THREAT ASSESSMENT BRIEF

Emergence of SARS-CoV-2 B.1.617 variants in India and situation in the EU/EEA

11 May 2021

Summary

- First reported in India in December 2020, SARS-CoV-2 lineages B.1.617.1, B.1.617.2 and B.1.617.3 have been increasingly detected in other countries.
- The aim of this Threat Assessment Brief is to assess the potential public health implications of the B.1.617 lineages for EU/EEA countries with a focus on lineage B.1.617.2.
- Over the past eight weeks India and some surrounding countries have seen a sharp increase in the number of reported SARS-CoV-2 cases and deaths. This has been associated with a rising proportion of sequenced viruses belonging to lineages B.1.617.1 and B.1.617.2.
- The United Kingdom has seen a rapid increase in detection of lineage B.1.617.1 and, to a greater extent, B.1.617.2, associated with travel to India and onward community transmission. On the 6 May, the United Kingdom (UK) designated lineage B.1.617.2 as a variant of concern.
- In the EU/EEA there are indications that the frequency of detection of both lineages B.1.617.1 and B.1.617.2 is increasing.
- Currently described lineages B.1.617.1, B.1.617.2 and B.1.617.3 have distinct mutation profiles and warrant individual assessment. Given the still very limited available data with respect to their transmissibility, disease severity and immune escape potential relative to other co-circulating SARS-CoV-2 variants in the EU/EEA, the full impact of these lineages on public health is not yet possible to assess.
- At this time, ECDC maintains its assessment of B.1.617.1, B.1.617.2 and B.1.617.3 as variants of interest and will continue to actively monitor the situation.

Options for response

- In order to better understand and inform assessments of the potential public health implications of these variants, targeted genomic surveillance should be enhanced (including of travel-associated cases, clusters or outbreaks and breakthrough infections) together with antigenic characterisation of SARS-CoV-2 variants and enhanced general surveillance.
- Diagnostic laboratories should remain vigilant to detect any mismatches of specific RT-PCR assay primers and probes in comparison to circulating virus genomes.
- COVID-19 vaccination rollout should continue to be a high priority to reduce COVID-19 mortality by vaccinating those at risk of severe illness in the shortest time possible, thereby reducing SARS-CoV-2 transmission, as has recently been documented in Israel and the UK.

Suggested citation: European Centre for Disease Prevention and Control. Emergence of SARS-CoV-2 B.1.617 variants in India and situation in the EU/EEA– 11 May 2021. ECDC: Stockholm; 2021.

Erratum: 12.05.2021: A missing reference (no.21) was added to the document.

- COVID-19 vaccine coverage remains at low levels in all EU/EEA countries, and as such, ECDC currently advises caution in the relaxation of current non-pharmaceutical measures including those related to travel. The limited information so far regarding these new variants does not change ECDC's current advice on non-pharmaceutical measures. Greater understanding of the risks related to these B.1.617 lineages is needed before any modification of current measures can be considered.
- Further characterisation of these lineages is needed to allow a full assessment of their potential public health implications.

Introduction

Viruses constantly change through mutation and the emergence of a new variant is an expected occurrence and not in itself a cause for concern. Diversification of SARS-CoV-2 due to evolution and adaptation processes has been observed globally and is expected [1]. Most mutations that emerge will not provide a selective advantage to the virus. However, some mutations or combinations of mutations may do so, such as increased transmissibility through an increase in receptor binding or the ability to evade the host immune response by altering surface structures recognised by antibodies [2].

ECDC regularly assesses new evidence on variants detected through epidemic intelligence, rules-based genomic variant screening, or other scientific sources. Currently, four variants designated as variants of concern (VOCs) by ECDC are under surveillance in the EU/EEA and around the world (B.1.1.7, B.1.1.7+E484K, B.1.351 and P.1). Another nine SARS-CoV-2 variants are considered variants of interest (VOI) by ECDC and additional variants are being monitoring [3].

First reported in India in December 2020, SARS-CoV-2 lineages B.1.617.1, B.1.617.2 and B.1.617.3 have been increasingly detected, these lineages are distinct and differ by their characteristic mutations [4,5].

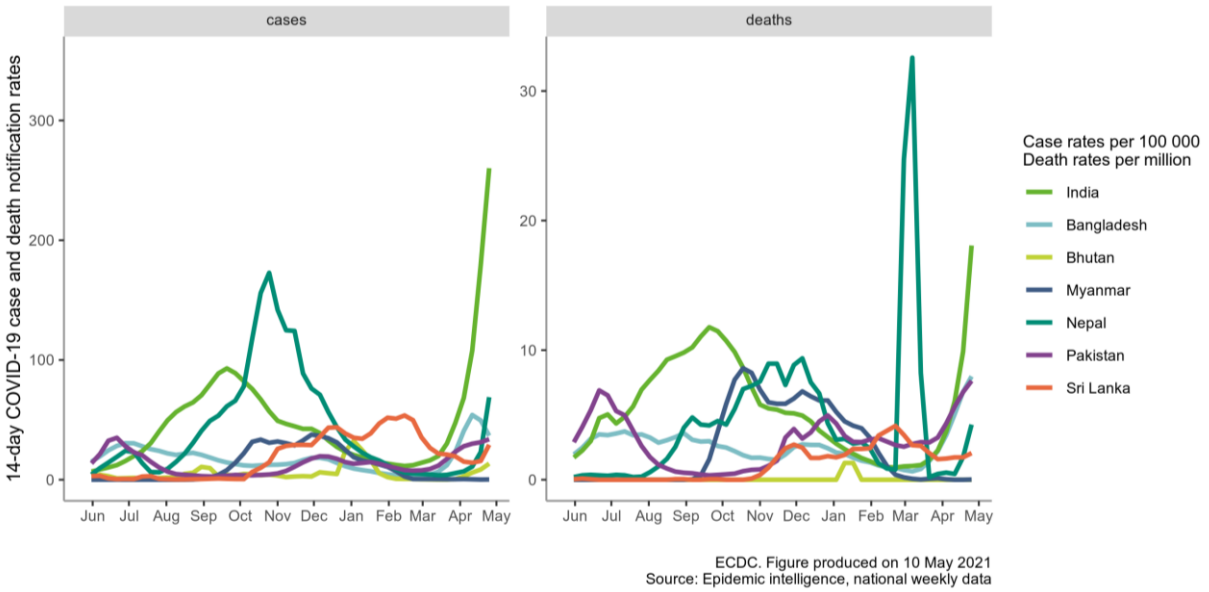
The aim of this Threat Assessment Brief is to assess potential public health implications of B.1.617 variants for EU/EEA countries, with a focus on lineage B.1.617.2.

Event background

Epidemiology

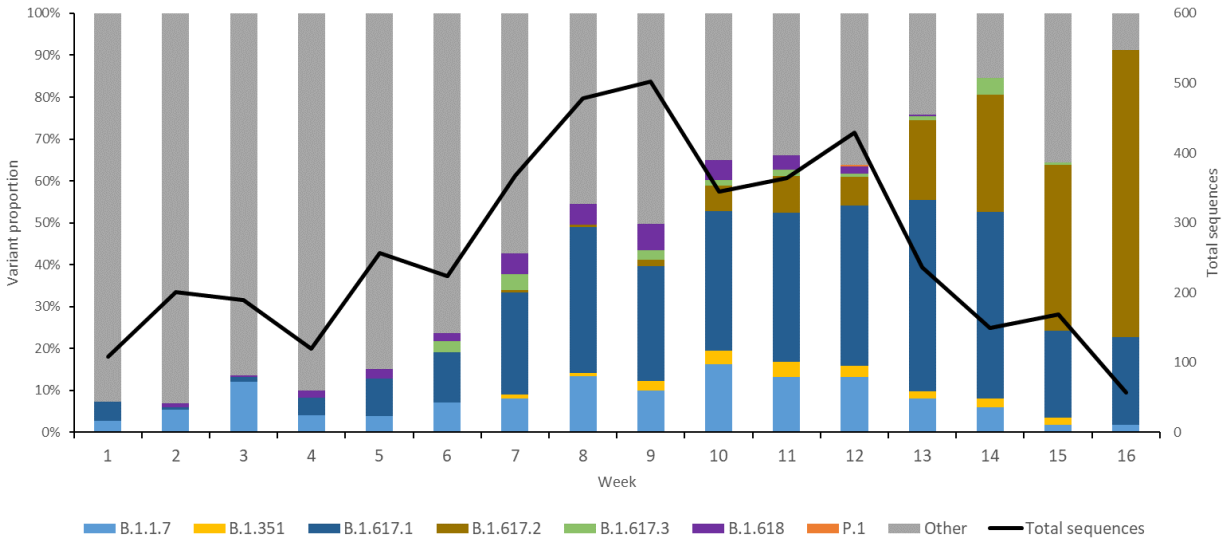
Over the past eight weeks, the number of reported SARS-CoV-2 cases and deaths have markedly increased in India and its neighbouring countries (Figure 1) [6].

Figure 1. COVID-19 14-day case notification rates per 100 000 and death rates per million population in India and land-bordering countries, 1 June 2020 to 2 May 2021



The increase in case numbers in India has been associated with rising proportions of sequenced viruses belonging to lineages B.1.617.1 and B.1.617.2 submitted to the GISAID EpiCoV database (Figure 2) [7,8]. Sequencing capacity and genomic surveillance strategies differ between countries, biasing detections towards countries with higher sequence reporting activity. For this reason, direct comparisons between countries is challenging, and it is important to take these factors into account when assessing reported changes in the levels of circulation for different variants. Reporting of sequences by country to GISAID EpiCoV worldwide is shown in Figure A1 in the Annex.

Figure 2. Variant distribution and total sequences reported from India during 2021. Based on data from GISAID EpiCoV available as of 10 May 2021



Data source: GISAID EpiCoV, accessed 10 May 2021

B.1.617.1 was first detected in India in December 2020. It initially increased in proportion in India and reached a peak of around 50% of weekly reported sequences in GISAID EpiCoV in late March 2021 before starting to decline in April 2021 (Figure 2). As of 10 May 2021, it has been detected in India (1 147), the United Kingdom (247), USA (137), Singapore (64), Germany (28), Australia (21), Denmark (21), Bahrain (9), Japan (9), Angola (8), Switzerland (8), Hong Kong (7), Ireland (7), Portugal (7), Belgium (5), Luxembourg (5), South Korea (5), Canada (4), the Netherlands (4), New Zealand (4), Sweden (4), France (3), Jordan (3), Czechia (2), Guadeloupe (2), Russia (2), Sint Maarten (2), Spain(2), Cambodia (1), Greece (1), Italy (1), Malaysia (1), and Mexico (1).

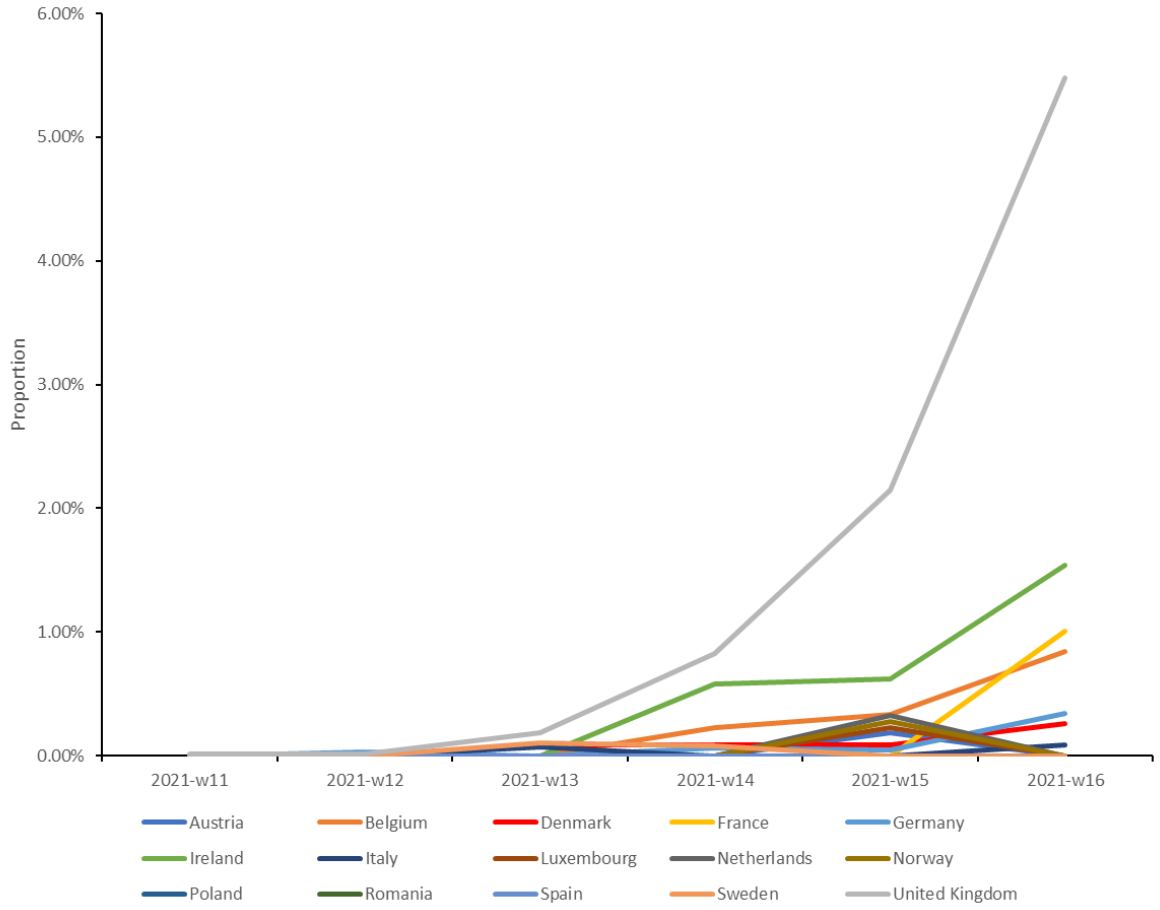
There are indications of the variant increasing in the EU/EEA, but it is currently only detected in a small proportion of sequences, with the highest proportions reported in Luxembourg (0.6%), and Spain (0.3%) in GISAID EpiCoV, for week 16 .

B.1.617.2 was first detected in India in December 2020, and remained rare in the country until early March 2021, when it started to increase, becoming the dominant variant amongst reported sequences in mid-April 2021 (Figure 2). As of 10 May 2021, it has been detected in the United Kingdom (676), India (290), USA (192), Singapore (91), Australia (58), Germany (31), Japan (20), Denmark (18), Bahrain (13), Belgium (12), France (12), Ireland (12), Switzerland (10), New Zealand (9), Italy (5), Poland (5), China (4), Spain (3), Sweden (3), Indonesia (2), the Netherlands (2), Aruba (1), Austria (1), Canada (1), Greece (1), Hong Kong (1), Luxembourg (1), Norway (1), Romania (1), Slovenia (1), and South Korea (1).

The United Kingdom has seen a rapid increase in the proportion of this variant, associated with travel to India and onward community transmission [9]. There is an increasing trend in some EU/EEA countries, but the variant remains at low levels, with the highest proportions being reported by Ireland (1.5%), France (1.0%), and Belgium (0.8%) in GISAID EpiCoV, for week 16. If these countries would follow the same pattern of increase of B.1.617.2 as the United Kingdom, they are at least two weeks behind in the evolution of the increase (Figure 3). When a variant is associated with travel, its proportion in the community can be overestimated as travellers and their contacts are more likely to be tested than others, so these data should be interpreted with caution.

B.1.617.3 was first detected in India in February 2021; it is a rare lineage in India and has remained at a low level since its detection (Figure 2). As of 10 May 2021, it has been detected in India (56), the United Kingdom (7), Russia (1), and USA (1). This lineage has so far not been detected in the EU/EEA.

Figure 3. Proportion of B.1.617.2 among sequences reported to GISAID EpiCoV by EU/EEA countries and the UK, with >60 weekly sequences, samples collected weeks 11 to 16 2021



Data source: GISAID EpiCoV, accessed 10 May 2021.

Vaccination rollout

As of 10 May 2021, COVID-19 vaccination coverage in India is 9.7% of the total population with at least one dose and 2.4% with full vaccination coverage. All other bordering countries (Bangladesh, Myanmar, Nepal, Pakistan, Sri Lanka) have lower vaccination coverage, with the exception of Bhutan which has recently achieved >60% COVID-19 vaccination coverage with one dose in its population [10].

In comparison, COVID-19 vaccination coverage in adults in EU/EEA countries for one dose varies between 11.2% in Bulgaria and 51.4% in Hungary as of 10 May 2021. The median one dose vaccination uptake was 31.6% across EU/EEA countries. The level of full vaccination uptake in adults across the EU/EEA varies between 3.4% (Latvia) and 28.7% (Hungary), with the cumulative full vaccination uptake as high as 12% across all EU/EEA countries as of 10 May 2021 [11].

Properties of the B.1.617 SARS-CoV-2 variants

There are three distinct lineages within B.1.617, all with distinct mutation profiles which warrant assessment at the individual lineage level rather than assessment as one. The classification of the variants listed below are as of 10 May 2021, according to the respective agencies [3,9,12].

B.1.617.1 is defined by the spike protein amino acid changes L452R, E484Q, D614G, P681R, and Q1071H (some viruses also carry V382L). This lineage has been classified as a VOI by ECDC and the World Health Organization (WHO) and as a variant under investigation (VUI) by the UK.

B.1.617.2 is defined by spike protein changes T19R, Δ157-158, L452R, T478K, D614G, P681R, and D950N. B.1.617.2 is increasing rapidly in the United Kingdom [9] (Figure 2) and it has also been detected in several other countries worldwide (Figure 3). This lineage has been classified as a VOI by ECDC and WHO, and as a VOC by the UK, due to an estimate of its transmissibility being at least as high as that of VOC B.1.1.7.

B.1.617.3 is defined by the spike protein changes T19R, Δ157-158, L452R, E484Q, D614G, P681R, and D950N. This lineage has been classified as a VOI by ECDC and WHO, and as a VUI by the UK.

Some of the specific spike protein changes associated with these lineages have been described as having an impact on viral properties, these include:

- L452R – associated with increased transmissibility and reduction in neutralisation by convalescent plasma and specific therapeutic antibodies [13].
- E484Q (only B.1.617.1 and B.1.617.3) – changes at this site are associated with reduction in neutralisation by convalescent sera [14].
- P681R – change is located directly adjacent to the furin cleave site and could potentially have an effect on S1/S2 cleavage, cell entry and infectivity, although this has not been demonstrated in practice.
- D614G – This change is associated with increased transmissibility with high confidence. It is however carried by the vast majority of currently circulating viruses [15].

Potential impact on transmissibility

There are no R_0 estimates, estimates of peak viral load or duration of shedding published for any of the B.1.617 lineages.

In the UK, secondary attack rates among close contacts of cases that had not travelled or with unknown travel status appear to be broadly similar for B.1.617.1 (9.6%; 95% CI 5.0%-17.9%) and B.1.617.2 (9.5%; 95% CI 5.9%-14.9%) compared with B.1.1.7 cases (10.1%; 95%CI 10.0-10.2%); these were all higher than secondary attack rates for close contacts of wild type SARS-CoV-2 cases (5.2%; 95% CI not provided). There was insufficient information to assess the secondary attack rate for B.1.617.3 due to low numbers [9,16]

Public Heath England (PHE) consider that B.1.617.2 is at least as transmissible as B.1.1.7 (currently the dominant variant in the UK). This assessment was based on evidence that the variant B.1.617.2 can compete with B.1.1.7 in the population, as well as on modelled growth estimates [17]. The assessment was made with 'moderate confidence' and it highlighted the need for further analyses to confirm this observation. Growth estimates, based on a logistic growth model for variants of concern relative to a B.1.1.7 baseline for B.1.617.1, were estimated by PHE on 20 April 2021 to be 0.51 (n=21; p=0.006) [17]. No growth rate assessment or any other transmissibility estimate is available from PHE for B.1.617.3.

Furthermore, all three lineages contain the mutations L452R and D614G, which are both associated with increased transmissibility.

Factors that may have increased the detections of all three lineages in the UK in recent weeks include increased travel to/from India for religious and other large gatherings [18]. Targeted testing of arrivals from India to the UK and countries in the EU/EEA may have caused an overrepresentation of all three lineages among cases detected and sequenced and further data are needed to assess their true incidence and transmissibility [9].

Potential impact on diagnostics

The viruses belonging to the three B.1.617 lineages do not carry specific genomic features (e.g. large deletions) indicative of an increased risk of possible primer/probe mismatch that would hinder the capacity of current RT-PCR assays to detect SARS-CoV-2. As of 10 May, there was also no indication of reduced effectiveness of currently used molecular diagnostic assays.

The detection capability of other assays, such as rapid antigen detection tests (RADTs), against the B.1.617 variants has not been assessed.

Potential impact on disease severity

No information is available in the pre-print or peer-reviewed literature, or in TESSy reporting, on severity related to any of the B.1.617 lineages. While death rates have increased sharply in India in correlation with the increase of the B.1.617 lineages, comparative data at patient level are not available and the increased death rates could be a function of increased transmission combined with insufficient healthcare services to meet the high demand for care [6].

As of 7 May 2021, no deaths had been reported among those infected with any of the B.1.617 lineages in the United Kingdom (235 cases of B.1.617.1, 509 cases of B.1.617.2 and 9 cases of B.1.617.3). However, PHE's assessment highlights that the identified cases of these variants were still too recent to allow enough time to assess this variant's impact on disease severity in comparison to other co-circulating SARS-CoV-2 strains [9].

Potential impact on immune escape

In a recently published study, Yadav et al. obtained virus isolates for use in neutralisation assays from asymptomatic/mildly symptomatic patients in India, with sequencing confirming the isolates were from the B.1.617.1 lineage. They observe that serum derived from recipients of the BBV152 vaccine (n=28) was able to neutralise B.1.617.1 virus *in vitro*. BBV152 is an inactivated virus-based COVID-19 vaccine being developed by Bharat Biotech in collaboration with the Indian Council of Medical Research [19].

An approximately two-fold reduction in neutralising capacity was observed against both the heterologous B.1.617.1 and B.1.1.7 variants when compared to the homologous vaccine strain virus B.1 (D614G). The authors additionally confirm that serum derived from recovered individuals (n=17; infected with B.1.1.7 (n=2), B.1.351 (n=2), B.1.1.28.2 (n=2), and B1 (n=11) virus) showed equivalent neutralising titres against B.1.617.1 when compared to serum samples from BBV152 vaccine recipients. This is a small study, with serum samples obtained from recovered individuals for whom the severity of disease experienced was not reported. The sampling strategy used to select vaccinated individuals was not presented, with no demographic, clinical or antibody data presented to establish how representative selected individuals are of the vaccinated population [20].

In a preprint study, Hoffmann et al. also observe that plasma derived from convalescent patients (n=15) was capable of neutralising pseutotype virus particles, expressing the spike protein of either the Wuhan-1 isolate (D614G), B.1.617.1, or B.1.351 *in vitro*. They observed a two-fold reduction in neutralising capacity for B.1.617.1 compared to Wuhan-1. This compared favourably to the almost six-fold reduction seen with B.1.351 compared to Wuhan-1. Additionally, plasma from BNT162b2 vaccine recipients (n=15) was also able to neutralise all three pseudotype virus particles; the authors observed a three-fold reduction for B.1.617.1 compared to Wuhan-1, with an 11-fold reduction in neutralising capacity reported for B.1.351. In the same study, the monoclonal antibodies casirivimab (REGN10933), imdevimab (REGN10987) and etesevimab (LY-CoV016) were able to neutralise B.1.617.1 pseudotype virus particles. B.1.617.1 pseudotype virus particles were resistant to neutralisation by bamlanivimab (LY-CoV555), however, B.1.351 pseudotype virus particles were resistant to both etesevimab (LY-CoV016) and bamlanivimab (LY-CoV555) [21]. Again, this was a small study with limitations. The authors use pseudotype viruses, rather than live virus in their neutralisation assays. Neutralising antibody titres have been shown to be lower amongst recovered COVID-19 cases that experience no, or only mild symptoms [22]. Here, convalescent plasma samples were obtained exclusively from hospitalised COVID-19 patients in intensive care who experienced moderate to critical disease, so their serum antibody responses may not be representative of all recovered individuals.

In summary, for lineage B.1.617.1, the results of two small studies indicate that monoclonal antibodies, as well as serum from previously infected and vaccinated individuals can neutralise B.1.617.1 equally, or more effectively than other currently circulating variants of concern. No studies evaluating immune escape potential are currently available for lineage B.1.617.2.

Summary

The aim of this Threat Assessment Brief is to assess potential public health implications of the B.1.617 lineages for EU/EEA countries, with a focus on lineage B.1.617.2.

Currently described lineages B.1.617.1, B.1.617.2 and B.1.617.3 have distinct mutation profiles and warrant individual assessment to understand differences in transmissibility, pathogenicity and immune escape potential relative to other circulating SARS-CoV-2 variants.

There is currently very limited data available to inform an assessment of the potential public health implications for these variants.

B.1.617.2 has emerged as the dominant variant circulating in India over an eight-week period where SARS-CoV-2 case numbers and deaths have risen dramatically in the context of large mass gatherings, a relaxing of non-pharmaceutical measures, and low vaccination coverage. Whilst increased detection of B.1.617.2 has been observed in the UK and the EU/EEA over the past four weeks, factors that may have increased the detection of all three lineages in the UK in recent weeks include increased travel to/from India for religious and other large gatherings. Targeted testing of arrivals from India to the UK and countries in the EU/EEA may have caused an overrepresentation of these variants and further data is needed to assess the true incidence and transmissibility of this lineage.

Whilst recognising that variant proportions are dynamic and potentially subject to rapid change, B.1.617.2 currently accounts for less than 1% of SARS-CoV-2 sequences in the EU/EEA. There is no indication that B.1.617.2 affects the performance of existing SARS-CoV-2 PCR diagnostics, however, data is currently lacking to assess the detection performance of RADTs for B.1.617.2.

The impact that B.1.617.2 might have on health systems in the EU/EEA cannot, at this stage, be fully assessed. This is based on the following:

- There is currently no data on the severity of disease caused by B.1.617.2 infections relative to other circulating variants in the EU/EEA;
- There is currently no *in vitro* neutralisation data evaluating the immune escape potential of B.1.617.2 against serum from previously infected or vaccinated individuals. Available evidence exists only for B.1.617.1, where serum from previously infected and vaccinated individuals has been shown to neutralise B.1.617.1 equally, or more effectively than other currently circulating variants of concern.

At this time, ECDC maintains its assessment of B.1.617.2 as a variant of interest and will continue to actively monitor and evaluate emerging data as part of continuous variant monitoring activities.

Options for response

Vaccination

Continued scaling-up of the vaccination rollout should remain a priority in order to reduce COVID-19 mortality, by vaccinating those at risk of severe illness in the shortest time possible [23]. In Israel, high vaccine uptake in the general population has been associated with marked and sustained declines in SARS-CoV-2 incidence [24].

Options for non-pharmaceutical interventions

COVID-19 vaccine coverage remains at low levels in all EU/EEA countries, and as such, ECDC currently advises caution in the relaxation of current non-pharmaceutical measures, including those related to travel. The limited information so far available regarding these new variants does not change ECDC's current advice on non-pharmaceutical measures [2,25]. Greater understanding of the risks related to these B.1.617 lineages is needed before any need to modify current measures can be considered.

Genomic surveillance and antigenic characterisation of SARS-CoV-2 variants

Early detection and antigenic characterisation of SARS-CoV-2 variants should be strengthened in all EU/EEA countries.

As part of targeted genomic surveillance, ECDC recommends increased sequencing of traveller-related cases according to ECDC's guidance for genomic SARS-CoV-2 monitoring [26]. In order to detect the importation into countries and to slow down the spread of B.1.617 variants in areas or countries where it is not yet present or only circulating at very low levels, ECDC recommends comprehensive sequencing of all SARS-CoV-2 positive cases with travel history to areas/countries where B.1.617 variants are circulating. This is particularly relevant for, but not limited to, those coming from areas where B.1.617 variants are endemic.

In addition, a representative sample of clusters or outbreaks associated with a specific setting/behaviour/age-group with a minimum of five specimens (to be able to assess whether the event is dominated by B.1.617) should be sequenced [26]. Other examples of situations that require sequencing, including to monitor for the B.1.617 lineages, can be cases with an unusual clinical presentation, such as severe infections and deaths in younger age groups with no underlying diseases, prolonged infections, a general change in the clinical presentation and cases where zoonotic transmission has been raised as a possibility and cannot be ruled out. This may indicate a change in pathogen virulence or inter-species transmission which should be monitored.

COVID-19-vaccinated individuals need to be closely monitored for breakthrough infections and virus isolates from these cases should be comprehensively sequenced and reported, irrespective of the strain identified [26]. Reports of suspected cases of COVID-19 reinfection also need to be investigated and sequence analysis of virus isolates from all these cases should be initiated. Mechanisms for antigenic characterisation to confirm or exclude vaccine escape mutants need to be established to support any need for reassessment of vaccine composition and strategy.

In addition to targeted genomic surveillance, representative sequencing should be performed in order to generate data that reflect the overall variant situation in the country [26]. Specimens for genome analysis should be selected as being representative of SARS-CoV-2 cases in the country. Sample collection should be made using methods that ensure the unbiased selection of cases for sequencing. It is important to ensure that sequencing is performed on a sufficient number of cases every week (representative in terms of time), at every level of healthcare systems (representative in terms of clinical spectrum), and in all regions or other administrative areas of a country (representative in terms of geography). This should ensure representativeness in terms of age, gender, and disease severity of cases.

ECDC offers the possibility for antigenic characterisation of SARS-CoV-2 isolates, to support the detection of variant viruses that may escape natural immunity and/or vaccines. This is done through antigenic characterisation of SARS-CoV-2 isolates and by supporting the scaling up of sequencing capacity in EU/EEA countries. Please contact PHE.Support.Microbiology@ecdc.europa.eu for more information.

Evidence of outbreaks or community transmission of any of the B.1.617 lineages should be reported immediately through the Early Warning and Response System (EWRS), while overall VOC and VOI detections should be reported to The European Surveillance System (TESSy) weekly. SARS-CoV-2 sequences should be submitted to GISAID or other public databases in a timely manner, i.e. ideally within one to two weeks from sample collection. Raw data can be deposited in the COVID-19 data portal [27].

Surveillance

ECDC encourages all EU/EEA countries, where possible, to report complete case-based data to TESSy using the NCOV record type for all cases for which information on variants is available. In addition to monitoring time trends in variant distributions, case-based data facilitates pooled analyses of virus variant cases to assess associations between different variants and factors such as severe outcome, re-infection, and vaccine breakthrough.

Enhanced surveillance and contact tracing of close contacts to confirmed variant cases should be maintained, particularly if a case is travel-related. The early identification of cases with an epidemiological link to B.1.617 cases or with a travel history to areas known to be affected will be key. This will allow rapid testing, isolation and follow-up of these cases' contacts and subsequently stop the spread of the new variant.

Diagnostics

Diagnostic laboratories should remain vigilant to detect any mismatches of specific RT-PCR assay primers and probes in comparison to circulating virus genomes. It should be noted that the vast majority of primer/probe binding sites of commercial assays are not publicly known. For in-house or commercial RT-PCR assays for which the primer/probe sequences are available, validation can be done via the ECDC PrimerScan [28] or similar tools that identify mismatches. For commercial assays where the primer/probe sequences are unknown, a validation procedure for the capacity of the molecular assays to detect variants is needed. In general, laboratories should have a quality assurance system in place and are encouraged to participate in external quality assessment (EQA) schemes or perform result comparison between laboratories, for a subset of samples. ECDC is planning a molecular External Quality Assessment (EQA) for national COVID-19 reference laboratories in June 2021. Please contact PHE.Support.Microbiology@ecdc.europa.eu for more information.

For Sanger sequencing or next generation sequencing (NGS), amplicon-based sequencing of selected parts of the viral genome are alternative methods for the identification of variants. For the differentiation of the B.1.617 variants, ideally, at least the S-gene region corresponding to amino acid residues 1-800 should be sequenced, which allows detection of all characteristic amino acid changes except D950N (B.1.617.2 and B.1.617.3) and Q1071H (B.1.617.1).

S-gene target failure is used in some laboratories to identify variants that have an S-gene deletion, a characteristic of B.1.1.7 that has predominated in Europe in recent months. The S-gene target is however detected in other variants, including viruses belonging to the three B.1.617 lineages. While this assay will fail to differentiate between different circulating variants that do not carry the specific S-gene deletion, it can be used to signal a decrease in the prevalence of B.1.1.7, and in combination with other specific mutation RT-PCR assays (e.g. Single-Nucleotide-Polymorphism (SNP) assays), to identify B.1.617.1, B.1.617.2, and B.1.617.3.

ECDC has published a document that presents the available methods (screening and sequencing) for detection and identification of circulating SARS-CoV-2 VOCs [29].

Evidence gaps

Key information that will improve the understanding and enable an assessment of the risk posed by the different B.1.617 lineages includes:

- Further epidemiological characterisation of these variants, particularly for non-travel related cases;
- Improved transmissibility estimates, including information on any differences in viral shedding or duration of infection associated with any of these variants;
- Clinical characterisation of cases infected with these variants;
- In vitro studies of neutralisation to assess immune escape potential using convalescent serum and serum from vaccinated individuals;
- Investigation and monitoring of reinfection and breakthrough infections.

Such characterisation and further information will support improved assessment of the impact that these lineages might have on EU/EEA countries.

Source and date of request

ECDC internal decision, 09 May 2020.

Consulted experts

ECDC experts (in alphabetic order): Cornelia Adlhoch, Erik Alm, Agoritsa Baka, Nick Bundle, Theresa Enkirch, Angeliki Melidou, Nathalie Nicolay, Ajibola Omokanye, Anastasia Pharris, Emma Wiltshire.

Disclaimer

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This report was written with the coordination and assistance of an Internal Response Team at the European Centre for Disease Prevention and Control. All data published in this threat assessment brief are correct to the best of our knowledge at the time of publication. Maps and figures published do not represent a statement on the part of ECDC or its partners on the legal or border status of the countries and territories shown.

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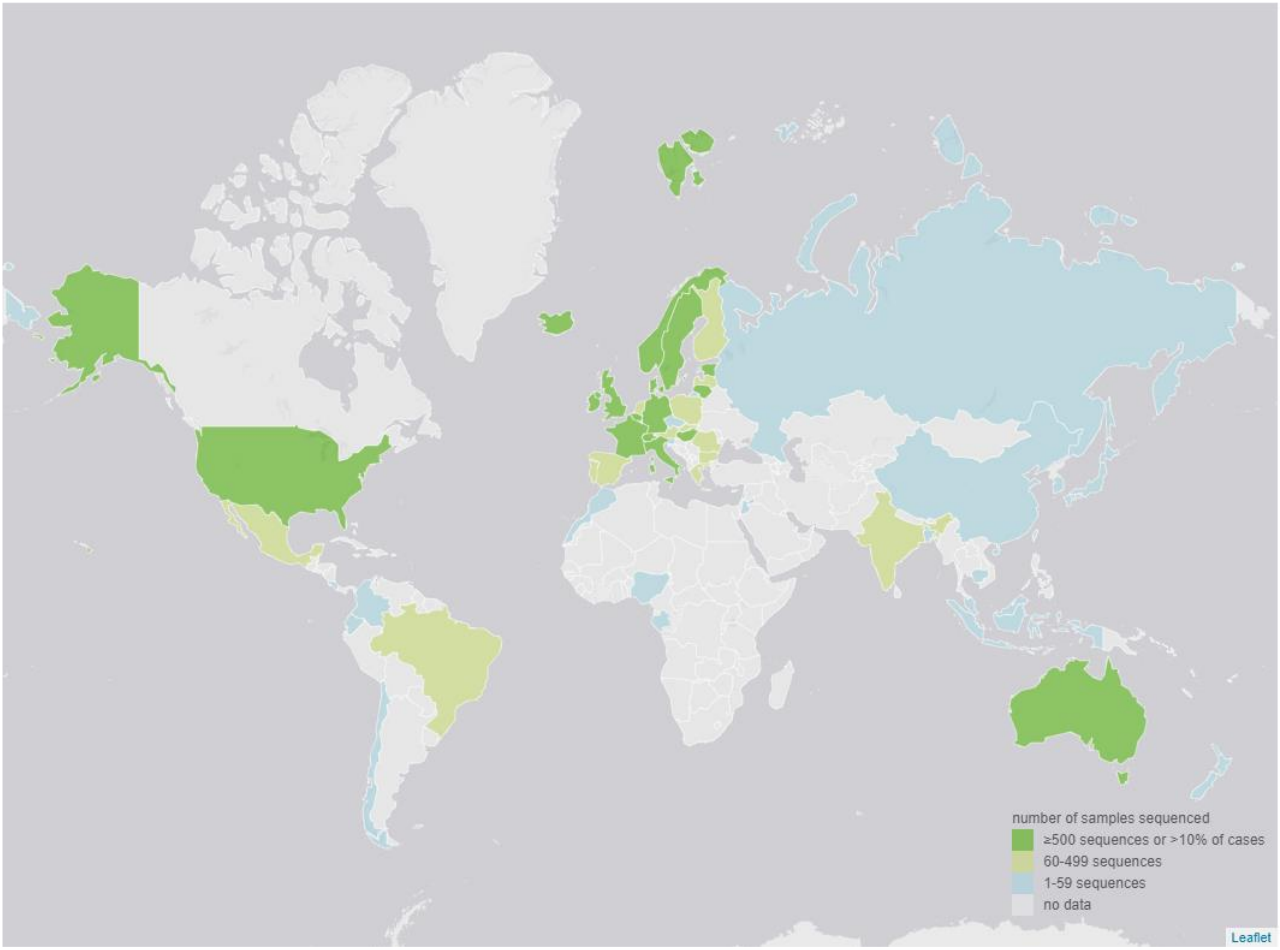
Annex

Figure A1. Sequence reporting worldwide for samples collected in weeks 15-16.



Data source: GISAID EpiCoV, accessed 10 May 2021.