

OC5 TIGS Genomics and wastewater

[00:00:02.11] Hello. My name is Farah Ishtiaq. I'm a scientist at Tata Institute for Genetics and Society. We lead the environmental surveillance programme for SARS-CoV-2 and other infectious diseases in Bangalore.

[00:00:16.51] Today I'm going to give a brief overview of how wastewater sampling and genomic surveillance can help us understand the diversity and distribution of infectious agents in our environment.

[00:00:29.70] Wastewater-based epidemiology is a population-wide monitoring tool, and it can be used for pathogens that can be excreted via human waste and can be found in sewage network. Wastewater monitoring has been used for a long time for monitoring many enteric pathogens, especially polio.

[00:00:49.42] And more recently, wastewater monitoring has been used as a complementary tool to track the rise and fall in COVID-19 cases. We have been combining it with genomic surveillance, which forms the backbone of monitoring for SARS-CoV-2 pandemic.

[00:01:07.42] So unlike clinical samples, wastewater-based monitoring collects sequence data at a community level which actually represents the population. So when you sequence these samples, you capture abundance and diversity of lineages circulating in there at the community level.

[00:01:25.35] And these data can be analysed in any ways. For example, wastewater genomic surveillance helps to gain insights in how the virus populations are changing, how the virus is evolving. And most detection of SARS-CoV-2 in wastewater have been used to correlate with the COVID-19 incidence data.

[00:01:47.03] But we have been combining it to understand what exactly is driving this rise in cases. So for example, here you see in this figure that you see a spike in cases going up here, which has been a real concern for the city very recently.

[00:02:02.36] But when we look at our data, we see a huge combination of BA.2 sublineages suddenly appearing in the community level, which helped us to understand there is not a new variant of concern in the population, but it's just a mix of lineages which is causing a spike in the viral load.

[00:02:24.32] And when we compared this data with the clinical data which has been submitted in the GISAID repository, it helps us to understand how a significant proportion of people at a community are infected with certain variants in a population and shedding the virus. So basically it allows you to explore the emergence of new variants that might have escaped in the clinical testing as well.

[00:02:53.25] And once you have this relative abundance and diversity data, you can analyse it using any kind of modelling to understand how the temporal trend is changing, and also at a spatial level as well.

[00:03:06.68] These data have been really useful for us to identify the disease hot spots in the city. So for example, in our city we have a well-defined sewage network, and we know the catchment area.

[00:03:18.37] By plotting the viral load, we know which areas are facing a significant rise in the COVID cases. But by combining our genomic surveillance, we know what variants are causing that spike in the viral load, and it helps us making very informed policy decisions.