Scientists tracking mutations of the new coronavirus say there is no evidence its changes have made the virus deadlier or more contagious. But they are tracking the virus’s genetic changes, which are common and typically benign, to better understand how it is being transmitted around the world and help combat its spread.

The novel coronavirus, or Sars-CoV-2, and all other coronaviruses are made up of RNA, which has a slightly different chemical makeup than DNA. Viruses with an RNA genetic code also mutate easily. When the virus makes a copy of itself, it often makes mistakes and changes a small piece of its genome, which helps it adapt to its environment.

“It’s a natural process of a virus being a virus,” said Nathan Grubaugh, an assistant professor of epidemiology of microbial diseases at the Yale School of Public Health. But those changes aren’t innately dangerous. Virologists say most mutations are “silent,” meaning they don’t change any of the virus’s behaviors.

Mutations could also cripple a virus and effectively kill it. Others could make the virus more infectious and dangerous or less severe, said Neville Sanjana, a human geneticist and bioengineer at the New York Genome Center, a nonprofit research institution. Though right now, infectious disease experts say there isn’t any evidence that Sars-CoV-2 mutations have made the virus behave differently.

These small tweaks in the genetic code also build up as a virus spreads, copying over all of the previous mutations when it replicates while adding new ones. And as the virus spreads in different geographic directions, so do its mutations, making genomic branches that researchers can follow back to the root.

“Just by these little fingerprints that are within each of these viruses, you can know who acquired it from whom,” said Elodie Ghedin, a molecular parasitologist and virologist at New York University School of Global Public Health. “You can track transmission.”

On Tuesday, researchers from the Peking University School of Life Sciences and the Institut Pasteur of Shanghai said that the novel coronavirus had evolved into two “major types,” according to a paper published in National Science Review. One of those types was more prevalent in 70% of the patient samples studied, leading the researchers to suggest that the variant might be more “aggressive,” though they noted the findings were still preliminary.

But the study only analyzed 103 genomes out of the more than 101,000 global infections, experts who weren’t involved in the study pointed out. And, while there was a slight genomic variation, which is expected, there wasn’t enough evidence to make claims about differences in severity or how easily the virus spreads, the virologists said.

“To say it’s infecting more people because it’s more aggressive is a huge leap,” Dr. Grubaugh said. “We don’t see that mutations are associated with higher case fatalities or rates of transmissions.”

The authors of the study didn’t respond to requests on Friday requesting comment.

Although mutations do occur, understanding what that means for fatality and spread rates is difficult to study, and takes years of lab experiments to come to a conclusion, Dr. Grubaugh added.

Still, researchers are keeping pace with the variations of the novel coronavirus, connecting the dots between cases by sharing the shifting genetic codes in different patient samples. On Jan. 10, scientists in China made the virus’s genome available online, and researchers have since sequenced at least 167 samples taken from different patients across the globe.
“There are groups all over the world that are sharing sequence data in real-time,” said Trevor Bedford, an associate member of the Vaccine and Infectious Disease Division at the Fred Hutchinson Cancer Research Center in Seattle.

Dr. Bedford is one of the creators of Nextstrain, an online platform that takes available genomic data and maps their relationships by following the accumulating mutations, with the goal of assisting the public health response to viruses.

Researchers earlier this week compared the genomes of two different patients in Washington state, one who had returned Jan. 15 from Wuhan, China—the original center of the outbreak—and one who was diagnosed in late February but didn’t travel abroad or have history with someone who was infected. Both cases were in Snohomish County, nearby Seattle’s King County.

The two viral genomes were highly similar, Dr. Bedford wrote on his website at the time, sharing one rare genetic variant. The connection strongly implies that the second case was related to the first, researchers say, rather than being connected to another unknown, more recent traveler.

Researchers now think that the virus has actually been circulating in the Seattle metropolitan area for several weeks. There are likely hundreds of undetected cases that are part of this cluster, researchers say, which called for a broader public health response and wider testing.

There have been at least 19 confirmed cases of Covid-19, the disease caused by the novel coronavirus, in Snohomish County and 58 cases in King County as of Friday, according to local health officials, who suspect there are more. At least 13 people in the state have died from the disease.

While these genetic links can provide powerful insights, scientists say much more information is needed to determine this pathogen’s transmission patterns, especially as the number of total genomes sequenced is still dwarfed by the total number of cases.

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