

# Why variants are most likely to blame for India's COVID surge

April 28 2021, by Rajib Dasgupta

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With [more than 300,000](#) new COVID cases a day and hospitals and crematoria facing collapse, Director-General of the World Health Organization Tedros Adhanom Ghebreyesus has called the situation in India "[beyond heartbreaking](#)".

India's [government](#) has blamed the people for not following COVID-safe public health directives, but recent data shows mask use has only [fallen](#)

[by 10 percentage points](#), from a high of 71% in August 2020 to a low of 61% by the end of February.

And the mobility index increased by about [20 percentage points](#), although most sectors of the economy and activity had opened up. These are modest changes and do not adequately explain the huge increase in cases.

A more likely explanation is the impact of variants that are more transmissible than the original SARS-CoV-2 virus.

## **Variants in India**

Viruses keep changing and adapting through mutations, and new variants of a virus are expected and tracked in a pandemic situation such as this.

The Indian SARS-CoV-2 Genomics Consortium (INSACOG), a group of ten national laboratories, [was set up](#) in December 2020 to monitor genetic variations in the [coronavirus](#). The labs are required to sequence 5% of COVID-positive samples from states and 100% of positive samples from international travelers.

The United Kingdom is currently testing about 8% of its positive samples and the United States about 4%. India has been testing about [1%](#) altogether. INSACOG has so far tested [15,133 SARS-CoV-2 genomes](#). This means of every 1,000 cases, the UK has sequenced 79.5, the US 8.59, and India [only 0.0552](#).

In the final week of December, India [detected six cases](#) of the UK variant (B.1.1.7) among international travelers.

The current second wave started in the northwestern state of Punjab in the first half of February and has not yet plateaued. One of the advisers

to the Punjab government confirmed that more than 80% of the cases were [attributed](#) to the UK variant.

Significantly, the most affected districts are from Punjab's Doaba region, known as the NRI (non-resident Indian) belt. An estimated [60-70% of the families](#) in these districts have relatives abroad, mostly in the UK or Canada, and a high volume of travel to and from these countries.

B.1.617, or what has been called the "Indian double mutation," has [drawn attention](#) because it contains two mutations (known as E484Q and L452R) that have been [linked](#) to increased transmissibility and an ability to evade our immune system.

[Many experts](#) in India now think this is [driving the surge](#).

Even as India's health ministry announced the detection of the mutants on March 24, it went on to [add](#): "[...] these have not been detected in numbers sufficient to either establish or direct relationship or explain the rapid increase in cases in some states."

The head of the Indian Council of Medical Research said there was [no reason for panic](#) because mutations are sporadic, and not significant. That day, the states of Maharashtra and Punjab [accounted for](#) 62.5% and 4.5% of 40,715 new cases, respectively.

Across the world, several key mutant strains have emerged thanks to ongoing virus replication in humans. Both ability to replicate and transmit, and a better ability to escape our immune systems, led to the variants [establishing themselves](#) as dominant strains across geographies and populations.

The UK variant (B.1.1.7) is at least 30% [more transmissible](#). At a recent

webinar, Indian experts observed the "Indian strain" (B.1.617) is similarly transmissible to the UK variant, but there is little evidence so far of it being more lethal than the original virus.

## **Why higher transmissibility is so concerning**

According to epidemiologist Adam Kucharski at the London School of Hygiene and Tropical Medicine, the conundrum [is this](#): "[...] suppose 10,000 people are infected in a city and each infects 1.1 other people on average, the low end for the estimated rate of infection in England. After a month, 16,000 people would have been infected. If the infection fatality rate is 0.8%, as it was in England at the end of the first wave of infections, it would mean 128 deaths. With a variant that is 50% more deadly, those 16,000 cases would result in 192 deaths. But with a variant that is 50% more transmissible, though no more deadly, there would be 122,000 cases after a month, leading to 976 deaths."

In all likelihood, this is the current Indian scenario: a higher overall death count despite the variants being no more fatal in relative terms.

Setting up a genomic surveillance system and consistently testing 5% of the positive samples is an expensive but important tool in the journey ahead. This can help us identify emerging hotspots, track transmission and enable nimble-footed decision-making and tailored interventions.

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