

Hello, my name is Thanat Chookajorn from Mahidol University, MIMS. I'm delighted to share my thoughts on running a genomic surveillance programme in Southeast Asia and, most important of all, our experience in working with local partners to generate impacts. The work shown to you has been made possible by my colleagues at COVID-19 Network Investigation Alliance, CONI. We are grateful for the support from our public health partners and funders.

At the start of the pandemic in early 2020, a group of researchers with links to Thailand formed a team to do genomic surveillance for the country. We work with local hospitals and health officials to run surveillance and to assist in outbreak investigations.

The data was analysed by the high performance supercomputer platform ThaiSC. And it has been our policy that every sequence with sufficient quality will immediately and automatically be shared on GISAID. We also run a local Nextstrain build specific to Thailand and Southeast Asia. This is to allow scientific and health care communities to visualise the evolving genomic repertoires in real time.

Of course, the work allow us to see the importation events into the country. It also reveals the lineage compositions of SARS-CoV-2 in Thailand. I'm sure that in the training material from COG-UK, you will be able to learn about these useful tools. But the focus of my presentations is on how to generate impacts using genomic surveillance data.

And from our experience, the genomic size shown in the last two slides are important. But to guarantee impacts, it is inevitably important to work on what the local health communities need. Running an outbreak investigation is perhaps a low-hanging fruit.

I'm sure that by now those of you who studied the material could see that genomic sequencing reveals more than the types of variant. It could show the connectivity over time of cases. This is very helpful in tracking highly contagious SARS-CoV-2.

Working with the local health officials, we combined the genomic and epi-[demiological] data to track the events leading to an outbreak at a quarantine facility in Bangkok by identifying which individuals were the source of the outbreak and track how the virus got transmitted. More importantly, the resolution provided by general data allows to see what is the weakness in the system which leads to the changes in policy, improving the work conditions of health care workers at a quarantine facility in Thailand.

And there is another example, perhaps on a larger scale. And this came from our commitment for a quick turnaround time and immediate data sharing. So after about one year of running surveillance, there it has been known in the community that we routinely perform surveillance. And our data sharing standard is also known to the community.

When local health officials suspected an unusual cluster in the most southern part of Thailand, we were approached to join the investigation. We flagged a cluster of Beta in Thailand. And we suspected that they were likely to come from Malaysia.

But it was not surprising that for a disease like COVID, the report of Beta would be politically and scientifically scrutinised. But by having a clear standard of how to release the data and how to analyse and how to share them on GISAID, it allows everyone to see that, ah, this Beta cluster, they seem to come from another country, not from the quarantine, and we could link to the source and the chains of transmission.

It allows the public health resource to be allocated in time. And within less than 24 hours, a lot of help was sent to the region. And we are proud to say that this Beta variant was the only VOC identified to have a local transmission that was largely contained in Thailand thanks to the dedication of the local community and health care workers.

And the final example is my favourite one is the cluster at a market at outskirts of Bangkok called the Pornpat. So let me give you some background. This market, red circle here, it is located very close to the biggest transportation hub in Thailand, the green box. And you can see that they're very close.

And in January of 2021, there was a cohort there that got that got controlled very quickly. But later in February, a month later, a new outbreak arose, a bigger one even. And at the time, it was suspected that the transportation of merchandise from other provinces might be the source of the second outbreak.

We were asked to join the investigation. And we compare the populations in January and February, keeping in mind that we also tracked the surveillance data at the population scale as well. And we found that the virus causing the outbreak in February was in fact the direct progeny of those from the outbreak in January. Basically, there is a hidden reservoir there.

When we shared the information through the public health authorities, it became clear to everyone that this second peak, the bigger one, is likely to come from the populations of people who did not get tested in the first round. And the reason was this market, people working there, people live with-- people living in the vicinity, they need the market to work, to survive.

It may be a foreign concept for some of us to understand that some for these folks they need to work to be able to get food for that to their family on every particular day, so they must work. And they were afraid that if they get tested, if they were found to be positive, the market will remain shut down.

And it takes local health officials, the local authorities to go door to door to meet these people, to share with them that it is the government's goal as well to reopen the market, to convince them that they need to come out to get checked and because that is the only way that everyone can help one another to open the market again.

And you can see that with this big cluster when the launch happened is that more people can get tested. It came down. And you can see that we have this graph showing the linkage of this population.

But it's meaningless without these people on the left who engage the public to convince people that they need to come out. Genomic surveillance data is important. It acts like a map. But it depends on the people, to the authorities, to the public to work together to contain COVID-19.

And I would like to end by mentioning that to do genomic surveillance, it means that one has to interact with multiple partners, with multiple organisations. I'm sure that during that process, you would hear these words. They're shown here.

And it's important to keep in mind that the people, that it's always about the people. Buildings, organisations cannot talk, cannot ever demand something. So we need to be patient, be kind to people who work there because the concept of data sharing may not be something that they're used to.

And if we are kind and stick to scientific and ethical standards, some people will start to appreciate the importance of data sharing, transparency, and good data QC. And when some of those people start to become the converts, then it's our job to help them achieve their goal and to generate impacts.

I'm counting-- we are counting on every one of you. It has been clear that the only way for humanity to get out of this pandemic is to not leave anyone behind and that your contributions to genomic surveillance will be important. Thank you for your time and attention. Feel free to say hello when we meet at the end of the pandemic. Thank you.