

## ‘A lot of secrets’ in coronavirus genomes: Why are some strains so deadly, while others remain more mild?

[In 1965, a] group of researchers in England, led by Dr. David Tyrrell, was learning more about the common cold. They, too, isolated what appeared to be a new type of virus in tissue culture. When Tyrrell’s team examined it under an electron microscope, they found that it resembled a virus that had been isolated in the 1930s from chickens with bronchitis. It was a coronavirus—the first proven to infect humans.

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[I]t’s still not altogether clear why three coronaviruses—SARS-CoV-1, MERS-CoV and [SARS-CoV-2](#) (the source of the COVID-19 pandemic)—have led to far more severe symptoms and a higher mortality rate, while the other four known human coronaviruses remain much milder.

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Dr. [Ken] McIntosh suspects that coronaviruses will continue to perplex researchers. First, because coronaviruses are large and complex, and second because they can change relatively easily on a genetic level. He notes that these viruses can also recombine fairly easily within the same cell, and that such mutations are likely what led to both the coronavirus that causes SARS and the novel coronavirus that has caused the [current pandemic](#).

“Coronaviruses have the largest RNA genome of any of the animal viruses,” Dr. McIntosh says. “And it has a lot of secrets.”

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