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ESSAY

So Where Did the Virus Come From?

Research into the origins of the new coronavirus raises questions about how it became so infectious in human beings



ILLUSTRATION: MITCH BLUNT

By Matt Ridley

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New research has deepened, rather than dispelled, the mystery surrounding the origin of the coronavirus responsible for Covid-19. Bats, wildlife markets, possibly pangolins and perhaps laboratories may all have played some role, but the simple story of an animal in a market infected by a bat that then infected several human beings no longer looks credible.

A study published in early May by scientists at the Broad Institute in Cambridge, Mass., and at the University of British Columbia has uncovered an unusual feature of the virus's recent development: It has evolved too slowly. The genomes of viruses sampled from cases during the

SARS epidemic of 2002-2003 showed rapid evolutionary change during the early months of the epidemic, as the virus adapted to its new host, followed by much slower change later. By contrast, samples taken from recent cases of the new coronavirus, SARS-CoV-2, have comparatively few genetic substitutions compared with an early case from December.

The authors, Shing Hei Zhan, Benjamin Deverman and Yujia Alina Chan, write: “We were surprised to find that SARS-CoV-2 exhibits low genetic diversity in contrast to SARS-CoV, which harbored considerable genetic diversity in its early-to-mid epidemic phase.” This implies, they argue, that “by the time SARS-CoV-2 was first detected in late 2019, it was already pre-adapted to human transmission to an extent similar to late epidemic SARS-CoV.” This is potentially very good news: Because the virus is relatively stable genetically, a vaccine that works against it, if we’re able to develop one, will be more likely to work against all strains.

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The same study seems to rule out the possibility that infected animals at the Huanan Seafood Market in Wuhan transmitted the virus to several human beings, as some have suggested as a point of origin. The Chinese authorities have now confirmed that no animal samples from the market were infected. This suggests that a single person brought a virus that was already adept at human transmission to the market and infected others.

Work published in March by Andrew Rambaut of Edinburgh University, analyzing the genomic sequences, calculates that the most recent common ancestor of the viruses now in circulation infected someone in late November or early December, though with a “confidence range” stretching back into October. That leaves little time for evolutionary adaptation, so the months during which the virus fine-tuned its ability to infect human beings were presumably before this and somewhere other than the market in Wuhan.

The closest animal version of the virus remains a bat sample collected by scientists in 2013 a thousand miles away in Yunnan. Details of where and how that sample was collected have been sketchy, but a new paper by two scientists from the Agharkar Research Institute in Pune, India, show that it is the same as a published sample with a different name that was collected from an abandoned mineshaft in southern Yunnan in 2013, following an outbreak of pneumonia-like illness that killed three miners there the year before.

One of the coronavirus's key genes resembles a virus found in smuggled pangolins.

But that virus cannot be the immediate source of Covid-19. Part of one of its key genes, coding for the “spike” protein that allows the virus to lock onto human cells, is distinct from the version that is causing the pandemic. In the human virus, this part of the gene, called the “receptor binding motif,” more closely resembles the virus found in smuggled pangolins, though the rest of the pangolin virus is less similar.

Compared with the bat and pangolin viruses, the one now infecting human beings also has an extra 12-letter nucleotide sequence, called a “furin cleavage site,” in the spike protein gene; this greatly enhances the virus’s ability to get into and out of different types of human cells. Kristian Andersen of the Scripps Institute in La Jolla, Calif., and colleagues argue that this might have arisen by mutation during “a period of unrecognized transmission in humans” after the original transmission from an animal.

What about the controversial claim that the virus may have originated in a laboratory? Both Ralph Baric’s team at the University of North Carolina at Chapel Hill and Shi Zhengli’s team at the Wuhan Institute of Virology have been working on SARS-like coronaviruses and testing their ability to infect human cells. They have for some years reported successful experiments in which they created new strains of the virus by manipulating the spike proteins that are now the focus of discovering the origin of SARS-CoV-2, and their research has included inserting furin cleavage sites.

The two teams made these so-called chimeric viruses in order to understand what makes viruses more or less dangerous and in the hope of being ready to protect people against a future SARS epidemic. In 2015 they published a joint experiment in which they combined parts of one mouse-adapted SARS-like coronavirus with a spike gene from a SARS-like coronavirus derived from Chinese bats.

The first case could have been a rural farmer or possibly a bat researcher collecting samples for virologists.

In reporting their results, they expressed caution about continuing such risky experiments: “On the basis of these findings, scientific review panels may deem similar studies building chimeric viruses based on circulating strains too risky to pursue, as increased pathogenicity in mammalian models cannot be excluded.” They added: “The potential to prepare for and mitigate future outbreaks must be weighed against the risk of creating more dangerous pathogens.”

Nikolai Petrovksy and colleagues at Flinders University in Australia have found that SARS-CoV-2 has a higher affinity for human receptors than for any other animal species they tested, including pangolins and horseshoe bats. He suggests that this could have happened if the virus was being cultured in human cells, adding that “We can’t exclude the possibility that this came from a laboratory experiment.”

So what did happen? At present, the evidence is pointing tentatively to a chain of person-to-person infections occurring somewhere outside a city before somebody brought the virus to Wuhan, where the market acted as an amplifier. The first case could have been a rural farmer or possibly a bat researcher collecting samples for virologists. Or it is possible that another animal was involved in some way, with the virus bouncing between a farmer and his animals, or a wildlife smuggler and his poor pangolins.

There are more coronaviruses out there. If the evidence is pointing away from wildlife markets, and if the Chinese authorities are confident it wasn’t a laboratory leak, they should be eager to help the world find out what did actually happen.

Whatever the initial spark, what turned a brush fire into a global conflagration was city life. Viruses have erupted into human beings from contact with nature many times in the past. When more of the population lived in rural areas, hunted animals for food and foraged in forests for firewood, contact with bats would have been more frequent. But chains of infection in rural villages would have petered out.

Today, all it takes is one infected individual to go to a crowded market and cough on somebody who is about to travel to another country, and the world catches the disease. It is sure to happen again.

—Mr. Ridley is a member of the House of Lords and the author, most recently, of “How Innovation Works: And Why It Flourishes in Freedom.”