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È possibile creare un virus in laboratorio senza lasciare traccia? La risposta dell'esperto

A Presa Diretta, in onda lunedì 14 settembre alle 21.20 su Rai3, parla per la prima volta in Italia il microbiologo Ralph Baric, il maggior studioso al mondo di coronavirus, tra i più grandi esperti nella costruzione di virus sintetici, autore della famosa chimera del 2015 di cui parlò il Tg Leonardo.

① 14/09/2020 11:43 CEST | Aggiornato 14/09/2020 14:17 CEST

HuffPost



Original source (in Italian):

https://www.huffingtonpost.it/amp/entry/e-possibile-creare-un-virus-in-laboratorio-senza-lasciare-traccia-la-risposta-dellesperto_it_5f5f3993c5b62874bc1f7339/

Archive:

https://www.huffingtonpost.it/amp/entry/e-possibile-creare-un-virus-in-laboratorio-senza-lasciare -traccia-la-risposta-dellesperto it 5f5f3993c5b62874bc1f7339/

The following is a translated version of the text in link above using google translate:

Is it possible to create a virus in the laboratory without a trace? The expert's answer

At Presa Diretta, broadcast on Monday 14 September at 21.20 on Rai3, the microbiologist Ralph Baric, the world's leading coronavirus scholar, one of the greatest experts in the construction of synthetic viruses, speaks for the first time in Italy, author of the famous chimera of 2015 which Tg Leonardo talked about.

09/14/2020 11:43 CEST | Updated 09/14/2020 2:17 PM CEST HuffPost

The microbiologist Ralph Baric, the world's leading coronavirus scholar, one of the greatest experts in the construction of synthetic viruses, author of the famous 2015 chimera of which Leonardo news spoke, speaks for the first time in Italy in an interview granted to PresaDiretta: "You can engineer a virus without leaving any trace. The answers you are looking for, however, can only be found in the archives of the Wuhan laboratory".

It is not true that the manipulations of the viruses in the laboratory would be seen, as has been repeated for all these months in the face of the mysterious origins of SARS-Cov-2. For at least ten years, in the two most advanced laboratories in the world, in North Carolina and Wuhan, where the pandemic broke out, researchers have used very sophisticated techniques called seamless, literally "seamless" thanks to which it is possible to combine genetic material of different types of viruses without leaving scars in the joints between one piece and another, as it used to be.

"If you want, you can choose to leave a trace, a kind of signature of your intervention. A bit like saying, this virus was made in Professor Baric's laboratory "he says - exclusively to Presadiretta in the investigation" SARS-CoV-2 IDENTIKIT OF A KILLER" broadcast tonight at 21.20 on Rai3 - Ralph Baric, professor of microbiology and immunology at North Carolina, which has been studying coronaviruses for thirty years.

"In the chimera we made in America in 2015 with the SARS virus, together with Professor Zheng-li Shi of the Wuhan Institute of Virology, we had left signature mutations, so it was clear that it was the result of genetic engineering. But, otherwise there is no way to distinguish a natural virus from one made in the laboratory ". The chimera, which we all heard about for the first time a few months ago because the 2015 news report from Tg Leonardo returned to the web, was part of a research project also funded by the American NIH to study bat viruses: Chinese and American researchers had inserted the Spike protein into the SARS virus, the one that allows the virus to enter human cells, and a supervirus capable of attacking humans was released.

So you rule out that SARS-CoV-2 is a laboratory chimera? we ask him. "Not with the viruses that have been sequenced and reported to date." Are the databases public? "Yes, the sequences can be downloaded. But then, I can't know if the researchers publish every single sequence. How could I know? There are millions of virus sequences...".

"In the databases there were sequences of a large number of SARS-like bat coronaviruses identified in China - explains Baric - And in that huge basin, one could imagine that there were strains that could have grown well in human cells. . The question in the scientific community was therefore: if a new strain emerges, is it capable of causing an epidemic or must it go through a series of mutations? That was what that 2015 experiment was for, and we now know that there are viruses in bats that are pre-programmed to jump from one species to another. If they do, they will reproduce well in humans. In that case we didn't have access to the viruses in China,

all we had was the sequence: you can chemically synthesize the sequence of the virus in the laboratory and then recreate the virus. "

Could SARS-CoV-2 have come out of the Wuhan laboratory? Perhaps we will never know, because the international investigation, which has been underway for months, has never started. And the Wuhan databases have disappeared: in the archives of the network we discovered that Professor Shi had made available to the scientific community a very rich database specialized in bat and rodent viruses that contained data relating to more than 20 thousand samples and viruses collected. over the years in different parts of China. It reported very detailed information: the GPS coordinates of the sampling site, the type of virus found, whether the virus had been sequenced or isolated (ie grown in cell cultures). The database provided for password access to consult data relating to viruses not yet published, with the only obligation not to disclose the information until the date of publication. However, since June the entire page has been removed from the web. Indeed, according to a portal that monitors China's scientific databases, the data were inaccessible as early as September 12, 2019. Why? What experiments were done in Wuhan?

The anomaly of this virus is investigated in the PresaDiretta investigation. It is not yet known which animal it came from, for Sars - a few weeks after it was identified as a coronavirus - the intermediate animal was found. And then the experiments that were carried out in the Chinese laboratory, financed by the USA; Gain of function experiments, which for a large part of the scientific world are as dangerous as playing with nuclear power.