

# ONE MUTATED CORONAVIRUS TYPE DOMINATES GLOBALLY

Relevant for: Developmental Issues | Topic: Health & Sanitation and related issues

A laboratory technician is seen the Inselspital Universitaetsspital Bern university hospital during researches for a vaccine against the coronavirus disease (COVID-19) in Bern, Switzerland on April 22, 2020. | Photo Credit: [Reuters](#)

Scientists at the National Institute of Biomedical Genomics (NIBMG), Kalyani, West Bengal, have found that the novel [coronavirus](#) has undergone mutations to form 10 different types (clades). Of the 10, one specific type called A2a has become predominant and is fast replacing both the original type (called "O") from China and other mutated types in many countries. The results of the study will soon be published in the *Indian Journal of Medical Research*.

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The A2a type seems to be predominant in New York, Italy, Australia, Spain, Iceland, Brazil, Congo and other countries. It is also the dominant type in India. Washington state and New York show contrasting predominance of the clades. While B1 type is predominant in Washington, A2a dominates in New York. The differences in patterns of travel contact with China and Europe could be a reason, they write. It is not known if A2a type has become predominant in China too as China has not been submitting sequence data for about a month.

The mutation that gives rise to the A2a type is seen in the spike protein of the virus. The spike protein is responsible for the virus binding to the cell receptor and entering the cells. The mutation seen in A2a has caused a change in the amino acid at a particular location of the spike protein.

"The mutation seen in A2a enhances the efficiency of entry of the virus into human cells. None of the other nine types has a mutation in the spike protein," says Dr. Partha Majumder from NIBGM who led a two-member team that carried out the research. "The increased infectivity may be the reason why the A2a type has become predominant in many countries."

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Does the enhanced efficiency to gain entry into cells responsible for increased disease severity and deaths? "The case fatality is not significant between the 10 types," he clarifies.

The researchers analysed 3,669 whole genome sequences of coronavirus isolated from COVID-19 patients from 55 countries. The sequences have been deposited in the GISAID public database. Of the 3,669 sequences studied, the A2a type was predominant — 1,848 sequences.

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Even in the case of India, 16 of 35 genome sequences belong to the A2a type. "Of the 16 sequences of A2a type, 10 were from people who did not have a travel history. We think the A2a type will be predominant in India," says Dr. Majumder. "The sample size from India is small and the number of sequences with A2a is also relatively small. We need more sequences from India before saying with confidence that A2a type is predominant in India."

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