdc.europa.eu/en/cases-2019-ncov-eueea>

North Africa and the Middle East

- Outbreaks in **North African** countries like **Morocco, Tunisia** and **Libya** are rapidly spiralling out of control.
- The numbers of new cases continue to increase in **Iran, Israel, Iraq, Lebanon, Palestine,** and **Jordan.**

The Americas

- In the **United States**, the number of cases has surpassed 7 million and the death toll has surpassed 210,000. New cases have been increasing in 27 of the 50 states over the past two weeks. The latest rise in cases has mostly been concentrated in the West and Midwest, where states like Colorado, Wyoming, Wisconsin, North and South Dakota, and Montana are seeing a surge. Test positivity rates have recently increased to 3.25% in New York City and schools have closed in some parts of the city. In Florida over the past two weeks the average test positivity rate is 11%.

- **Canada** is experiencing a clear second wave with new cases focused in the large cities of Montreal and Toronto. New case counts have surpassed 2,000 on several days for the first time since early May.
- Six **Latin American** countries – Brazil, Colombia, Peru, Argentina, Mexico and Chile – account for 25% of global COVID-19 cases. The capital of **Chile**, Santiago, is only just emerging from the world’s longest lockdown of seven months. The cumulative test positivity rate of 38.4% in **Argentina** is the highest in the world followed by **Mexico** at 37%.

African Region

- While so much about the virus and how it operates remains unclear, **sub-Saharan Africa** so far has avoided a deadly wave of coronavirus cases. Many factors have contributed to this. A number of West African nations already had a pandemic response infrastructure in place from the Ebola outbreak of late 2013 to 2016. Just six years ago, Liberia lost nearly 5,000 people to Ebola. At the beginning of this year, **Liberia** began screening for COVID-19 at airports. Travellers coming in from countries with more than 200 cases were quarantined. To date, Liberia, a country of some 5 million, has 1,335 cases and around 82 deaths³.
- After the Ebola pandemic, **Senegal** set up an emergency operations centre to manage public health crises. Some COVID-19 test results come back in 24 hours, and the country employs aggressive contact tracing. Every coronavirus patient is given a bed in hospital or other health-care facility. Senegal has a population of 16 million but has 302 registered deaths. Several countries have come up with innovations. **Rwanda**, a country of 12 million, also responded early and aggressively to the virus, using equipment and infrastructure that was in place to deal with HIV/AIDS. Testing and treatment for the virus are free. Rwanda has recorded 26 deaths.
- In **South Africa**, where daily new cases surpassed 13,000 on numerous days in July, the numbers in September have been fewer than 2,000. However, other southern African countries, including **Mozambique, Botswana** and **Namibia**, are experiencing significant first waves that began in July.
- Elsewhere in sub-Saharan Africa, the number of new cases has been declining in most countries, with the exception of **Ethiopia**, which experienced a late first wave, and **Uganda**, which is experiencing a second wave with 200 to 400 new cases per day.

Asia-Pacific Region

- **India’s** epidemic has continued to grow at an alarming rate. The country has recorded over 7 million cases 12 days after it hit 6 million. This accelerating epidemic is of great concern, and the country is expected to become the worst-hit in the world within the next few weeks. India has reported more than 100,000 deaths, the third highest in the world after the US and Brazil. The fatalities are primarily concentrated in the large cities such as Mumbai, Delhi and Chennai.

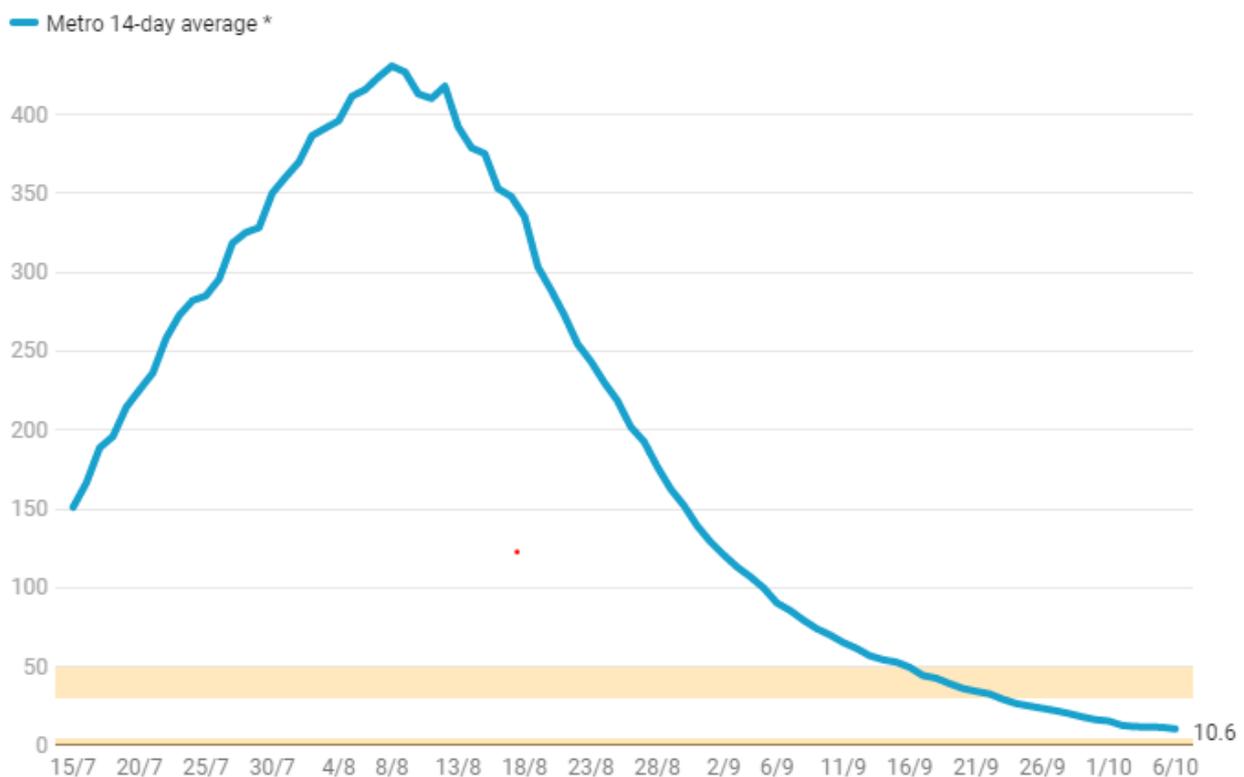
³ <https://www.washingtonpost.com/opinions/2020/09/22/africa-has-defied-covid-19-nightmare-scenarios-we-shouldnt-be-surprised/>

- **Indonesia**'s case numbers have shown no signs of slowing down and continue to grow reporting more than 4,000 new daily cases on most days since 19 September. New cases and deaths are exploding in **Bali**, which has reported more than 9,000 cases, most since early September when the island opened up to tourists from other parts of Indonesia.
- Daily new cases in the **Philippines** have been in steady decline after a new lockdown was imposed in Metro Manila – down from around 5,000 in mid-September to around 2,500 in early October.
- **Myanmar** has reported 18,781 cases and 444 deaths and reported an all-time high of 1,291 new cases on 4 October. The outbreaks are centred in a number of townships in Yangon but also spreading in Mandalay. There is now a lockdown in Yangon.
- **Papua New Guinea** has reported 570 cases and seven deaths. During the past two weeks, 23 new cases have been recorded.

Australia

- Since the last update, the **Victorian** daily case numbers have continued to decline. The number of active cases was 241 on 6 October. Of those cases, 29 (12%) are healthcare workers and 77 (32%) are aged care facility residents.
- To trigger the next stage of release from lockdown, Metro **Melbourne** must continue to average fewer than five cases over a period of 14 days. On 6 October that number was 10.6. A further metric is zero cases of unknown source of infection. In the past 14 days there have been 13 such cases in Melbourne.

Figure 2: Metro Melbourne Rolling 14-Day Average of New Cases



SCIENCE AND RESEARCH UPDATES | MUTATIONS OF SARS-CoV-2⁴

Mutations, or changes in an organism's genetic material, are natural effects of evolution after replication. Although these changes can be interpreted as errors in the replication process, mutations that occur at certain sites can give the virus new properties, making them more likely to survive⁵. Although the virus SARS-CoV-2 is a relatively new pathogen, it has accumulated mutations across its genes from the start of this pandemic.

The Spike protein D614G mutation, for instance, which has a Gly614 amino acid replacement in the spike protein, was first detected in viruses collected in China and Germany in late January; most scientists suspect the mutation arose in China⁶. Fortunately, SARS-CoV-2 is mutating slower than other viruses, like influenza and HIV, with about two new changes in its genome every month.

So, what happens when a SARS-CoV-2 gene is mutated?

The cell's machinery within the host organism helps each gene to make a specific protein. The resultant mutant protein usually has a slightly different shape than the normal protein, particularly around the area where the mutation lies. For example, if a protein is mutated at the site where another protein or drug would usually bind, this interaction might be compromised⁷.

Because therapies like vaccines and drugs typically target proteins specifically, mutations that compromise drug interactions present a major challenge in therapeutic drug development, especially as new mutations may render some of these therapies ineffective over time⁷.

In March 2020, researchers at Duke University in North Carolina and the Los Alamos National Laboratory in New Mexico, had already started screening thousands of coronavirus genetic sequences for mutations that might have changed the virus's properties as it made its way around the world⁸.

In April, they warned in a preprint posted to the bioRxiv server that "D614G is increasing in frequency at an alarming rate". It had rapidly become the dominant SARS-CoV-2 lineage in Europe and had then taken hold in the United States, Canada and Australia. D614G represented a "more transmissible form of SARS-CoV-2", the paper declared.

These assertions dismayed many scientists because viruses usually mutate to better co-exist with the host not harm it. It wasn't clear that the D614G viral lineage was more transmissible, or that its rise indicated anything

⁴ We acknowledge Professor Gilda Tachedjian for her review and comments on an earlier draft.

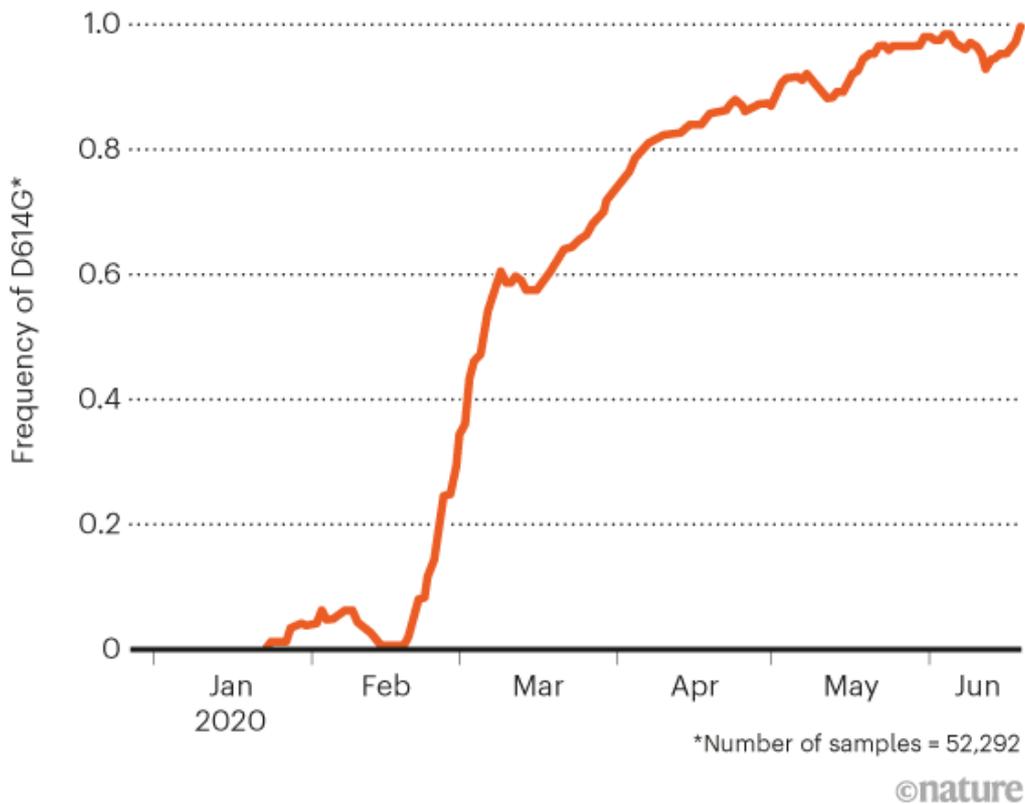
⁵ <https://pursuit.unimelb.edu.au/articles/locked-and-loaded-using-genomic-sequencing-to-target-covid-19-s-weak-spots>

⁶ <https://www.nature.com/articles/d41586-020-02544-6>

unusual, they said. But alarm spread fast across the media. Although many news stories included researchers' caveats, some headlines declared that the virus was mutating to become more dangerous. In retrospect, the lead author said that he and his colleagues regretted describing the variant's rise as "alarming". The word was removed from the peer-reviewed version of the paper, published in Cell in July⁷.

GLOBAL SPREAD

By the end of June, the D614G mutation was found in almost all SARS-CoV-2 samples worldwide.



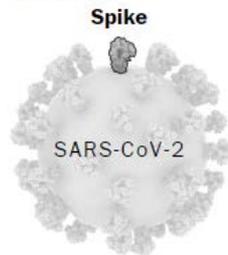
In a pre-print paper posted on the medRxiv server on 20 September, researchers sequenced the genomes of 5,085 SARS-CoV-2 strains causing two COVID-19 waves in metropolitan Houston, Texas⁸. The genomes were from viruses recovered in the earliest recognised phase of the pandemic in Houston, and an ongoing massive second wave of infections. Virtually all strains in the second wave had the Gly614 amino acid replacement in the spike protein typical of the D614G strain. Patients infected with the Gly614 (or D614G) variant strains had significantly higher virus loads in the nasopharynx on initial diagnosis. They found little evidence of a significant relationship between virus genotypes and altered pathogenicity.

⁷ [https://www.cell.com/cell/fulltext/S0092-8674\(20\)30820-5?returnURL=https%3A%2F%2Flinkinghub.elsevier.com%2Fretrieve%2Fpii%2FS0092867420308205%3Fshowall%3Dtrue](https://www.cell.com/cell/fulltext/S0092-8674(20)30820-5?returnURL=https%3A%2F%2Flinkinghub.elsevier.com%2Fretrieve%2Fpii%2FS0092867420308205%3Fshowall%3Dtrue)

⁸ <https://www.medrxiv.org/content/10.1101/2020.09.22.20199125v3>

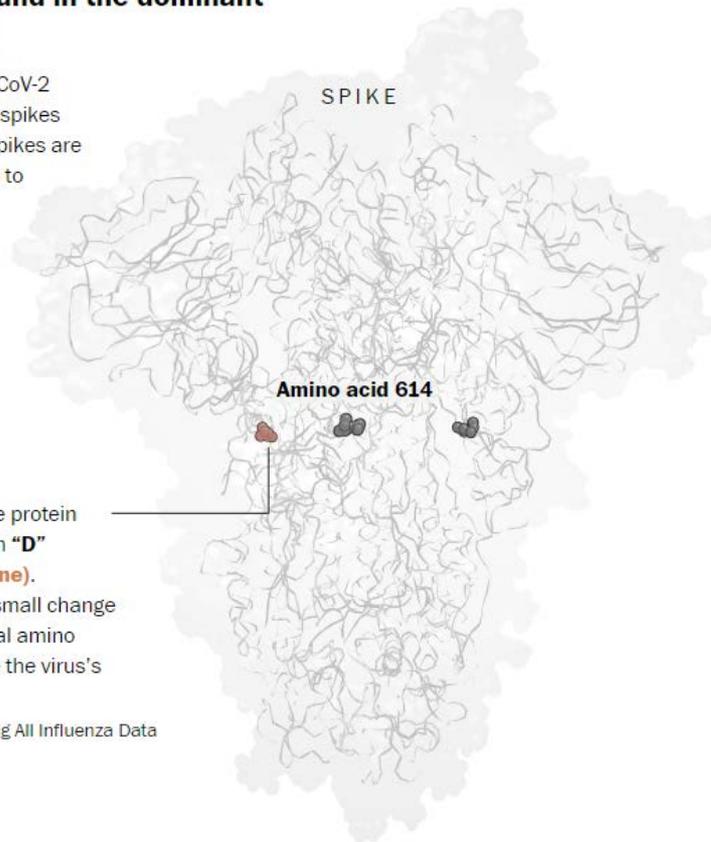
The tiny mutation found in the dominant coronavirus variant

Like all coronaviruses, SARS-CoV-2 has a series of characteristic spikes surrounding its core. These spikes are what allow the virus to attach to human cells.



A mutation affecting the spike protein changed amino acid 614 from “**D**” (aspartic acid) to “**G**” (glycine). Research suggests that this small change — which affects three identical amino acid chains — might enhance the virus’s transmissibility.

Source: Global Initiative on Sharing All Influenza Data



Source: <https://www.washingtonpost.com/health/2020/09/23/houston-coronavirus-mutations/?arc404=true>

Another study, posted on the medRxiv server on 1 September investigated the positive selection of Spike 614G in the United Kingdom, using more than 25,000 whole genome SARS-CoV-2 sequences collected by the COVID-19 Genomics UK Consortium⁹. Using phylogenetic analysis, they identified Spike 614G and 614D clades with unique origins in the UK and they extrapolated and compared growth rates of co-circulating transmission clusters.

Population genetic modelling indicated that 614G increases in frequency relative to 614D in a manner consistent with a selective advantage. They also investigated the potential influence of Spike 614D versus G on virulence by matching a subset of records to clinical data on patient outcomes. They did not find any indication that patients infected with the Spike 614G variant have higher COVID-19 mortality.

Most available evidence suggests that D614G doesn’t stop the immune system’s neutralising antibodies from recognising SARS-CoV-2. That might be because the mutation is not in the spike protein’s receptor-binding domain (RBD), a region that many neutralising antibodies target: the RBD binds to the cell-receptor protein ACE-2, a key step in the virus’s entry to cells. The 614G mutation has been reported to change the structure of the spike protein so that it is more likely in an ‘open orientation’ - ready to interact with the ACE-2 receptor, which may explain its ability to enter cells more efficiently compared to the 614D counterpart which tends to be in a ‘closed orientation’¹⁰.

⁹ <https://www.medrxiv.org/content/10.1101/2020.07.31.20166082v2>

¹⁰ [Yurkovestskiy, L et al Preprint at bioRxiv https://doi.org/10.1101/2020.07.04.187757 \(2020\)](https://doi.org/10.1101/2020.07.04.187757)

With most of the world still susceptible to SARS-CoV-2, it's unlikely that immunity is currently a major factor in the virus's evolution. But as population-wide immunity rises, whether through infection or vaccination, a steady trickle of immune-evading mutations could help SARS-CoV-2 to establish itself permanently, potentially causing mostly mild symptoms when it infects individuals who have some residual immunity from a previous infection or vaccination¹¹.

Summary

The D614G mutation of SARS-CoV-2, which probably originated in China, spread rapidly around the world and had almost become the universal form of the virus by June. There is still no consensus on whether this mutation made the virus more transmissible but some laboratory studies and population-based genetic epidemiology studies in the US and UK suggest that it may be more infectious than its predecessor. There is general agreement that this mutation has not made the virus more clinically virulent. It also appears that the D614G mutation has not affected the immune system's ability to recognise the virus.

¹¹ <https://www.nature.com/articles/d41586-020-02544-6>

OVERDISPERSION AND SUPERSPREADING OF COVID-19

The Problem with the Metric R_0

The well-known R_0 (pronounced as “r-naught”) is an *average* measure of a pathogen’s infectiousness, or the mean number of susceptible people expected to become infected after being exposed to a person with the disease. If one infected person infects three others on average, the R_0 is 3. This characteristic has been widely promoted as a key factor in understanding how the pandemic spreads. However, averages aren’t always useful for understanding the distribution of a phenomenon, especially if it has widely varying behaviour. Heterogenous transmission of SARS-CoV-2 means that while one person may pass it onto a few, another may pass it on to many, requiring a more nuanced metric to determine transmissibility.

Superspreading Events

A database at the London School of Hygiene and Tropical Medicine (LSHTM) lists an outbreak in a dormitory for migrant workers in Singapore linked to almost 800 cases; 80 infections tied to live music venues in Osaka, Japan; and a cluster of 65 cases resulting from Zumba classes in South Korea¹². Clusters have also occurred aboard ships and at nursing homes, meatpacking plants, ski resorts, churches, restaurants, hospitals, and prisons. Sometimes a single person infects dozens of people, whereas other clusters unfold across several generations of spread, in multiple venues.

In **Melbourne**, a recent cluster that began in a retail meat shop spread rapidly to infect at least 28 people dispersed across the city and into a rural shire.

There are COVID-19 incidents in which a single person likely infected 80 percent or more of the people in the room in just a few hours. For example, in the US state of **Washington**, following a 2.5-hour choir practice attended by 61 persons, including a symptomatic index patient, 52 COVID-19 cases occurred (attack rate 86.7%); three patients were hospitalised, and two died¹³. In Shejian province of **China**, an asymptomatic infected individual infected 23 of the 67 other passengers of a bus during a 50-minute journey¹⁴.

One well-publicised potential superspreading event occurred at the **White House** when the president introduced his nominee for the Supreme Court in the Rose Garden to a crowd of around 150 people who were not physically distanced and few of whom wore masks. Although this was an outdoor event, a number of guests mingled in rooms inside the White House. As of 6 October, 12 attendees had tested positive to COVID-19 including the president and the first lady.

¹² <https://wellcomeopenresearch.org/articles/5-83>

¹³ <https://www.cdc.gov/mmwr/volumes/69/wr/mm6919e6.htm>

¹⁴ <https://jamanetwork.com/journals/jamainternalmedicine/fullarticle/2770172>

But, at other times, COVID-19 can be surprisingly much less contagious. For example, in **Guangzhou** earlier this year, 195 contact groups were identified for 349 laboratory-confirmed cases. Of these, 138 (71%) did not lead to any secondary cases¹⁵. Growing numbers of studies estimate that a majority of infected people may not infect a single other person. A recent paper found that in **Hong Kong**, which had extensive testing and contact tracing, about 19 per cent of cases were responsible for 80 per cent of transmission, while 69 per cent of cases did not infect another person¹⁶. This finding is not rare: Multiple studies from the beginning have suggested that as few as 10 to 20 per cent of infected people may be responsible for as much as 80 to 90 per cent of transmission, and that many people barely transmit it.

Scientists looked globally at known early-introduction events, in which an infected person comes into a country, and found that in some places, such imported cases led to no known infections, while in others, they sparked sizable outbreaks. Using genomic analysis, researchers in **New Zealand** looked at more than half the confirmed cases in the country and found a staggering 277 *separate* introductions in the early months, but that only 19 per cent of introductions led to more than one additional case¹⁷.

Overdispersion Parameter, k

This kind of behaviour, alternating between being super infectious and fairly non-infectious, is exactly what k captures, and what focusing solely on the average value of R obscures.

That's why in addition to R , scientists use a value called the overdispersion parameter (k), which describes how much a disease cluster. The lower k is the more transmission comes from a small number of people. In a seminal **2005 Nature paper**, Lloyd-Smith and co-authors estimated that SARS—in which superspreading played a major role—had a k of 0.16¹⁸. The estimated k for MERS, which emerged in 2012, is about 0.25.

Researchers at the London School of Hygiene and Tropical Medicine quantified individual-level variation in COVID-19 transmission by applying a mathematical model to observe outbreak sizes in affected countries, using a WHO database. **The method of calculating k can be found in this reference**¹⁹. Their model suggested a high degree of individual-level variation in the transmission of COVID-19. Within the current consensus range of R_0 (2-3), the over-dispersion factor k was estimated to be around 0.1, suggesting that **80% of secondary transmissions may have been caused by a small fraction of infectious individuals (~10%)**.

Risks for Superspreading Clusters

Much is still unknown about the super-spreading of SARS-CoV-2. Some people shed far more virus, and for a longer period of time, than others, perhaps because of differences in their immune system or the distribution of virus receptors in their body. A 2019 study of healthy people showed some breathe out many more particles than

¹⁵ [https://www.thelancet.com/journals/laninf/article/PIIS1473-3099\(20\)30471-0/fulltext#seccestitle130](https://www.thelancet.com/journals/laninf/article/PIIS1473-3099(20)30471-0/fulltext#seccestitle130)

¹⁶ <https://www.nature.com/articles/s41591-020-1092-0>

¹⁷ <https://www.medrxiv.org/content/10.1101/2020.08.05.20168930v3>

¹⁸ <https://www.nature.com/articles/nature04153>

¹⁹ <https://wellcomeopenresearch.org/articles/5-67/v3>

others when they talk²⁰. The volume at which they spoke explained some of the variation. In study after study, super-spreading clusters of COVID-19 almost overwhelmingly occur in poorly ventilated, indoor environments where many people congregate over time—weddings, churches, choirs, gyms, funerals, restaurants, bars and such—especially when there is loud talking or singing without masks.

Researchers in China studying the spread of the coronavirus outside Hubei province—ground zero for the pandemic—identified 318 clusters of three or more cases between 4 January and 11 February, only one of which originated outdoors²¹. A study in Japan found that the risk of infection indoors is almost 19 times higher than outdoors. Japan, which was hit early but has kept the epidemic under control, has built its COVID-19 strategy explicitly around avoiding clusters, advising citizens to avoid closed spaces and crowded conditions.²²

Countries that have controlled the virus to low levels need to be especially vigilant for superspreading events, because they can easily undo hard-won gains. After South Korea relaxed social distancing rules in early May, a man who later tested positive for COVID-19 visited several night clubs in Seoul; public health officials proceeded to identify thousands of potential contacts and found 170 new cases²³.

Summary

COVID-19, like other diseases caused by coronaviruses, such as SARS and MERS, tend to cluster rather than spread linearly like influenza. COVID-19 is also subject to large superspreading events where one person may infect dozens or hundreds of others. Thus, the metric R_0 does not reflect the reality of SARS-CoV-2 transmission.

On the other hand, the over-dispersion factor k is a better metric to characterise transmission. The lower the value of k the fewer people are causing most spread of the virus. This value has been estimated as 0.12 for SARS and 0.25 for MERS while estimates for COVID-19 are as low as 0.1 meaning that just 10% of infected cases are infecting more than 80% of people.

Superspreading events have been associated with large indoor gatherings in poorly ventilated spaces and where people may be singing (choir practices and church services) or speaking loudly (nightclubs and bars). It is likely that in this environment an individual with a high viral load in their pharynx has introduced the virus into an environment where it spreads rapidly.

The concept of over-dispersion has implications for contact tracing. Rather than focusing only on ‘forward’ tracing, namely finding people that have been in contact since the person was infected, there should also be efforts to see who first infected the subject. This may reveal new previously unidentified infected individuals within the cluster.

²⁰ <https://www.nature.com/articles/s41598-019-38808-z>

²¹ <https://www.medrxiv.org/content/10.1101/2020.04.04.20053058v1.full.pdf>

²² <https://www.medrxiv.org/content/10.1101/2020.02.28.20029272v2.full.pdf>

²³ <https://www.sciencemag.org/news/2020/05/why-do-some-covid-19-patients-infect-many-others-whereas-most-don-t-spread-virus-all>

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