YNHHS/YM Statement on SARS-CoV-2 Mutations

SARS-CoV-2 is the virus known to cause coronavirus-19 disease (COVID-19). The SARS-CoV-2 RNA genome has approximately 30,000 nucleotides that encode 29 genes.

All viruses are known to mutate. Over 40 variants of significance have been identified in SARS-CoV-2, including in the receptor binding domain of the Spike protein. The Spike protein is key as it binds to the host cell receptor (ACE2) and mediates virus infection of the cell. Neutralizing antibodies, induced by natural infection or vaccination, bind to the Spike protein and prevent infection of the host cell.

The strain in the news, B.1.17, initially found in the UK, is noted to increase transmission only.

Most variants are not associated with resistance to medications, changes in the effectiveness of vaccines or changes in the severity of clinical disease.

This situation is being carefully monitored by Yale University and Yale New Haven Health clinicians, scientists, epidemiologists, and laboratories.

Accuracy of PCR tests done at YNHHS is not reduced as most do not target the Spike gene and none target the Spike gene only.

YNHH is helping to detect the appearance of new variants through genetic sequencing in collaboration with Yale School of Public Health and Connecticut Department of Public Health.

- COVID-19 Testing Stewardship Committee

This statement is based on current information, recommendations, and evidence and will be subject to revision or retraction based on continued monitoring by the Committee.