

## **OC5 2-15 establishing genomics surveillance**

[00:00:16.79] And it's wonderful that we have you guys here because you have worked, I think, during the pandemic actively. And we got a lot of help from your teams in making sure that we have a lot of surveillance data from all over the world.

[00:00:31.13] And how is your experience? I guess it must be stressful. Tell me about your work in the Caribbean. You established your surveillance team there.

[00:00:41.75] Yeah, so we started off our work on SARS-CoV-2, the virus we didn't work on before. And we didn't have capacity to do any sequencing in the Caribbean, at least in the English-speaking Caribbean. We started off as a little research project, just to establish some sequencing capacity.

[00:00:58.91] And then when the variants of concern emerged, we converted into a sequencing service for several countries in the region. And we were more involved in more formal surveillance and interacting with the Ministry of Health and things like that. So it was stressful. It was stressful, it's a lot of work.

[00:01:18.50] And how did you manage with the bioinformatics? Because I think it's something very important. Very often people think, oh, surveillance, just sequence it. But really to look at the data is important, as well.

[00:01:31.85] Right. So luckily, although we didn't have sequencing capacity in the region before, at least in internal Tobago, luckily, we had been working on virus evolution for a while. So we were very familiar with the phylogenetic tools and the bioinformatics and things like that that we've used on other viruses. That aspect of it, being a user of the tools, was not an issue for us.

[00:01:54.05] What was more difficult was adapting the sort of workflow and tools and managing the data and stuff. And that needed someone who had computing and computer coding skills. That is what we were missing. And it took us a while to get that. And once that was there, we did a much better job.

[00:02:14.01] And I think the other thing that was really useful was the collaborations we had with people overseas who were able to give us a lot of support throughout the entire thing. So it was very useful.

[00:02:28.35] You were asked about working well. What's your thought on your work during the pandemics and what happened in other countries?

[00:02:36.99] So I think the key to our success was being part of the COG-UK consortium. So we were involved right from the start of sequencing Scottish tissue samples, primarily. And we were able to use the Arctic bioinformatics pipelines, which made generating the genome sequences very straightforward. And then we were able to upload that data to the COG-UK framework, and then COG-UK were then able to upload that to GISAID to share globally.

[00:03:04.80] So I think that was the key, was having already publicly available tools, pipelines to share data quite easily and generate the data quite easily. We did have issues with, once you went from 100 sequences to 10,000 and then a million, things started breaking, and things needed to be tweaked to cope with the kind of unique amount of data. But it all worked out in the end, I think. It was good.

[00:03:31.13] We never reached a million.

[00:03:32.30] [LAUGHTER]

[00:03:33.04] Soon, soon.

[00:03:34.28] I don't think anyone expected it to reach a million.

[00:03:37.34] [INTERPOSING VOICES]

[00:03:38.13] But it went far beyond it.