

# Are COVID-19 vaccines working?

## What you need to know about the impact of viral variants on global vaccine effectiveness.

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Not all vaccines being used in the world are equal. Most globally available vaccines have some level of protective activity against the initial SARS-CoV-2 strains, but not all have activity against the more recent, and now dominant, variants. When the vaccine being administered in a given global location does not protect against the region's predominant variant, there will be a substantial impact on the dynamics of the virus as it spreads throughout the population.

### Varied Vaccine Utilization

CoronaVac, also known as the Sinovac COVID-19 vaccine, is an inactivated, or killed, SARS-CoV-2 virus product developed and manufactured by the Chinese company Sinovac Biotech. CoronaVac has some effectiveness in preventing serious illness and death against the initial SARS-CoV-2 strains, and it is inexpensive and quick-to-produce. This Affordability and ease of access allowed less affluent nations to provide the vaccine for its citizens. This has resulted in CoronaVac being widely used.

Historically, killed-virus vaccines, or viral sub-unit vaccines, have not been very successful in fighting any coronavirus. Since CoronaVac is a killed-virus product, it is largely ineffective in stopping the spread of recent SARS-CoV-2 variants, such as Alpha, Delta and [Lambda](#). These findings have been critical to the pandemic discussions in countries where variants are widespread, such as [South America](#).

Fortunately, the mRNA vaccines available in the United States remain [remarkably effective against serious infection from all known SARS-CoV-2 variants](#).

### The Evolution of Viral Variants

Variants can alter the protection given by vaccines and the utility of some of our treatments. Major variants can result in regional outbreaks with increased morbidity and mortality. In some cases, such as the Alpha and [Delta variants](#), they replace most of the SARS-CoV-2 viral types globally within a few months.

We know that SARS-CoV-2 undergoes mutation where single nucleotides of its RNA change. It mutates at a rate of approximately two single-nucleotide changes every 30 days, which is about half of the influenza rate. Initially, these numbers gave us hope that we could more quickly defeat the virus with public health measures, testing, vaccines and treatments.

# SARS-CoV-2 Reassortment

We now know that the SARS-CoV-2 virus also vigorously participates in an evolutionary process called “reassortment” or “antigenic shift” similar to the influenza virus. During reassortment, the host cell is infected with two different SARS-CoV-2 viral types, and as they replicate, the genomes of the two viruses mix and recombine to create entirely new viral genomes with new characteristics. The reassortment process is likely why serious variants of the SARS-CoV-2 virus can develop so quickly, and the large amount of virus in the global human population allows the reassortment process to continually occur.

[A recent paper](#) suggests that when mutations or other genomic changes occur in specific locations on the SARS-CoV-2 genome, the risk for a more serious variant is increased. We frequently see mutations in these areas can cause the virus to become more infectious, more pathogenic, or both. Recent variants of concern, Alpha, Delta and Lambda, have mutations that cluster within certain regions of the viral genome. Additionally, specific mutations, such as the L452Q, appear to enhance infectivity and spread of the virus by altering its receptor-binding characteristics.

Its worth noting, all variants with mutations in these regions are not all increasingly dangerous. As we gain more knowledge about [how SARS-CoV-2 mutates](#), we may learn to better predict its future behaviors.