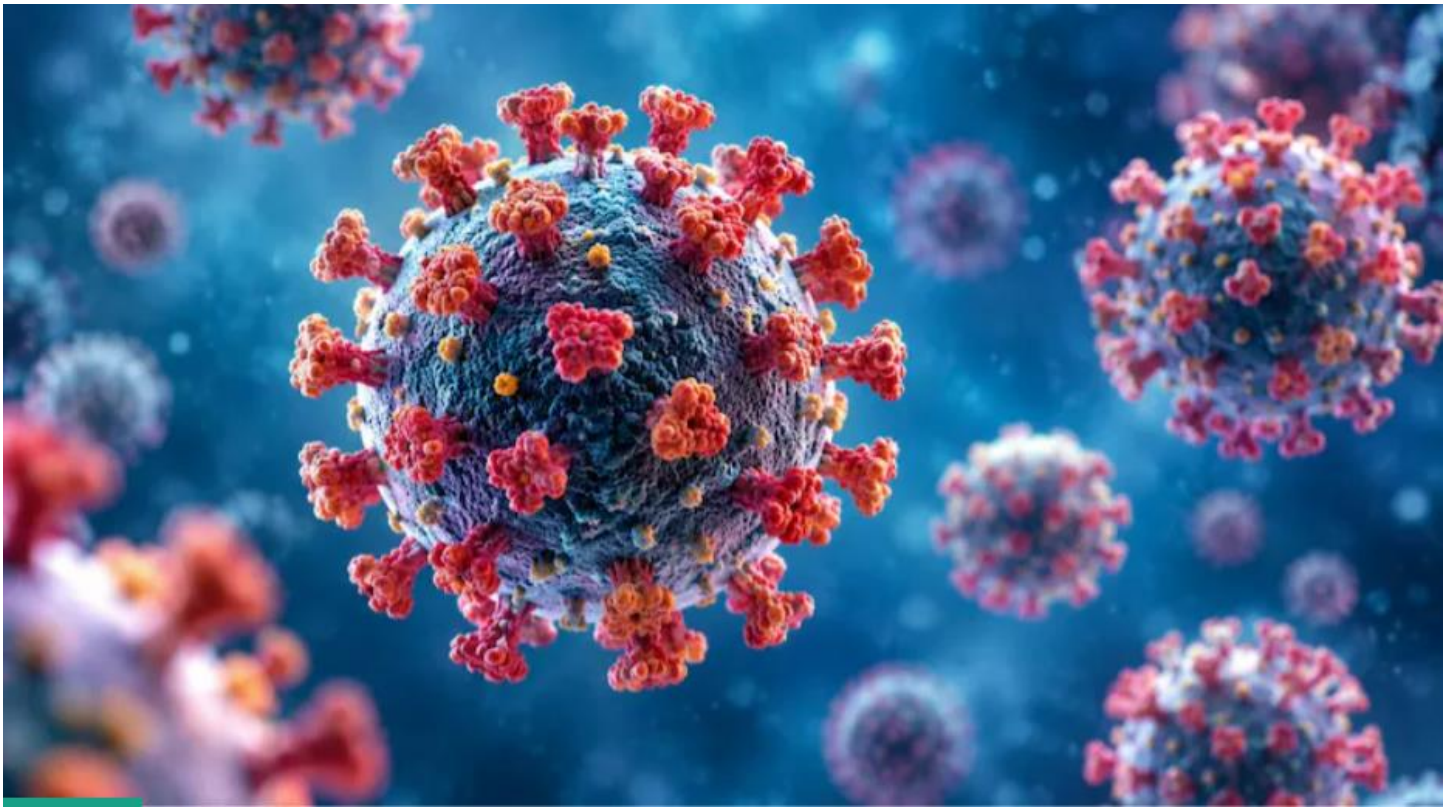
New COVID-19 variant with highly mutated spike protein spreads globally: Symptoms, vaccine protection and risks

A newly identified COVID-19 lineage, PJ.2.1, is being studied for its highly mutated spike protein and growing presence in several countries. Here is what researchers have found about its spread, symptoms, vaccine response and potential risks.



The new PJ.2.1 variant has been detected in several countries, but there is no established symptom profile unique to the lineage.

A newly identified COVID-19 variant, PJ.2.1, has been detected in several countries after first being identified in Canada's Ontario province in May 2026. Its growing presence in parts of North America, Europe, Asia and Oceania has prompted researchers to examine its genetic changes, ability to enter human cells and response to vaccine-induced antibodies.

Preliminary findings published in the *Journal of Infection* in October 2026 suggest that PJ.2.1 may have an increased ability to bind to ACE2, the receptor that the coronavirus uses to enter human cells. However, the research did not find evidence of substantially greater resistance to vaccine-induced antibodies than most of the other variants examined.

There is currently insufficient clinical evidence to establish whether PJ.2.1 causes more severe illness, increases hospitalisations or leads to more deaths. Researchers have also not identified a distinct set of symptoms associated with this lineage.

The World Health Organization (WHO) has highlighted that COVID-19 symptoms can overlap with those of influenza and other respiratory infections. This makes it difficult to identify the cause of an illness based on symptoms alone.

PJ.2.1 is a lineage of SARS-CoV-2, the virus that causes COVID-19. Researchers have described it as a *saltation variant*, a term used for a virus that emerges with a relatively large number of genetic changes rather than acquiring mutations gradually over time.

According to research by Markus Hoffmann and colleagues published in the *Journal of Infection* in October 2026, PJ.2.1 originated from MC.10.1.7, a descendant of the JN.1 lineage that circulated until May 2025.

The first documented sample of PJ.2.1 was identified in Ontario on May 2, 2026. It was subsequently detected in other Canadian provinces, including Alberta, British Columbia and New Brunswick.

The United States recorded its first detection in New York City on June 30. Further detections were reported in California, Arizona, New Jersey, Virginia, North Carolina, Missouri, Oklahoma, Colorado and Florida.

The lineage has also been identified in Singapore, Australia, New Zealand, Israel, France and Spain. Researchers in Spain reported evidence of local transmission chains across multiple regions.

Data from Public Health Ontario indicate that PJ.2.1's share of sequenced SARS-CoV-2 samples increased from 16.9% in the preceding four-week period to 25.2% between September 20 and October 17.

These figures reflect its proportion among the samples that were sequenced, rather than the share of all COVID-19 infections in the population.

Why is PJ.2.1 spreading? What does the research say?

A key area of investigation is the variant's spike protein, the structure that allows SARS-CoV-2 to attach to human cells. PJ.2.1 carries several changes in this protein, which can influence how the virus interacts with the ACE2 receptor.

ACE2 is found on the surface of human cells and acts as an entry point for the coronavirus. The researchers examined whether changes in PJ.2.1's spike protein affected its interaction with this receptor.

In laboratory experiments, PJ.2.1 was less susceptible to inhibition by an antibody targeting ACE2 than the other variants examined. The finding suggests that its spike protein may bind more effectively to the receptor.

The researchers also assessed whether the variant could evade antibodies generated after COVID-19 vaccination.

Their findings did not indicate substantially greater immune evasion compared with most of the other variants tested. Antibodies from people who had received an LP.8.1-adapted COVID-19 vaccine were able to neutralise PJ.2.1. Its sensitivity to neutralisation was 1.8 times lower than that of the LP.8.1 reference variant.

The study therefore points to increased ACE2 binding as a possible factor behind PJ.2.1's growth, rather than a substantial increase in its ability to evade vaccine-induced antibodies.

However, these findings are based on laboratory experiments. They do not establish how efficiently the variant spreads between people or how it affects patients in real-world conditions.

What are the symptoms of PJ.2.1?

There is no established symptom profile that distinguishes PJ.2.1 from other COVID-19 variants.

Common COVID-19 symptoms identified by the WHO include:

- Fever or chills
- Cough
- Sore throat
- Runny or blocked nose
- Headache
- Muscle and body aches
- Fatigue and weakness

Some people may also experience shortness of breath, gastrointestinal symptoms or changes in their sense of smell and taste.

The WHO has noted that several symptoms of COVID-19 overlap with those of influenza, including fever, cough, a runny nose, sore throat, headache and fatigue. Similar symptoms can also occur with other respiratory infections.

As a result, symptoms alone cannot reliably establish whether someone has COVID-19, influenza or another respiratory illness. Diagnostic testing can help identify the infection, while genomic sequencing is used by public health laboratories to determine which SARS-CoV-2 lineage is circulating.

Does PJ.2.1 cause more severe COVID-19?

There is currently insufficient clinical evidence to conclude that PJ.2.1 causes more severe illness than previously circulating variants.

The research published in the *Journal of Infection* focused primarily on the variant's genetic characteristics, its interaction with human cells and its susceptibility to antibodies. It did not establish an increase in hospitalisations or deaths among people infected with PJ.2.1.

It is important to distinguish between a variant's ability to spread, its capacity to evade immune responses and the severity of the illness it causes. These are separate characteristics, and an increase in one does not automatically mean an increase in the others.

The researchers also reported that PJ.2.1 was detected more frequently among older age groups, particularly people aged 70 and above. However, this observation does not establish that the variant specifically targets older people or causes more severe disease in this group.

Older adults, people with weakened immune systems and those with underlying conditions such as diabetes, heart disease and chronic respiratory illnesses remain at greater risk of severe COVID-19 complications.

Do existing COVID-19 vaccines protect against PJ.2.1?

The laboratory findings offer some indication that vaccine-induced antibodies can still recognise and neutralise PJ.2.1.

In particular, the study found that antibodies from people who had received an LP.8.1-adapted vaccine were able to neutralise the variant. Researchers reported that its sensitivity to neutralisation was only 1.8 times lower than that of the LP.8.1 reference variant.

However, laboratory neutralisation results do not provide a complete picture of how well vaccines prevent infection in real-world conditions. The study does not establish the effectiveness of vaccination against PJ.2.1 in terms of preventing infection, hospitalisation or severe disease.

COVID-19 vaccination remains an important measure for reducing the risk of severe illness, hospitalisation and death. People at higher risk should consult their healthcare providers about recommended vaccinations and booster doses.

Has WHO classified PJ.2.1 as a variant of concern?

The emergence of PJ.2.1 warrants continued monitoring, but its detection across several countries should not be confused with a formal WHO classification.

The WHO uses a variant-tracking framework to assess emerging SARS-CoV-2 lineages and their potential public health implications. Its last update in July 2026 did not include PJ.2.1 among the variants of interest or variants under monitoring listed at the time.

The absence of a formal designation does not mean that the lineage is not being studied. Genomic surveillance helps public health authorities track changes in the virus and assess whether emerging variants have characteristics that could affect public health.

Has PJ.2.1 been detected in India?

The available information does not establish whether PJ.2.1 has been detected in India.

The Indian SARS-CoV-2 Genomics Consortium (INSACOG) provides a framework for monitoring genetic changes in circulating coronavirus strains through genomic sequencing. Such surveillance helps identify emerging lineages and track their spread.

No conclusion about the presence of PJ.2.1 in India can be drawn from the international detections and research findings outlined above.

What does the emergence of PJ.2.1 mean?

PJ.2.1 is among the newer SARS-CoV-2 lineages being investigated as the virus continues to evolve. Its increasing share of sequenced samples in Ontario and detections in several other countries have made it a subject of scientific attention.

Current laboratory research suggests that its growth may be linked to stronger interaction with the ACE2 receptor. The same research has not found substantially greater immune evasion compared with most of the variants tested.

There is also no established evidence that PJ.2.1 causes more severe illness. Further research and genomic surveillance will be needed to understand its behaviour outside laboratory settings.

For now, testing when respiratory symptoms develop, following public health guidance and keeping vaccinations up to date, particularly among people at higher risk, remain relevant measures for managing COVID-19.

News Source:

https://www.moneycontrol.com/world/new-covid-19-variant-with-highly-mutated-spike-protein-spreads-globally-symptoms-vaccine-protection-and-risks-article-14076311.html