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New China virus: Five questions scientists are asking

Researchers are racing to find out more about the epidemiology and genetic sequence of the coronavirus spreading in Asia and beyond.

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Medical staff at a hospital in Wuhan, China, where most cases of the viral infection have occurred. Credit: Getty

Health authorities around the world are worried about an outbreak of a mysterious virus that originated in Wuhan, China, last month. Officials there have confirmed more than 500 cases of the infection, which causes a respiratory illness, and 17 deaths. Several cases have been spotted elsewhere in Asia and one in the United States.

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Researchers are racing to learn more about the virus and to discover whether it has the potential to cause an outbreak similar to the 2002–03 epidemic of severe acute respiratory syndrome (SARS), which emerged in southern China and killed 774 people in 37 countries. Both are members of a large virus family, called coronaviruses, that also includes those responsible for the common cold.

Efforts to understand the outbreak are especially crucial, because mass travel from Friday for the Chinese New Year holiday could spread the virus farther and faster.

How does the virus spread?

The most urgent question surrounding the outbreak is determining how it spreads. Chinese authorities have confirmed that some cases have been caused by transmission between humans, but it's still unclear whether this can happen routinely.

“What’s critical to understand is whether that’s occurring at a rate and with a level of efficiency which would sustain a human epidemic,” says Neil Ferguson, a mathematical epidemiologist at Imperial College London. Monitoring the rate at which new cases appear, and when symptoms began for each case, should tell scientists how easily the virus can pass between humans and whether the outbreak has the potential to persist.

How deadly is the virus?

High rates of pneumonia among the first people infected had many researchers worried that the Wuhan virus was especially pernicious. Those concerns have receded slightly, as more mild cases turn up. With at least 17 deaths in more than 500 cases, the virus does not seem to be as deadly as SARS – which killed an estimated 11% of the people it infected. But “It’s too early to be sanguine about the severity,” Ferguson says.

Where did the virus come from?

Authorities are working on the theory that the virus originated in an unidentified animal or animals, and then spread to humans at a large animal and seafood market in Wuhan.

Identifying the animal source of the virus could help to control the current outbreak and gauge its threat – and potentially prevent future epidemics, say researchers. Genetic sequencing suggests that the Wuhan virus is related to coronaviruses that circulate in bats,

including SARS and its close relatives. But other mammals can transmit these viruses – SARS was probably spread to humans by civet cats.

The live-seafood market where the outbreak seems to have originated – now closed – also sells wild animals. Tracing other cases to the market could help to identify the source, as could tests of animals from the market, or containers and cages, for viral genetic material, says Ben Cowling, an epidemiologist at the University of Hong Kong.

What can we learn from the virus's genetic sequence?

Genetic sequencing of the Wuhan coronavirus offers clues to its origins and spread.

Laboratories in China and Thailand have sequenced the genomes of at least 19 strains found in infected people and have made them publicly available. That's "pretty remarkable, given that we're two weeks after work has begun," says Trevor Bedford, an evolutionary geneticist at Fred Hutchinson Cancer Research Center in Seattle, Washington, who is analysing the sequences as they come in. "People are extremely fast and excellent about data sharing," Bedford adds.

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Bedford says that the most striking thing about the sequences is how similar they are to one another. "There's very little diversity. I expected to see more and I think other people did as well." The lack of genetic diversity suggests that the common ancestor of the different human strains emerged in November or December and has spread rapidly, and hasn't gained many mutations. Those it has gained tend to be distinct for each virus sequence. However, Bedford adds, the genomes don't yet indicate whether the rapid expansion of the virus occurred in humans or in an animal reservoir. Evolutionary geneticist Andrew Rambaut at the University of Edinburgh, UK, posted an analysis on 20 January that came to a similar conclusion.

Bedford says that, with further virus sequences, it might be possible to find out whether most cases are caused by repeated spillover of the virus from animals into humans, with limited human-to-human transmission, or whether the virus spread to a small number of humans and most cases are now being caused by secondary human-to-human transmission. "I think that would be the big epidemiological goal for everyone at the moment," he says. Genetic information from the animal or animals that transmitted the virus to humans would also be helpful in identifying the extent of human-to-human transmission, Bedford adds.

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Such sequences, he says, could also identify any genetic changes that might have helped the virus make the jump from animals to humans. And if the outbreak drags on because of extensive human-to-human transmission, Bedford and other geneticists will be looking for signs that the virus has gained further mutations enabling it to spread more efficiently in humans.

Bedford cautions that these conclusions are preliminary, because so few data are available. “Adding a few key samples can change the story significantly,” he says.

Can a drug be developed to treat the coronavirus?

No drugs have been shown to be effective in treating SARS or other coronavirus infections in humans, and no vaccines aimed at preventing these infections have been licensed.

A team at China’s National Engineering Research Center for the Emergence Drugs in Beijing is working on finding therapies that would work by blocking the receptor on human cells that the virus latches on to and uses to infect. A comparison of the SARS and new China virus sequences, published on 16 January, found that they bind to the same receptor. The team is hoping to revive efforts to develop treatments for SARS and adapt them in a bid to make a drug could work against the latest virus.

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