

Searching for answers in the genome of China's mysterious coronavirus

As public health officials respond in real-time to the unfolding of the outbreak, so too are scientists. Just one month after the first case of the pneumonia-causing virus was reported on December 8, Chinese scientists [sequenced the viral genome and made it public](#). Now, researchers around the globe are scrutinizing the sequence for insight into this mystery disease.

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When a man in Washington state developed mild symptoms two days after returning from Wuhan on January 15, his doctors shipped his sample overnight to the US Centers for Disease Control and Prevention, which used real-time reverse transcription polymerase chain reaction (rRT-PCR) to confirm that the sample matched the genetic sequence of 2019-nCoV. The strategy can also be used to determine the presence of the virus in individuals who don't show symptoms but may still be able to spread it to others. Without the genome, officials would not have been able to definitively diagnose the disease.

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"The other thing the sequence allows us to do," says [virologist Anthony] Fehr, "is see if the virus is evolving in real time."

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The genome does give scientists some insight, though. For example, there was very little genetic variation between the first 10 patient samples sequenced by various teams across the world. Menachery says that's a sign the virus recently jumped from animals to humans.

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