Scientists at Arizona State University sequenced SARS-CoV-2 genomes collected from hundreds of infected individuals. They found a deletion of 81 nucleotides in some of the viruses. This large deletion is in a gene that codes for a protein that helps the virus escape the immune system. Predict how the frequency of viruses with this deletion will change in the population over time. Use evidence to support your answer

How could sequencing many SARS-CoV-2 genomes be used to track how the virus has changed over time due to mutations?

Step 1:

SARS-CoV-2: The coronavirus illness virus, which causes a respiratory ailment (COVID-19). The coronaviruses are a broad family of viruses that includes the SARS-CoV-2. Both people and some animals can contract these viruses. In 2019, SARS-CoV-2 was first identified as a human pathogen. The virus is believed to be transmitted from person to person through droplets expelled during coughing, sneezing, or talking by an infected person. A less prevalent method of transmission is through contacting one's mouth, nose, or eyes after touching a surface that has the virus on it. Treatment for COVID-19 and SARS-CoV-2 infection prevention are the subjects of research. also known as coronavirus 2, the severe acute respiratory illness.

Step 2:

Over time, it's expected that viruses with this deletion will appear less frequently. As mentioned in the query, this deletion eliminates a portion of a protein's coding sequence that aids SARS-CoV-2 in evading the human immune system. This protein's function will probably be compromised with a sizable loss, making the virus simpler for the immune system to destroy. As more viruses with the deletion are destroyed by the immune system, the frequency of viruses with this deletion will naturally decline over time.

Step 3:

The prevalence of various alterations in the viral genome throughout time might be determined by sequencing the genomes of several SARS-CoV-2 strains. This could provide information on when new mutations appeared as well as which mutations changed in frequency throughout the course of numerous viral infections. This would thus serve to illustrate how SARS-CoV-2 evolved over time as a result of mutations.