

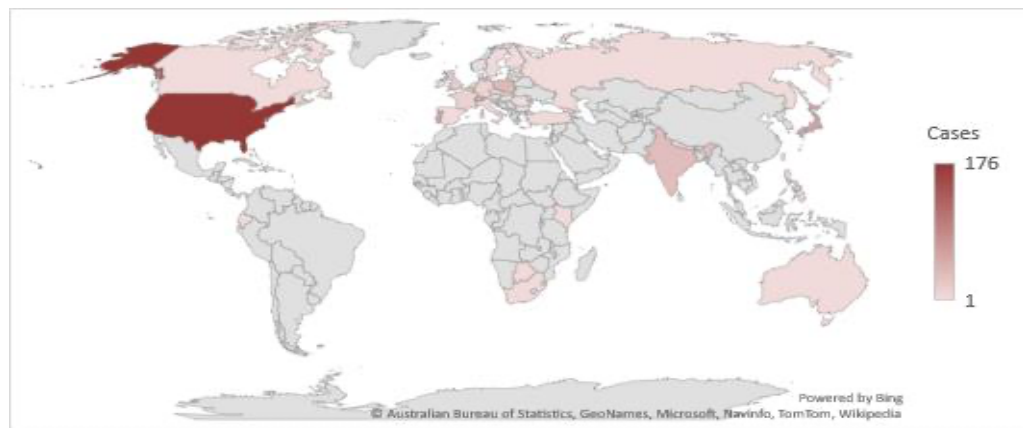
Feedback from operational stakeholders who manage or respond to outbreaks is that they are often too busy to review literature or obtain relevant background information to assist them with acute response. Unlike a traditional analytical outbreak investigation report, **Watching Briefs** are intended as a rapid resource for public health or other first responders in the field on topical, serious or current outbreaks, and provide a digest of relevant information including key features of an outbreak, comparison with past outbreaks and a literature review. They can be completed by responders to an outbreak, or by anyone interested in or following an outbreak using public or open source data, including news reports.

<b>Watching brief</b>	
<b>Title</b>	Is the Delta Plus Variant (B.1.617.2/AY1) more serious than the Delta Variant?
<b>Authors</b>	Mohana Priya Kunasekaran, Danielle Hutchinson, Xin Chen, Haley Stone,
<b>Date of first report of the outbreak</b>	Public Health England (PHE) reported that a new variant, Delta Plus (B.1.617.2/AY1), was present in six genomes sequenced in India, as of 7 June 2021 (1). Retrospective sequencing suggests it was likely circulating earlier in India, as a sample collected on 5 April 2021 tested positive for the Delta Plus variant (1). According to World Health Organization (WHO) variant tracker, the first Delta Plus sequence in Europe was from a sample taken on 31 March 2021 (2), and according to Global initiative on sharing avian influenza data (GSAID), the first Delta Plus sample was collected on 23 February 2021 in North America (3).
<b>Disease or outbreak</b>	<p>The WHO has designated the original Delta (B.1.617.2) strain as a variant of concern (VOC), and sublineages of this variant, which are given the alias AY, are currently being monitored closely. As of 23 September 2021, there have been 33 sub-lineages of Delta identified (AY1 to AY33) (2). The AY.1 sublineage is characterised by the K417N mutation and is known as Delta Plus K417N, or more commonly Delta Plus (4).</p> <p>Indian health authorities designated Delta Plus as a Variant of Concern (VOC) on 22 June 2021, and other countries including the United States followed (4). Assessment by European Centre of Disease Intelligence is ongoing, with only some evidence that the properties of Delta Plus fit the criteria for a VOC (5).</p> <p>Variants of Concern are designated such by the WHO if they have one or more of the following characteristics (6) :</p> <ul style="list-style-type: none"> <li>• Increase in transmissibility</li> <li>• Increase in virulence or clinical disease presentation</li> <li>• Decrease in effectiveness of public health measures or available diagnostics, therapies or vaccines</li> </ul>

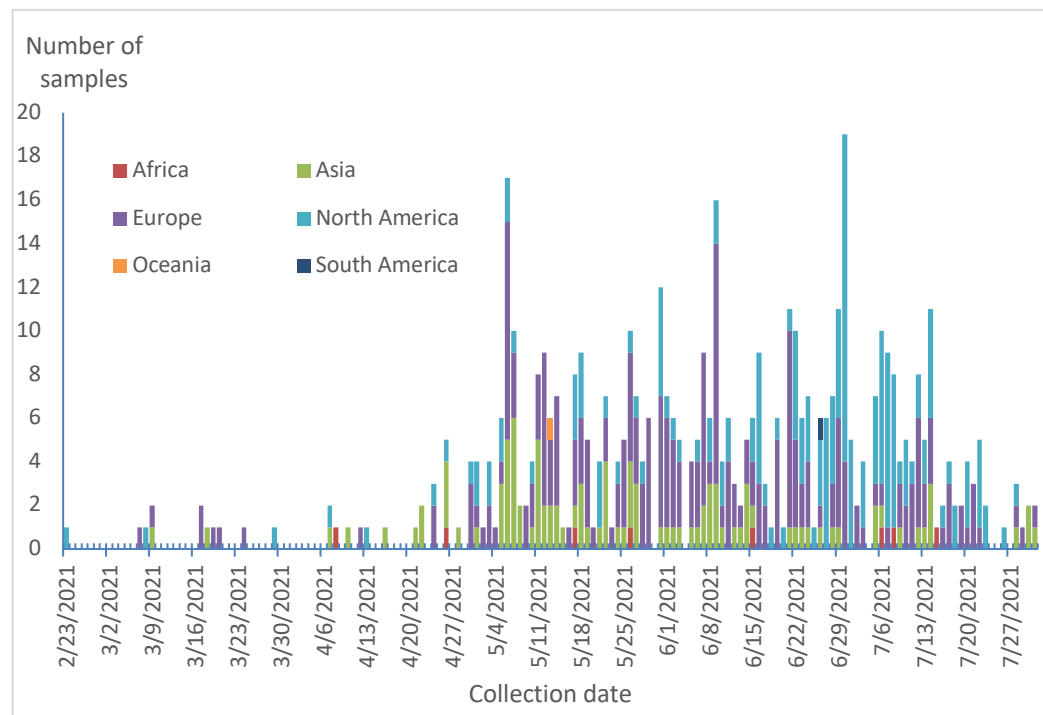
<p><b>Origin</b> (country, city, region)</p>	<p>Original strain: Wuhan, Hubei Province, China (7).</p> <p>According to the GSAID database, the first sample collected was on 23 February 2021 from the US. However, further information on this sample is not available (8) (Figure 2).</p> <p>In the United Kingdom, AY.1 was detected in samples dating as early as mid-March 2021, and by April, 41 cases were found in England, prompting the United Kingdom to ban international travel on 16 June 2021. Several patients with no history of travel or contact with travellers had tested positive for the Delta Plus variant, which suggests that the variant had begun to circulate in the community (9).</p> <p>In India, the earliest identification of the Delta Plus strain was on 5 April 2021, and by mid-April 2021 it had been found in the states of Maharashtra, Kerala and Madhya Pradesh (10). One report claimed that it was quite likely that the Delta Plus variant was first identified in Nepal, as the first cases sequenced in the United Kingdom had travelled from that area (11). Nepal has very little sequencing capacity, and the WHO Nepal office did not report any new variants being detected in Nepal during that time (11).</p>
<p><b>Suspected Source</b> (specify food source, zoonotic or human origin or other)</p>	<p>Similar to many RNA viruses, SARS-CoV-2 has been evolving into new variants as transmission progress. Although transmissibility may differ across variants, the mode of transmission appears to be similar to the Delta variant (12).</p>
<p><b>Date of outbreak beginning</b></p>	<p>Likely between February and March 2021, depending on locations (2,3)</p>
<p><b>Date outbreak declared over</b></p>	<p>Ongoing, cases of Delta Plus variant detected currently world-wide</p>
<p><b>Affected countries &amp; regions</b></p>	<p>Delta Plus variant reporting is not consistent across countries, as several countries include it with reporting of Delta variant cases and all data is subject to the genomic sequencing capacity of respective countries (Table 1).</p> <p>On 22 June 2021, it was reported that the Delta Plus variant has been found in nine countries (13). By 26 September, the AY.1 lineage had been detected in at least 44 countries, including India, the United States, the United Kingdom, Portugal, Switzerland, Japan, Poland, Nepal, China, Russia, South Korea and Peru, as well as 40 US states (14).</p> <p>According to the samples collected in Pangolin database, a large proportion of the samples come from the United States of America 68.0%, Japan 5.0%, Portugal 5.0%, United Kingdom 5.0% and Switzerland 3.0% (14) (Figure 1 &amp; 2). However, the total proportion is relatively small; Delta Plus cases peaked in the US in late June at less than 5% of the nation's sequenced cases.</p>

In Australia, Delta Plus was mentioned by the NSW Chief Health Officer on 9 October 2021, although no specific mention was given to case numbers. The first sample of Delta Plus was recorded on GSAID for Australia on 8 July 2021 (15).

**Figure 1.** Spread of Delta Plus (AY.1) variant samples from GSAID as of 10 August 2021.



**Figure 2.** Delta Plus samples collected by region as of 10 August 2021 in GSAID(15)



**Table 1.** Information for first case of Delta Plus by country

Country	Date of detection of first case of Delta Plus/Date of report from online news media	Sample collection date in GSAID	Last reported sample collection date in GSAID	Details
Peru	3 September 2021 (16)	Not uploaded	NA	Three cases were identified, including a healthcare worker who had already been vaccinated and two others who were unvaccinated. All experienced mild symptoms
Georgia	26 July 2021 (17)	5 July 2021	11 July 2021	Two cases identified
Egypt	Mid-July 2021 (18)	Not uploaded	NA	35-year-old female who had shown very mild symptoms and did not require hospitalization
Czech Republic	19 July 2021 (19)	29 June 2021	8 August 2021	30-year-old female patient from Southern Moravia
Israel	7 July 2021 (20)	25 June 2021	10 August 2021	1 vaccinated female entering Israel from abroad
Turkey	6 July 2021 (21)	1 September 2021	1 September 2021	3 unconnected cases in different cities. One of them in Istanbul, no mention of the other two. Those affected are in good condition.
Russia	29 June 2021 (22)	12 April 2021	12 April 2021	1 female who had mild form of disease
Denmark	21 June 2021 (23)	21 June 2021	3 September 2021	Diagnosed in a passenger travelled by plane from Portugal.

1. This list includes countries where information on first case of Delta Plus was available on google news since Delta Plus was identified.
2. The search was limited to 31 March 2021 onwards, with the search terms First case, Delta Plus, B.1.617.2, [country: one by one through WHO member countries list]

**Number of cases (specify at what date if ongoing)**

As of 26 September 2021, 1454 sequences of the AY.1 lineage have been detected globally (14). However, as reporting of Delta Plus (AY.1) in many

	<p>countries is combined with Delta, the exact number of cases of AY.1 and other sublineages is difficult to obtain.</p> <p>The India SARS-COV-2 Genomics Consortium (INSACOG), as of 1 September 2021, reported the total number of Delta Plus cases in India was 856 after analysing 51,561 samples (24).</p>
<b>Clinical features</b>	<p>Some studies suggest that Delta Plus symptoms may manifest over a longer period (25, 26). At present there is no evidence to suggest that the symptoms of infection with Delta Plus are different to the Delta strain (12, 27, 28) and may include dry cough, tiredness or fever, and if exacerbated shortness of breath and abdominal pain (29).</p>
<b>Mode of transmission (dominant mode and other documented modes)</b>	<p>Studies show that the mode of transmission for Delta Plus variant is similar to that of the Delta strain (12). A low proportion of global sequences suggest that Delta Plus has reduced transmissibility compared to the globally dominant Delta strain (30). Further study needs to be done to elicit if there are any differences in mode of transmission between Delta Plus strain and the other variants.</p>
<b>Demographics of cases</b>	<p>It has been noted that Delta Plus cases have primarily been in younger people, however, this sample was quite small, and more information needs to be gathered on susceptible population (31). Data collected in Maharashtra in July 2021 showed no difference between sexes and the majority of cases were in the 19-49 year age group (32). Although studies have showed that children and adults under 50 were 2.5 times likely to become infected with Delta, no such data has been available for delta plus in children (33).</p> <p>Likelihood of travel and therefore increased risk of exposure to Delta Plus variant, as well as lower vaccination rates compared to the elderly population, may contribute to higher case numbers in the younger age groups (34).</p>
<b>Case fatality rate</b>	<p>Since April 2021, 0.5% of 11 968 samples in the state of Maharashtra (66 cases) were identified as Delta Plus and there were five deaths among these cases, giving a rough case fatality rate estimate of 7.6% (35). This data is based on rough estimates in a single state of India and not verified by any other sources. It is likely that the CFR reported here may be biased as the proportion of delta plus cases may be underreported (based on sample tested). Hence, the actual CFR may be lower than expected.</p>
<b>Complications</b>	<p>The K417 position within the region of the spike protein interacts with the ACE2 receptor protein and enables the virus to infect the cells of the lung, heart, kidney</p>

	<p>and even the intestine (28). Information to date suggests that the Delta Plus variant is likely to result in less severe disease than the Delta strain (34).</p>
<p><b>Available prevention</b></p>	<p>Preliminary data shows that existing vaccines are still effective against Delta Plus variant. Half of the cases in the UK occurred among people who were not vaccinated and as of 5 July 2021, there were no deaths in those infected with Delta Plus (36).</p> <p>A sero-prevalence study, although with a relatively small sample size, showed that Delta Plus displayed a degree of resistance to mRNA vaccine-elicited antibodies similar to that of the Beta and Delta variant (37, 38). While it is too early to conclude whether vaccines will be affected by Delta Plus, initial studies suggest K417N mutation is unlikely to have a significant impact (38, 39).</p> <p>In a pre-print vaccine study, the Pfizer vaccine was tested against Delta Plus using a computational tool PROVEAN that carried out a 2D interaction diagram analysis to find amino acid residue's interaction against antibodies (39). The authors suggested that the mutation appeared to have not led to virus escape from vaccine-elicited neutralising antibodies (39).</p> <p>Therefore, the preventive measures recommended against the Delta Plus strain are similar to that of the Delta strain (38) However, there has not been any published information on the effectiveness of control measures such as mask use, social distancing specific to Delta Plus strain.</p>
<p><b>Available treatment</b></p>	<p>Similar treatment modalities as for Delta strain are recommended (27, 38).</p> <p>In a preprint study that assessed the sensitivity of Delta Plus variant to various monoclonal antibodies (mAb) targeting various targets of spike protein, some therapeutic mAb, including Bamlanivimab, lost binding to the variant Spike and no longer neutralized Delta Plus (41).</p> <p>There is also some evidence from India that Delta Plus is resistant to monoclonal antibody cocktail treatment (Casirivimab and Imdevimab formulated by Regeneron and Roche) for COVID-19, which was authorised in recent months (37, 40). However, these results have not been released by the Indian SARS-CoV-2 Genomics Consortium.</p>
<p><b>Comparison with past outbreaks</b></p>	<p>Compared to the Delta strain, the proportion of Delta Plus sequences and cases are much lower (below 1% of the available sequences from India in June 2021); therefore, the rate of increase of cases and number of deaths reported is also much lower (41). This could be due to the molecular differences in the Delta Plus, with an extra mutation (K417N) location in the spike protein which covers the surface of the SARS-CoV-2 virus.</p>

	<p>The impact of the vigorous global vaccination roll out that commenced since January 2021 may also contribute to the outbreak dynamic of Delta Plus (27, 39).</p>
<p><b>Unusual features</b></p>	<p>The limited number of sequences of Delta Plus are not sufficient to determine the Delta Plus variant's transmissibility, the severity of its unique pattern of mutations at every level, or its impact on vaccination efficacy.</p> <p>Previous studies on the Beta variant, which carries the same K417N mutation, suggests that this mutation increases the ability of the virus to infect the cell and these traits are also seen in other highly transmissible and antibody resistant variants (28). Studies have also shown the mutations in the K417N location have helped the Beta variant evade antibodies, which could be a possible mechanism by which Delta Plus variant could evade vaccines and antibodies better than Delta variant (42-44). However, initial theories suggesting that the K417N mutation would result in increased transmissibility have been unfounded, with the impact of Delta Plus less than expected.</p> <p>The impact of individual mutations on proteins may not have a simple additive effect. From empirical data, there does not seem to be an increase in ACE2 binding due to K417N mutation in Delta Plus variant(44); and some experts suggest that the K417N mutation might actually weaken Delta Plus, similar to Alpha variant, which was not as transmissible or severe as Delta variant (44). A single mutation cannot be the sole target of vaccines and treatment modalities, and it is uncertain how long such variants will be in circulation or if their perceived impact will be as severe as expected (42).</p> <p>The preliminary data presented in this watching brief suggests that the impact of the Delta Plus variant has not been as severe as Delta variant, with lower transmission rates, case numbers, and severity of disease; with existing vaccines remaining effective.</p>
<p><b>Critical analysis</b></p>	<p><u>Importance of VOC classification</u></p> <p>The classification of VOCs is country-specific and depends very much on genomic sequencing capacity. The WHO classifies variants dependent upon transmissibility, disease severity (such as increased hospitalizations or deaths), the extent of reduction in neutralization by antibodies generated during previous infection or vaccination, reduced effectiveness of treatments, or diagnostic detection failures. Variants with these characteristics will be classified as a Variant of Concern (VOC), a Variant of Interest (VOI) or Variants that are being monitored (4, 6). However, national-level VOC classification may not necessarily follow the global standard or other countries (45, 46). This assignment of priority for concern usually depends on local assessment by countries according to their pre-defined criterion. Sublineages such as Delta Plus are not routinely reported separately to Delta variant in most countries. Inconsistent emphasis and disparity in surveillance systems of emerging variants could result in a huge gap in information available on circulating variants (47-49).</p>

	<p><u>Importance of improved genomic surveillance</u>  Country-level surveillance of variants depends on capacity for genomic sequencing and rigorous sample collection. Low genomic sequencing capacity may negatively impact some countries, for example, if a new strain were to emerge from a country with low genomic sequencing capacity, it would result in delayed identification of the new strain, while cases continued to increase. In this instance, the first case of Delta Plus may have emerged in Nepal, however, it had limited surveillance capacity and by the time it was identified, the Delta Plus variant had spread to more countries and resulted in more cases. Fortunately, based on empirical data, the impact of Delta Plus variant has not been as severe as Delta variant to date.</p> <p>A genomic surveillance system, like the COG-UK or GISAID, is required internationally to coordinate collection and documentation of the variants, as genomic sequencing is not readily available in many low-income and middle-income (47, 49). The emergence of Delta Plus may be an opportunity to consider how to close the gap in genomic information collected across countries, in preparation of a potentially more pathogenic strain yet to emerge.</p> <p><u>Vaccination disparity across regions</u>  Evolutionary biologists theorise that the emergence of new variants, like Delta, is likely driven by uncontrolled transmission (50). There is a strong push to improve vaccination rates globally, and in low-income countries specifically, to reduce the case numbers, and thereby reduce the opportunity for mutations of the virus and the potential for more pathogenic strains to emerge (51) In July 2021, the WHO issued strong messages to pharmaceutical companies promoting booster doses of their vaccine, particularly addressing affluent countries with excess doses of vaccine, and comparing vaccination coverage of low-income countries, where only 2.2% of the population had received at least one dose as of 26 September 2021 (52, 53). If the global difference in vaccinations persists between more affluent and low-income countries, more variants of concern could emerge, posing further challenge to current treatment modalities. Effective policies are required to control the pandemic worldwide and in addition to vaccination roll out, genomic surveillance will facilitate defining and implementing better countermeasures.</p>
<p><b>Key questions</b></p>	<ol style="list-style-type: none"> <li>1. How effective are N95 masks against the Delta Plus variant compared to other variants?</li> <li>2. Are children more susceptible to Delta Plus variant?</li> <li>3. What is the case-fatality rate of Delta Plus variant globally?</li> </ol>



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