

## Infographic: Tracking coronavirus strains with genetic ‘barcodes’

Drexel University researchers have reported a method to quickly identify and label mutated versions of the virus that causes COVID-19. Their preliminary analysis, using information from a global database of genetic information gleaned from coronavirus testing, suggests that there are at least six to 10 slightly different versions of the virus infecting people in America, some of which are either the same as, or have subsequently evolved from, strains directly from Asia, while others are the same as those found in Europe.

...

“It’s the equivalent of scanning a barcode instead of typing in the full product code number,” [researcher Gail] Rosen said. “And right now, we’re all trying to get through the grocery store a bit faster. For scientists this means being able to move to higher-level analysis much faster. For example, it can be a faster process in studying which virus versions could be affecting [health outcomes](#). Or, public health officials can track whether new cases are the result of local transmission or coming from other regions of the United States or parts of the world.”

...

[T]his method can also reveal the portion of its genetic code that appears to remain resistant to mutations—a discovery that could be exploited by treatments to combat the virus.

[genetictraci](#) for type unknown

Major SARS-CoV-2 genetic subtypes in countries/regions with the most sequences (indicating date subtype was first sequenced in that country/region). Subtypes with less than 5% abundance are plotted as “OTHER.” Credit: Drexel University

[Read the original post](#)