

New York COVID-19 Genomics Research Network Coalesces to Battle Pandemic

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Source: NYGC

A laboratory at the New York Genome Center

NEW YORK – A new consortium spearheaded by the New York Genome Center aims to foster and organize genomic COVID-19 research in the New York metropolitan area.

With approximately \$2.5 million in philanthropy funding to start, the [COVID-19 Genomics Research Network](#) plans to launch a number of research projects and to establish a data commons for storing and sharing results.

According to Tom Maniatis, CEO and scientific director of the New York Genome Center, the new effort fits in with the center's mission to foster genomics collaborations between research and medical institutions in New York. When the pandemic started to take hold of the city last month, he and his colleagues convened a local working group to discuss all aspects of COVID-19. That group has met online twice so far, attracting about 200 participants last week, and is scheduled to meet again later this month.

The network aims to engage in international COVID-19 research efforts and to get four local projects off the ground that will leverage the genome center's technical expertise and sequencing capacity. In addition, it plans to establish a data commons that will allow investigators to store, access, and analyze the data collected in these projects.

While there are no formal written agreements in place yet, there appears to be a lot of interest to participate, Maniatis said, both from NYGC members and from two companies, Illumina and Regeneron.

On the international side, the network plans to participate in the [COVID-19 Host Genetics Initiative](#), an effort led by the Broad Institute and the Institute for Molecular Medicine Finland (FIMM) that focuses on [host genetic factors](#) that influence disease severity in individuals infected with SARS-CoV-2. In addition, the network is part of a project led by [Jean-Laurent Casanova at Rockefeller University](#) to identify inborn errors of immunity that can lead to severe COVID-19 in otherwise healthy individuals.

The consortium also plans four research projects that will cover different aspects of the disease.

According to Mike Zody, NYGC's scientific director of computational biology, a viral sequencing project that is already ongoing will trace how the virus spreads over time and will contribute to existing databases, "so we can use that going forward to make estimates about viral spread and, when we get to that point, viral recurrence, and have a better understanding of how the virus is moving through the population." The genome center has the capacity to sequence 10,000 samples for this project, he said, both during the current wave of infection and, later on, as part of surveillance efforts. The center is already getting samples from Hackensack Meridian Health and from Weill Cornell, which will soon be joined by Northwell Health, and the project is open for other collaborators to join.

Several [ongoing coronavirus sequencing projects](#) at New York institutions will continue in parallel with this one, Zody said. "We would love to have them contribute data to the consortium effort but we don't see a need to move a protocol that's working for them already," he said. However, other member institutions don't have sufficient sequencing capacity, he said, so the NYGC can serve as a resource for them to get their sequencing done.

A second project aims to genotype up to 10,000 COVID-19 patients with varying degrees of disease severity in order to identify common genetic variants that associate with disease outcome. The plan is to partner with NYGC spinout Gencove to generate low-pass whole-genome sequencing data at relatively low cost and to impute variants.

Zody said that a number of institutions are interested in participating in this project but appropriate consent mechanisms need to be put in place before the first samples can arrive. "What we're hearing from the hospitals, in general, is that people are very happy to be part of a study, but this is an issue," he said. "We have to be careful not to be doing anything that's obstructing clinical care or that puts the research personnel under unnecessary risk, to be going into the hospitals where active treatment is going on."

A number of hospitals have already collected patient samples that are consented for sequencing, and others have ongoing biobank projects with permissions that could be extended. "For us right now, the logistical issue is making sure that we have protocols in place that are consistent with the consent from the protocols approved at the collecting sites," Zody said, "so we can have a smooth handoff of samples from the hospitals to us."

Another project, a collaboration with Casanova's international consortium, aims to recruit and sequence the genomes of COVID-19 patients at New York hospitals who are under the age of 50 and have severe disease but no comorbidities that would put them at risk. The center has sufficient capacity to sequence on the order of 1,000 genomes for this project, Zody said, depending on how many samples become available.

"The idea behind this is that these individuals may have very severe defects of immunity that we will be able to learn fairly quickly by sequencing whole genomes of a few people," he explained. "If that saturates and we will not find anything new, that will be the end point for that project." Maniatis added that the first samples from Casanova's cohort could become available for sequencing as soon as next week.

Lastly, a project focusing on functional studies aims to leverage some of the strengths of the genome center in single-cell genomics and spatial transcriptomics. The goal is to analyze blood and tissue samples from patients to learn how the infection impacts them, which could reveal disease mechanisms and potentially lead to new treatments. For this project, which might involve a few dozen samples in total, the center plans to partner with member institutions that can handle and help prepare infected tissue that contains live virus.

According to Maniatis, the genome center plans to provide its services for these projects free of charge to its partners. The \$2.5 million in philanthropy funding it has raised so far will only be the beginning, "and we're hoping we can raise much more," he said. He declined to specify a fundraising target or potential sources of funding, though the research network's website lists a number of funding opportunities from government agencies and others.

The planned data commons would be hosted by the NYGC. "We're working very hard on that but of course we have a lot of negotiations and discussions before this can be fully implemented," Maniatis said.

The hope is that patients participating in the research projects will share broader and deeper clinical data and medical history than what typically goes into public repositories, Zody said. This would allow for more detailed studies of clinical outcomes, even independent of genetics. "We are aware that other efforts on aggregation are going forward with this," he said. "Our hope is that we will be consistent with the methods and protocols that everyone else is using, so that all the data could be aggregated when we get to the point when that can happen."

Eventually, the network wants to make its data available to other researchers and contribute it to international data repositories like the European Bioinformatics Institute's COVID-19 Data Portal or dbGAP. "That's the whole point of our data commons," Maniatis said. "Obviously, there could be obstacles from our partners, but we're committed to that goal."

Zody said the network will ensure its protocols will allow for human genome sequence data to go into data repositories that researchers can access. "Obviously, those data are going to have to be accompanied by some clinical data about

the severity of [the patient's] COVID disease, and we're closely following the standards that are being set by the international group on host genetics," he said.

"We believe that the only way we can really be impactful is if we share the data widely outside of New York, so it can be compared to other datasets," Maniatis added. " The hope is that there will be a two-way sharing of data across the world."

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