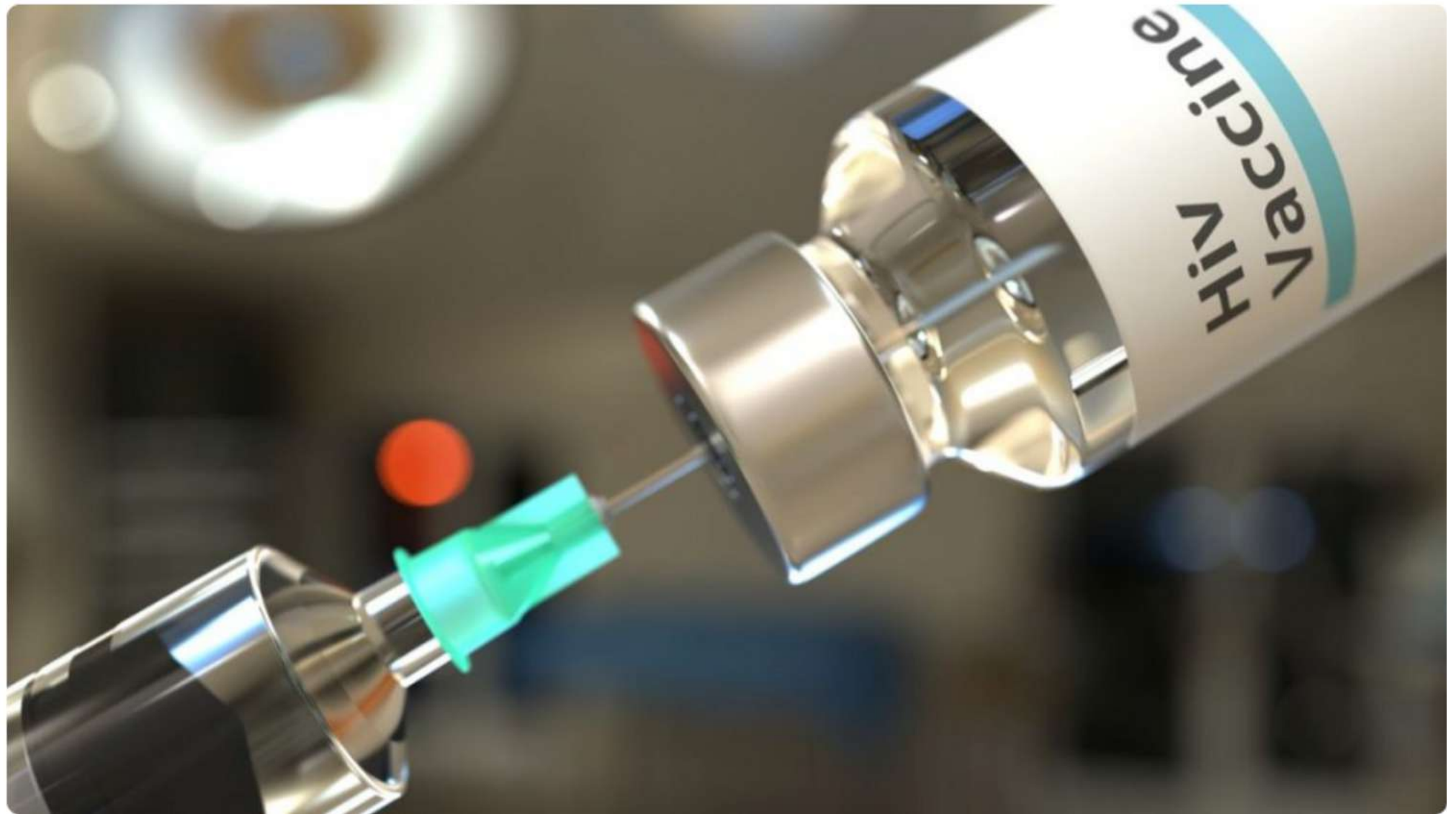


VIH : un vaccin particulièrement prometteur passe la première phase d'essais cliniques

L'approche novatrice employée pourrait également s'avérer efficace contre le virus de la grippe, l'hépatite C ou le paludisme



UNE VERSION ARNM PRÉVUE

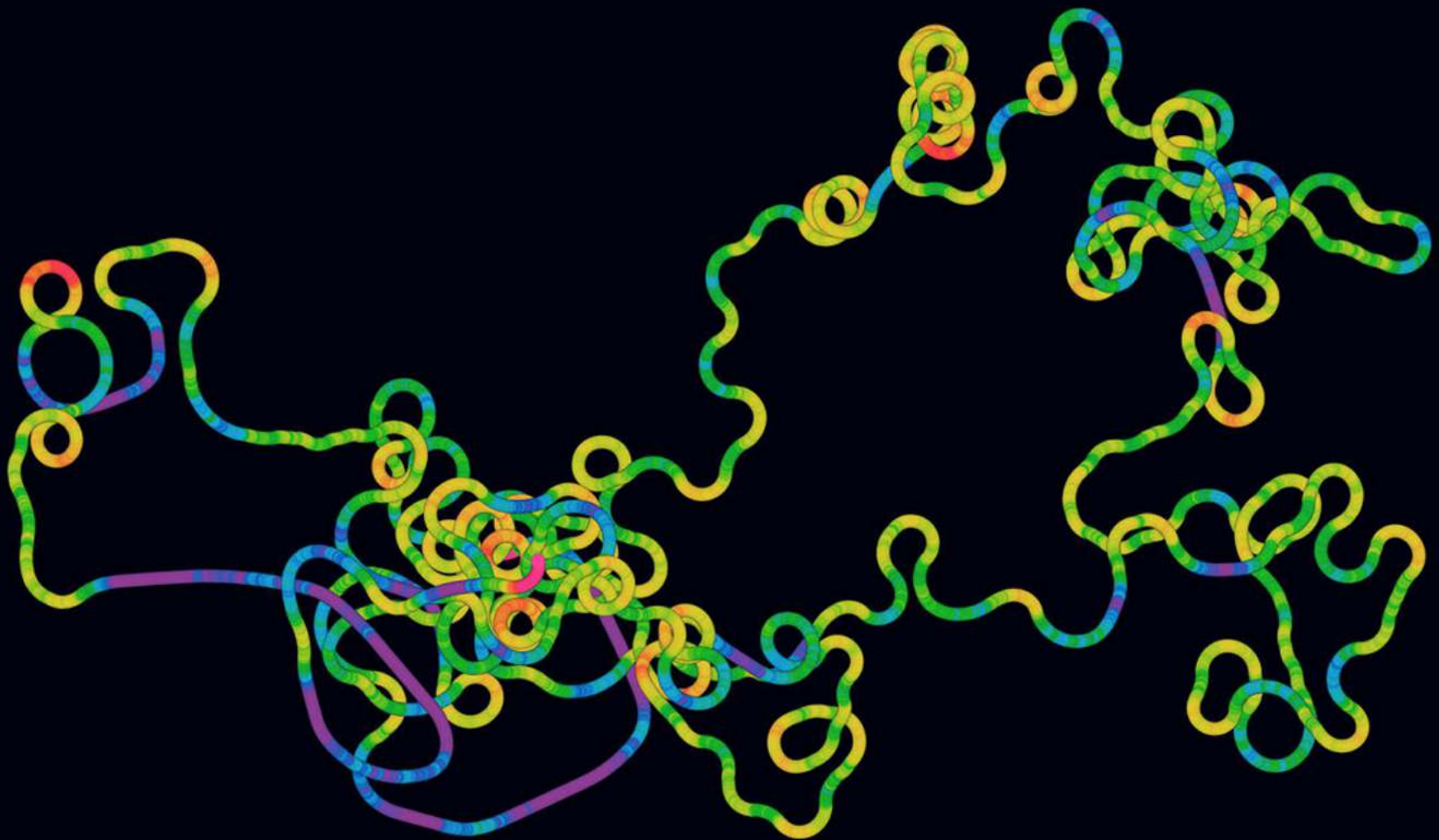
Planifiant actuellement de nouveaux essais, les chercheurs prévoient également de collaborer avec le laboratoire **Moderna** afin de créer une version **ARNm** du vaccin visant à induire les mêmes cellules B.

Les scientifiques estiment que cette nouvelle approche pourrait également s'avérer efficace contre d'autres agents pathogènes, comme le virus de la grippe, le virus de la dengue, le virus **Zika**, les virus de l'hépatite C et le parasite du paludisme.

*« Cet essai clinique a montré que nous pouvons stimuler les réponses immunitaires de manière prévisible afin de créer de nouveaux vaccins plus efficaces, et pas uniquement pour le VIH », a déclaré **Dennis Burton**, professeur au **Scripps Research**. « Nous pensons que ce type d'ingénierie vaccinale peut être appliqué à plus grande échelle, ce qui ouvrira une nouvelle ère dans la vaccinologie. »*

Source : **The Hill**

Par **Yann Contegat**, le 12 avril 2021



Critics decry access, transparency issues with
key trove of coronavirus sequences 10 Mar 2021

In December 2020, software developer Angie Hinrichs at the University of California, Santa Cruz (UCSC), applied for access to a labor-saving data feed from GISAID, a **nonprofit database** of viral sequences including those of the pandemic coronavirus, SARS-CoV-2. She wanted GISAID's data so she could display mutations on UCSC's **coronavirus Genome Browser**. That tool ties any position in the virus' nearly 30,000-letter genome to other scientific information, much as Google Maps shows gas stations and restaurants near addresses.

With more than 700,000 genomes from more than 160 countries, GISAID is by far the world's largest database of SARS-CoV-2 sequences. Access to the free, nonprofit repository has become vital to Hinrichs and thousands of other scientists and public health agencies tracking the virus' alarmingly rapid evolution.

But instead of getting a direct data feed, Hinrichs lost her existing access to two conveniently packaged GISAID files that are the next best thing. She emailed GISAID repeatedly pleading for restored access, but hasn't gotten it. Since December, she has had to download GISAID's sequences 10,000 at a time, with no access to most of the metadata unless she looks at each of the 10,000 sequences individually. As a result, she says, "My [phylogenetic] trees that use GISAID data are falling behind."

Hinrichs's experience is not unique. A dozen scientists spoke with *Science* raising complaints about their interactions with GISAID. They reported an opaque process of gaining access, unexplained interruptions once access was won, and phone harangues or threatening legal letters when they got on the wrong side of GISAID's strict rules against resharing data.

Many scientists who voiced criticisms declined to be identified for fear of losing GISAID access. They say that even as they race to study coronavirus evolution, they are walking on eggshells around their chief data supplier.

“I am so tired of being scared all the time, of being terrified that if I take a step wrong I will lose access to the data that I base my research on,” says one scientist who declines to be identified. “[GISAID] has that sword hanging over any scientist that works on SARS-CoV-2.”

In a statement, GISAID said, “Any individual who registers with GISAID and agrees to the GISAID terms of use will be granted access credentials. ...

On rare occasions, GISAID has found it necessary to temporarily suspend access credentials to protect the GISAID sharing mechanism.”

Both fans and critics emphasize that GISAID has provided an invaluable service during the pandemic, gathering many more coronavirus sequences than open-access databases like the United States’s GenBank. Even critics note that data are much easier to upload to GISAID than to open-access repositories, and that GISAID speedily curates sequences.

Many scientists trace what they view as a secretive, controlling organizational culture to GISAID's co-creator and head, **former Time Warner studio executive Peter Bogner**. GISAID "has a personality behind it that is fiercely protective of the organization [and] very insulted if somebody else ... is praised for SARS-CoV-2 data," Hinrichs says.

Bogner **has said** he invested several million dollars to **launch GISAID in 2008**. Its goal was to open up access to then-restricted avian flu sequences, and to protect scientists in non-Western countries against having their data scooped for publication or profit by requiring users to credit and try to collaborate with depositors.

GISAID, which stands for the Global Initiative on Sharing All Influenza Data, is today supported by private donors, governments, and nonprofits and is based in Germany; it says it remains "*independent* of government and corporate interests." With about 30 staff and more than 50 volunteers globally, it says it received €3.5 million in cash and in-kind contributions in 2020.