

News in focus

according to the Florida Keys Mosquito Control District (FKMCD), which is working closely with Oxitec on the project. Researchers and technicians will release bioengineered male *A. aegypti* mosquitoes, which don't bite, to mate with the wild female population, responsible for biting prey and transmitting disease. The genetically engineered males carry a gene that passes to their offspring and kills female progeny in early larval stages. Male offspring won't die, but instead will become carriers of the gene and pass it to future generations. As more females die, the *A. aegypti* population should dwindle.

The FKMCD approached Oxitec in 2010 about testing its approach in the Keys, because Florida was – and still is – experiencing an increase in mosquito-borne disease. In 2009, the state began seeing cases of locally transmitted dengue, and, a few years later, locally transmitted Zika.

Experiment launched

In late April of this year, project researchers placed boxes containing Oxitec's mosquito eggs at six locations in three areas of the Keys. The first males are expected to emerge in the first two weeks of May. About 12,000 males will exit the boxes each week over the next 12 weeks. In a second phase later this year, intended to collect even more data, nearly 20 million mosquitoes will emerge over a period of about 16 weeks, according to Oxitec.

Genetically engineered mosquitoes are an alternative to insecticides, which are used heavily in the United States to control insect populations. This has resulted in the evolution of mosquitoes that are resistant to insecticides.

"Unfortunately, we're seeing our toolbox shrinking due to resistance," said Andrea Leal, executive director of the FKMCD, at a press conference last week. "That's one of the reasons why we're really looking at these new innovative tools and new ways to control this mosquito."

To monitor the trial's progress, researchers will use capture devices to trap mosquitoes for study. They will measure how far the male mosquitoes travel from the boxes, how long they live, how effectively they squelch the wild female mosquito population and whether all of the females with the gene are indeed dying. Oxitec mosquitoes carry a fluorescent marker gene that makes them glow when exposed to a specific colour of light, which makes identification easier.

The biotech firm plans to present the results to the US Environmental Protection Agency (EPA), which gave the green light for the trial. The data will help the EPA to determine whether Oxitec can release the mosquitoes more broadly in the United States. The company is still testing them in

Brazil and other countries.

Opposition to the Florida field trial has been fierce from some residents in the Keys. Worried about being bitten by the mosquitoes or that the insects will disrupt the Florida ecosystem – and generally unhappy about being chosen as a test site – some have threatened to derail

“The fact that Oxitec was able to get the trial on the ground in the United States is a big deal.”

the experiments by spraying insecticides near the release points.

"As you can imagine, emotions run high, and there are people who feel really strongly either for or against it," says molecular biologist Natalie Kofler, who lectures at Harvard Medical School in Cambridge, Massachusetts, and is the founder of Editing Nature, an organization that advocates for responsible development and oversight of gene-editing technologies.

"And I can see how, if you didn't agree to this, it could be really concerning to have mosquitoes released in your neighbourhood."

Many of the concerns stem from the uncertainty of a new technology, says Kofler, who has been following this project for years. Oxitec has been engaging with the Florida Keys community to provide answers to queries. It explained, for instance, the very low likelihood that female mosquitoes with the lethal gene could reproduce. But many people don't have confidence in what they're hearing, because it's coming from a company, says Kofler.

Kofler is hoping that enough data are gathered to assess the mosquitoes' impact, including on other species in the Keys and local ecosystems, and that it's done "in a way that's transparent, and in a way that can make some community members feel better about the whole situation".

Oxitec employees have taken precautions against vandalism by placing their mosquito boxes on private, fenced-in properties, and not disclosing the boxes' precise locations to the public.

THE FLIP SIDE OF UNRESTRICTED VIRAL GENOME SHARING

Global-south scientists say open-access movement led by wealthy nations could exploit their COVID work.

By Amy Maxmen

"I was up all last night," says Nnaemeka Ndodo, a molecular bioengineer at the Nigeria Centre for Disease Control (CDC) in Abuja. He sequences coronavirus genomes during the day, and then analyses and uploads the results to an online database at night, working tirelessly alongside his colleagues. "We don't know Saturday, we don't know Sunday," he says.

Researchers around the world are racing to spot variants of the coronavirus SARS-CoV-2 so that they can determine whether the mutated viruses will evade vaccines or make COVID-19 deadlier. Like many scientists, Ndodo shares SARS-CoV-2 genome sequences in a popular data repository, GISAID, that requires users to sign in and to credit those whose data they analyse.

But a growing faction of scientists, mostly from wealthy nations, argues that sequences should be shared on databases with no gatekeeping at all. They say this would allow huge analyses combining hundreds of thousands

of genomes from different databases to flow seamlessly, and therefore deliver results more rapidly.

The debate has caught the attention of the US National Institutes of Health (NIH) – which runs its own genome repository, called GenBank – and the Bill & Melinda Gates Foundation, which has considered encouraging grantees to share on sites without such strong protections, *Nature* has learnt.

But many researchers – particularly those in resource-limited countries – are pushing back. They tell *Nature* that they see potential for exploitation in this no-strings-attached approach – and that GISAID's gatekeeping is one of its biggest attractions because it ensures that users who analyse sequences from GISAID acknowledge those who deposited them. The database also requests that users seek to collaborate with the depositors.

Fears of inequitable data use are amplified by the fact that only 0.3% of COVID-19 vaccines have gone to low-income countries. "Imagine Africans working so hard to contribute to a database that's used to make or



Microbiologist Christian Happi sequences SARS-CoV-2 samples in Nigeria.

update vaccines, and then we don't get access to the vaccines," says Christian Happi, a microbiologist at the African Centre of Excellence for Genomics of Infectious Diseases in Ede, Nigeria. "It's very demoralizing."

Getting credit

GISAID is the most popular repository for SARS-CoV-2 genome sequences, holding 1.4 million sequences as of 4 May. Researchers from under-resourced laboratories say it gives them a chance to participate in big-data analyses or do their own, because of the platform's terms on acknowledgement and collaboration. Without those, researchers such as Ndodo worry that the fruits of their fieldwork and lab work will be scooped up by computer scientists who aren't burdened with such tasks. Big-data analyses can result in top-tier journal publications – and that, in turn, might lead to lucrative grants and patents for technologies, such as diagnostic tests and vaccines.

Continental Africa and South America more than doubled the number of SARS-CoV-2 sequences they contributed to GISAID between January and April this year. For researchers at the Democratic Republic of the Congo's National Institute for Biomedical Research (INRB) in Kinshasa, the decision to share those sequences was initially fraught. While working in Guinea during the Ebola virus outbreak of 2014–16, one senior scientist was alarmed to learn that all of the specimens collected by African researchers were being shipped out of the country. Most of the scientific papers and patents on those samples were authored by scientists from wealthy countries. Labs in Guinea didn't sustainably benefit from that work and today remain unable to sequence samples.

So researchers at the INRB were wary of sharing SARS-CoV-2 genome data, says Eddy Kinganda-Lusamaki, a microbiologist at the institute. But after reviewing GISAID's crediting and collaboration requirements, Kinganda says, they decided to share their data before publication.

But such caution runs contrary to the growing open-source movement. As of 4 May, an online letter calling for researchers to put genome sequences in the public domain (see go.nature.com/3rtjg5) was signed by 778 scientists at universities and pharmaceutical companies – 99% of them based in

"If one is not careful, one will go back to the model of depositing data only after publication."

Europe, the United States and Canada. Rolf Apweiler, the co-director of the group that posted the letter in late January, the European Bioinformatics Institute near Cambridge, UK, tells *Nature*, "Sequencing is not for enriching the career of individual researchers, but for fighting a pandemic."

Tulio de Oliveira, director of the KwaZulu-Natal Research Innovation and Sequencing Platform in Durban, South Africa, agrees. But he counters that the most immediate goal for those sequencing SARS-CoV-2 is guiding their own country's outbreak response, and that governments listen most often to their own scientists.

Apweiler's letter caught the attention of NIH director Francis Collins recently. In a 21 April e-mail to dozens of international scientists

– shared anonymously with *Nature* – Collins links to the letter, along with news articles in *Nature* and *Science* about complaints over GISAID's data-sharing policies. He says global health funders, such as the NIH, are best positioned to set standards on sharing, and requests a meeting to discuss how to improve data access while protecting the interests of the scientists depositing data. Glenda Gray, president of the South African Medical Research Council in Cape Town, replied in the e-mail chain that if an open-access requirement comes to fruition, many scientists will stop sharing rapidly. "If one is not careful," she writes, "one will go back to the model of depositing data only after publication, which can take months or even years."

Collins did not respond to a request for comment from *Nature*.

Future requirements

The Gates Foundation is also talking about data sharing. It has told the Africa Centres for Disease Control and Prevention that, in the future, it might encourage grant recipients to share their results on open-access databases, says Yewew Kebede Tebeje, a microbiologist at the agency in Addis Ababa. A representative of the Gates Foundation says that GISAID or any accessible database suffices for sharing genome sequences, but did not answer *Nature's* question about future requirements.

An anonymous editorial posted on 4 May on the South African online news outlet *IOL* argues that a push from wealthy countries for open data is suspect, given how often scientists in the global south go unacknowledged (see go.nature.com/3upedvz). "A neocolonial mentality has long permeated the scientific community," the editorial says.

Fears of exploitation haven't changed Apweiler's mind, however. "The focus on low- and middle-income countries is bizarre because their amount of data is relatively little," he says. Africa has uploaded around 13,000 sequences to GISAID, and South America has uploaded 14,000 sequences, for instance, compared with about 380,000 from the United Kingdom alone.

But others note that, as COVID-19 rates drop in Europe and the United States, dangerous variants are more likely to pop up in low- and middle-income countries with few vaccines. Sequences from these places will therefore be in demand, says Nuno Faria, a computational virologist at the Institute for Tropical Medicine at the University of São Paulo in Brazil and Imperial College London. Because Brazilian researchers have shared data on GISAID, Faria points out, the P.1 variant, against which vaccines seem to be slightly less effective (P. Wang *et al.* Preprint at bioRxiv <https://doi.org/gjmwvx>; 2021), is known to now account for 82% of all coronavirus genomes sequenced in the country.