

Scientists find extensive wildlife DNA from the Wuhan wet market mixed with SARS-CoV-2

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A devastating blow has been dealt to the claims by US right-wing politicians and media outlets that the COVID-19 pandemic is the product of a lab leak at the Wuhan Institute of Virology, with a new study documenting scientifically, for the first time, the presence of SARS-CoV-2 RNA mixed with the DNA of numerous wild animals being sold at the Huanan wet market in Wuhan.

A preliminary finding of SARS-CoV-2 RNA mixed with the DNA of a raccoon dog from the Huanan wet market was made public late last week, and the WWS commented on it March 20. Now the full report has been released linking the DNA of several other wild animals from the market to the virus that causes COVID-19.

The study adds to the mountain of evidence supporting that theory of a zoonotic origin for the coronavirus, with the virus jumping from animals to humans when they came into contact at the market. SARS-CoV-2 is a natural virus, not an artificial one, manufactured in a Chinese laboratory, as the US media campaign claims, on the basis of zero evidence except for the sick imagination of fascists like former Trump adviser Steve Bannon and racist former *New York Times* science writer Nicholas Wade.

The study was released Monday on the *Zenodo* website by Dr. Florence Débarre, an evolutionary biologist at the French National Centre for Scientific Research (NCSR) and lead author. Dr. Débarre and her co-authors found genetic evidence of susceptible wildlife among positive SARS-CoV-2 samples at the Huanan Wholesale Seafood Market taken in January and February of 2020.

It is precisely the recent identification of raccoon dog and other wild animals' DNA at the Huanan market mixed with SARS-CoV-2 RNA that provides further compelling evidence that this was the epicenter for the origin of the pandemic in late 2019.

As Débarre noted in introductory remarks, she and her team, almost by chance, had on March 4, 2023 come across a set of genetic sequences publicly posted on the database of the GISAID, the Global Initiative on Sharing Avian Influenza Data, from environmental samples collected at the wet market in Wuhan. Débarre told *Nature*, "Basically, [they're] the ones we've been waiting for, for a year."

She and her colleagues downloaded approximately half-a-terabyte of genetic sequences for around fifty different samples that included drains, market stalls and carts, as well as the grounds in the Huanan market. What was remarkable was finding genetic sequences for multiple animals.

The Chinese authorities had denied the existence of such wild animals known to be susceptible to SARS-Cov-2 and able to function as potential intermediary hosts for a zoonotic spillover into human.

But a paper published on June 7, 2021, in *Nature* under the title, "Animal sales from Wuhan wet markets immediately prior to the COVID-19 pandemic," reported that between May 2017 and November 2019 some 47,381 individual animals from 38 species (including 31 protected species) had been sold.

The paper additionally noted that no pangolins were traded there, which supported an earlier finding that these animals were not likely to have caused the spillover into human populations. Dr. Peter Daszak had explained that "it was doubtful that this species played a role in the outbreak. We need to keep looking for the original reservoir." The president of EcoHealth Alliance, Daszak has for more than two decades worked tirelessly on the question of potential pandemic pathogens. He has become the target of the right-wing conspiracy theorists because his group had collegial connections with the Wuhan Institute of Virology.

Indeed, the present report corroborates that no pangolin DNA was found. However, DNA samples for five different species of wildlife—raccoon dog, Malayan porcupine, Amur Hedgehog, masked palm civet, and hoary bamboo rat—were present.

Débarre and colleagues wrote that when they notified the former head of the Chinese CDC, George Gao, on March 10, 2023, that they had found animal species linked to SARS-CoV-2 in the genetic samples, the sequences were made unavailable the next day and the CCDC declined to respond to inquiries. The NCSR researchers were also admonished by the GISAID Secretariat for supposedly not complying with terms of use and their privileges suspended, until objections were raised that there were no violations of the terms of use.

The Chinese CDC had said in a February 2022 report on their investigation, released in preprint form, that no infected animals had been identified after the market was closed down on January 1, 2020.

As the CCDC report stated, "Herein, we presented the SARS-CoV-2 detection results of 1,380 samples collected from the environment and the animals within the market in early 2020. By SARS-CoV-2 specific RT-qPCR, 73 environmental samples tested positive for SARS-Cov-2 and three live viruses were successfully isolated ... In contrast, no virus was detected in the animal swabs covering 18 species of animals in the market. The SARS-CoV-2 nucleic acids in the positive environmental samples showed significant correlation of abundance of *Homo sapiens* with SARS-CoV-2. In summary, this study provided convincing evidence of the prevalence of SARS-CoV-2 in the Huanan Seafood Market during the early stage of COVID-19 outbreak."

On March 11, the World Health Organization (WHO) was informed

of the Débarre group's findings. The next day, leading epidemiologists Michael Worobey, Edward Holmes, and Kristian Andersen met some of the members SAGO (the WHO-convened Scientific Advisory Group for the Origins of Novel pathogens) to review the findings.

As the introductory comment from the published report notes, "We cannot comment on the CCDC team's findings, as those are theirs to share, but some findings from our analyses have already been shared in the media and in public statements by the WHO. This meeting constitutes one of several efforts to establish a collaborative relationship with our colleagues at CCDC to share data and findings as rapidly as possible."

Moreover, Débarre recognizes the important work that was done by the CCDC when she said, "They did what needed to be done. We wouldn't have this data, if it wasn't for their work." Behind her comments stands the need to address the origin question through scientific and open collaboration, rather than the right-wing imperialist demonization of China that is escalating once again.

Although it is understood that SARS-CoV-2's ancestors originated in bats, how coronavirus passed into human populations is a critical question that scientists have been attempting to study in the laboratory since the SARS epidemic two decades ago. Field research has been critical in identifying recent SARS-CoV-2 related viruses. Additionally, research into such specific features as the furin cleavage site and the adaptive mechanisms these viruses evolve to jump into other species is critical. Apparently, the acquisition of such genetic characteristics is more commonplace than previously understood.

This is an issue of political as well as scientific importance, because right-wing conspiracy theorists have sought to capitalize on the lack of understanding of the scientific complexities to suggest that the furin cleavage site had to be specially engineered in a laboratory and could not have evolved naturally.

A report from 2021 on the global diversification and distribution of furin cleavage sites in coronaviruses found that at least "86 types of furin cleavage sites have been detected in strains of three coronavirus genera in 24 animal hosts in 28 countries since 1954, including at least 25 types in Beta-coronaviruses recorded in the years 1988-2019 in 14 countries. Most of them could cause unexpected threats to human beings or other mammals. Four of seven coronaviruses known to infect humans carry furin cleavage sites, including two with low pathogenicity (HCoV-OC43 and HCoV-HKU1) and two highly pathogenic zoonotic viruses (MERS-CoV and SARS-CoV-2)."

They added, "Moreover, evidence of frequent interchange of furin cleavage site motifs among the three coronavirus genera indicates that frequencies of recombination of coronaviruses' furin cleavage sites may have been underestimated."

In the early days of February 2020, Dr. Anthony Fauci, head of the National Institute of Allergy and Infectious Diseases (NIAID), NIH Director Francis Collins, and Dr. Jeremy Farrar, then Director of the Wellcome Trust, assembled an international cadre of foremost virologists and scientists to study the question of where COVID-19 came from, which eventually led to the critically important and still relevant paper titled "The proximal origin of SARS-CoV-2."

After extensive debate and analysis of the extant data, the scientists wrote, "Our analyses clearly shows that SARS-CoV-2 is not a laboratory construct or a purposefully manipulated virus."

Most extraordinary is the list of authors on the report who have been at the forefront of studying the question, including several directly

involved in this question in late January 2020 when they first raised their concerns that the novel coronavirus may have been bio-engineered. But their investigation convinced them otherwise.

They concluded, "Although the evidence shows that SARS-CoV-2 is not a purposefully manipulated virus, it is currently impossible to prove or disprove the other theories of its origin described here [various notions of *how* the zoonotic transfer took place]. However, since we observed all notable SARS-CoV-2 features, including the optimized RBD [Receptor Binding Domain] and polybasic cleavage site [Furin Cleavage Site], in related coronaviruses in nature, we do not believe that any type of laboratory-based scenario is plausible."

They noted, "More scientific data could swing the balance of evidence to favor one hypothesis over another. Obtaining related viral sequences from animal sources would be the most definitive way of revealing viral origins."

Despite the continued accumulation of evidence corroborating the zoonotic spillover of SARS-CoV-2, the highly provocative and malicious congressional hearings held on March 8 on the COVID origins attempted to give political credence and legitimacy to the reactionary conspiracy theory that posits the virus that causes COVID was bio-engineered and leaked from the WIV.

This week President Joe Biden signed the COVID-19 Origin Act of 2023, a bill sponsored by the fascistic Republican Senator Josh Hawley of Missouri. This new legislation which passed the Senate and House earlier and has unanimous support from both parties, ordered the Director of National Intelligence to declassify within 90 days all pertinent information pertaining to the Wuhan institute and COVID-19.

By all accounts, the release of the intelligence data of low confidence, will be couched in the most obvious and malignant terms. Regardless of the weight of evidence that continues to be discovered, the ruling elites in Washington will seize the opportunity to use the bogus lab-leak conspiracy theory to further their anti-China agenda.



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