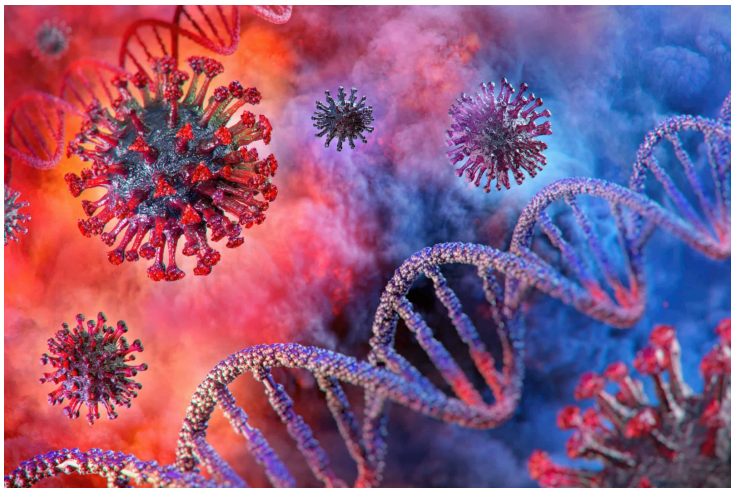
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Japan studies genetic differences of COVID-19 and SARS viruses

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The research team named their technique Fate-seq



Researchers at the University of Tokyo in Japan have identified specific portions of the genetic codes of the COVID-19 and SARS viruses that may promote the viruses' lifecycles. The new technique is researchers' first tool for determining what genetic sequences stored as RNA - DNA's chemical cousin - are more stable.

The research team named their technique Fate-seq because it aims to determine the fate of a genetic sequence, whether it will persist or degrade based on its stability.

Researchers compared 21 SARS-CoV stable genome fragments to the full genetic sequence data available for other types of coronaviruses.

Two of the stable fragments from the SARS-CoV are very common in other evolutionarily similar coronaviruses, including the virus that causes COVID-19, SARS-CoV-2.

In addition to better understanding dangerous viruses, researchers hope to use Fate-seq to understand the fundamental rules of RNA stability and advance new types of medicine.