

[MUSIC PLAYING]

My name is Gerald Mboowa. I'm a bioinformatics implementation expert at Africa CDC. Looking at the network-- we have the sample-referring network on the continent. So Africa has 55 member states or countries for that reason. And at the onset of SARS-CoV pandemic, different countries were at different levels of bioinformatics and genomics expertise. A country like South Africa was very much advanced compared to any other country in Africa when it came to pathogen genomics and sequencing itself.

So what happens is Africa CDC had to mobilise the available resources then. So Happi's (Prof Christian Happi) lab in Nigeria had to offer training and sequencing for a big number of the member states in Western Africa. And then also KRISP in South Africa had to offer its services to receive samples from different countries in Africa. UVRI in Uganda had to also offer services to receive SARS-CoV samples from different parts.

So each of these specialised sequencing facilities that were present then was opened up to receive SARS-CoV samples for sequencing outside the country itself. So UVRI received samples within Uganda and even outside Uganda. For example, Sudan, Somalia, Burundi, and all those samples are coming to UVRI.

Then Nigeria also-- the African Centre of Excellence for Genomics of Infectious Diseases also had received samples from that part of the continent. And also passages in their country received samples from that part of West Africa. So about seven to eight countries were assigned to collect samples and also ship them to the specialised sequencing facility for sequencing, and then results were sent back to the individual countries so that they can use them for decision-making in the different kind of circumstances they were in.

So the network that was set up almost a year ago has been working up to date, and we continue to see that we deliver within that network. We realised when SARS-CoV was initially hit the continent, some countries don't even have the sequencing capacity. In some cases, even the actual testing capacity was maybe thousands of kilometres away from even the countries themselves. So that network managed to-- , to date, has managed to deliver more than 30,000 SARS-CoV samples for sequencing across the different sequencing facilities.

At the beginning, we needed to sequence as much as we could from as wide a geographical region as possible. And that was based on the capacity that we had for sequencing. Every country has different capacities for sequencing. So you need to think about what you have available and what you can address with that capacity.

So when we started COG-UK, we started off with much lower sequencing capacity than we have right now. And we focused on that broad, random sampling and tried also to capture samples from the hospitals, from the severely ill patients. Now, as time has evolved, we've split our sequencing capacity into different priorities.

However, we've always tried to maintain a minimum of 50% of our sequencing capacity from random surveillance of community and hospital samples. And the other 50% has been split across other priorities, such as the severely ill patients. And that's for those in intensive care units. Also for National Core Studies so we can look at how the virus is spreading and how it changes in different populations, such as care homes and different populations in hospital. Also in prisons and other groups' population.

It's really important that we don't just focus on hospital samples. Yes, we want to understand why a virus is circulating in the hospitals and how it's affecting the patients, but we need to be able to spot what's also circulating in the community. If we want to detect new variants that are circulating in low frequency, we need to be sampling a random sampling set of individuals from the community so we can spot those new samples at low frequency and be able to respond as quickly as possible.

We are now at the stage where we have an algorithm where we can select samples at random from the community for sequencing. And this means that we can see a random representation of what's circulating in the community. And this helps to spot new variants that may be circulating at low frequency. This is what we've always wanted to achieve. It's difficult to get there at the beginning, but I think it's what we should all be working towards.

So there's a huge amount of questions that we can answer with genomics, but we really need to consider what capacity we have available and what is the key questions you need to address in your country at that time. And it's also important to always have a little bit of contingency. You don't know what's coming around the corner and you don't want to be maxed out every week. You want to have that little bit left aside so if a sample needs repeat sequencing, or if you get a new outbreak, or there's a new investigation of border samples, that you have that contingency so that you can do that sequencing rapidly. But it also means that you have the staff available that can respond because we need to build a sustainable system for the future of infectious disease genomics.

So my name is Carlo Lapid, and I am a bioinformatician at the Core Facility for Bioinformatics at the Philippine Genome Centre. One thing I've learned during the course of our effort is that getting good representative sampling during a pandemic, it's virtually impossible because it's a moving target. Different populations, different geographic regions get different case counts at different times, and it's a massive coordination.

Also I don't want to take credit because sampling isn't handled at the Philippine Genome Centre. We are working in cooperation with our Department of Health, specifically the Epidemiology Bureau at the Department of Health, who really does the hard work of coordinating with who knows how many clinics and testing centres, and so on, in order to collect samples and send them over to us for sequencing. They also make a lot of decisions regarding which samples get sequenced regarding on whatever priorities they have with cases they need to investigate, which can depend on so many factors that are outside of our control.