

Current major event

New variants of interest B.1.617

Recently, WHO has recognized a new SARS-CoV-2 variant of interest (VOI) that has been reported by India in December 2020. The emergence of VOI B.1.617 has coincided with the increased number of COVID-19 cases recently observed in India. However, there is still little evidence regarding the role played by this variant in the observed increase.

Editorial note

Evolution or mutation is an inherent phenomena observed in all viruses. Viruses including SARS-CoV-2 are changing over time resulting in the emergence of new variants that might have an impact on transmissibility, immunity and infection severity. Therefore, WHO, in collaboration with national authorities, institutions and researchers, continues to monitor SARS-CoV-2 variants of interest (VOIs) and variants of concern (VOCs), and assess these and other emerging variants based on the risk posed to global public health, including impacts on epidemiology and public health and social measures (PHSM). Evidence on vaccination protection against VOCs and prevention of infection from these variants are carefully studied (*see table*).

The new SARS-CoV-2 variants within Pango lineage B.1.617 were recently reported as a VOI from India and has recently been designated as VOIs by WHO. As of the end of April, over 1200 sequences have been uploaded to GISAID and assigned to lineage B.1.617 (collectively) from at least 17 countries. Most sequences were uploaded from India, the United Kingdom, the United States of America and Singapore. However, this lineage comprises several sub-lineages, including B.1.617.1, B.1.617.2 and B.1.617.3, which slightly differ by their characteristic mutations. Both B.1.617.1 and B.1.617.2 were first identified in India in December 2020, and have been detected at increasing prevalence concurrent to the major upsurge observed in the country. B.1.617.3 was first detected in India in October 2020, but relatively fewer viruses matching this sub-lineage have been reported to date.

B.1.617 includes several mutations present in other VOIs and VOCs that have been associated with phenotypic impacts and associated with increased transmissibility, a reduction in neutralization by some (but not all) monoclonal antibody treatments, and a moderate reduction in neutralization in post-vaccination sera. Preliminary laboratory studies of a small number of convalescent sera samples of COVID-19 cases (n=17) and recipients of Novavax-Covaxin (n=28) were able to neutralize B.1.617.

Countries, territories and areas reporting SARS-CoV-2 VOC 202012/01, as of 4 May 2021



SARS-CoV-2 VOC and VOI, 4 May 2021

	Pango lineage	First detected in	Earliest samples	Characteristic spike mutations
VOC	B.1.1.7	United Kingdom	Sep 2020	69/70del, 144del, N501Y, A570D, D614G, P681H, T716I, S982A, D1118H
	B.1.351	South Africa	Aug 2020	D80A, D215G, 241/243del, K417N, E484K, N501Y, D614G, A701V
	B.1.1.28.1, alias P.1	Brazil and Japan	Dec 2020	L18F, T20N, P26S, D138Y, R190S, K417T, E484K, N501Y, D614G, H655Y, T1027I, V1176F
VOI	B.1.525	United Kingdom and Nigeria	Dec 2020	Q52R, A67V, 69/70del, 144del, E484K, D614G, Q677H, F888L
	B.1.427/ B.1.429	United States of America	Jan 2020	S13I, W152C, L452R, D614G
	B.1.1.28.2, alias P.2	Brazil	April 2020	E484K, D614G, V1176F
	B.1.1.28.3, alias P.3	Philippines and Japan	Feb 2021	141/143del, E484K, N501Y, D614G, P681H, E1092K, H1101Y, V1176F
	B.1.526 with E484K or S477N	United States of America	Nov 2020	L5F, T95I, D253G, D614G, A701V, E484K or S477N
	B.1.616	France	Jan 2020	H66D, G142V, 144del, D215G, V483A, D614G, H655Y, G669S, Q949R, N1187D
	B.1.617	India	Oct 2020	L452R, D614G, P681R, ±E484Q

In India, preliminary modelling by WHO based on sequences submitted to GISAID suggest that B.1.617 has a higher growth rate than other circulating variants in India, suggesting potential increased transmissibility.

WHO continues to support Member States in reducing transmission by strengthening their surveillance capacities, enhancing sequencing capacities and variant detection, and applying a systematic approach to provide a representative indication of the extent of transmission of SARS-CoV-2 variants based on the local context, and to detect unusual events. PHSM remain critical to limit the spread of SARS-CoV-2 and its variants.

Countries are encouraged to continue strengthening existing PHSM, infection prevention and control, and disease control activities. Avoiding introduction to animal populations by decreasing the animal-human interface will be a critical aspect to the global strategy to reduce the occurrence of mutations that have negative public health implications.

Update on outbreaks

COVID-19 in 22 EMR countries

Current public health events of concern [cumulative N° of cases (deaths), CFR %]

Coronavirus disease 2019 (COVID-19): 2019-2021

Afghanistan	[62 063 (2698), 4.3%]
Bahrain	[187 905 (678), 0.4%]
Djibouti	[11 335 (149), 1.3%]
Egypt	[236 272 (13 845), 5.9%]
Iran (Islamic Republic of)	[2 640 670 (74 524), 2.8%]
Iraq	[1 108 558 (15741), 1.4%]
Jordan	[719 223 (9 076), 1.3%]
Kuwait	[284 076 (1635), 0.6%]
Lebanon	[532 269 (7460), 1.4%]
Libya	[179 970 (3070), 1.7%]
Morocco	[513 628 (9064), 1.8%]
occupied Palestinian territory (oPt)	[330 278 (3619), 1.1%]
Oman	[200 716 (2105), 1%]
Pakistan	[858 026 (18 915), 2.2%]
Qatar	[210 603 (502), 0.2%]
Saudi Arabia	[425 442 (7059), 1.7%]
Somalia	[14 415 (747), 5.2%]
Sudan	[34 889 (2446), 7%]
Syrian Arab Republic	[23 319 (1648), 7.1%]
Tunisia	[320 813 (11 429), 3.6%]
United Arab Emirates	[534 445 (1610), 0.3%]
Yemen	[6466 (1271), 19.7%]