COVID Information Commons (CIC) Research Lightning Talk

Transcript of a Presentation by Helena Solo-Gabriele (University of Miami), June 11, 2024

Title: *Wastewater Based Epidemiology Beyond the COVID-19 Pandemic: Opportunities and Next Steps*

Award CIC Database Profile

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Youtube Recording with Slides

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Transcript

Helena Solo-Gabriele:

Slide 1

Yes, I just presented on this slide, so I will continue on.

Slide 2

I wanted to start with our acknowledgements. This project was a huge team effort, all the way from the president of the University, including faculty, staff, and students.

Slide 3

I also wanted to acknowledge the many departments and units of the University of Miami, including the CFAR Center for AIDS Research, which is also part of the University of Miami Weill Cornell Medicine and also MetaSUB.

Slide 4

Our sample analysis plan was designed to split the sample into three splits. One was sent to the Center for AIDS Research where it was analyzed by Dr. Mark Sharkey using a new innovative technology called Volcano Second Generation PCR. That was our backbone for our rapid response. We were able to turn around samples within 12 hours. We also sent samples to the Onco-Genomic Shared Resource where they were analyzed by RT-qPCR for comparative purposes. Also at the Onco-Genomic Shared Resource, we had the samples analyzed for variants using a deep targeted sequencing approach. Samples were also sent to Weill Cornell Medicine where they were analyzed by Metatranscriptomics using RNA-seq. And all the bioinformatics were done through Weill Cornell Medicine.

Slide 5

All of our sample collection plans were mapped to human surveillance programs at the University of Miami. We had an extensive testing, tracking, and tracing program of our students and faculty and staff. We also at the university hospital had access to electronic medical records. We also had access to zip code level data through the Florida Department of Health. Through Miami Dade County Public Schools we had information on absenteeism. The most extreme aspect of the pandemic were the lockdowns which were motivated by the hospitals getting overwhelmed.

Slide 6

We know that from the wastewater - the hospitalizations can be predicted from the wastewater. Here, we have a black line corresponding to the hospitalizations. The green corresponds to the wastewater numbers. What we found throughout the pandemic is that - early during the pandemic, a small amount in the wastewater represented a lot of hospitalizations. As we were going through the various phases of the pandemic, the slope flattens so that now we're still seeing it in the wastewater but it's not resulting in as many hospitalizations.

Slide 7

In terms of the variance, on the right, we see the colors showing the different variants in both the clinical samples and the wastewater samples. They were both tracking each other. From the wastewater we can also see the variance. On the left hand side we see the relative timing of the variance observed in the wastewater versus the clinical samples. We see that for the Delta variant, for example, we saw it in the wastewater one week or seven days prior to seeing it in the clinical samples.

Slide 8

In terms of the hospital data, we also were able to evaluate comorbidities and we were able to observe correlations between the hospital wastewater SARS-CoV-2 numbers and the number of patients. Also, early during the pandemic, with remdesivir administration. Also from the hospital wastewater we were able to observe the Monkeypox virus in the wastewater and we were able to compare that to the number of patients in the hospital. It coincided in time. Similarly, for Candida auris - a fungal pathogen - we were able to correlate the presence of Candida auris in the wastewater with the presence of Candida auris patients in the hospital. Now, for Candida auris, not only were we able to see this fungal pathogen molecularly, we were also able to culture it as well.

Slide 9

So our next steps are really focusing on additional targets. We've teamed up with another group at Yale University. We've downloaded data from a wastewater scan from Biobot - all of these different laboratories are analyzing for SARS-CoV-2.

Slide 10

Just to give an update as to where they all stand - this is positivity or positive cases in Miami Dade County. You can see, the number of cases are decreasing over time because of - people are not going to get tested, but if we divide by the number of tests so the percentage that are positive amongst those who are tested, we're still seeing significant positivity and it's remaining pretty consistent over time. If we compare that to the wastewater from all the different labs, again and we see the correlation with the Delta wave, during the Omicron wave, between the wastewater and the positivity, and also, during the post-Omicron waves. We're seeing consistency across all the different labs.

Slide 11

In addition, from the shotgun sequencing as you can see on the green to the right. What's fascinating about the sequencing is now we can see abundances of pathogens directly. In the past, typically, you couldn't get to the pathogen level, but the green shows the bacterial pathogens that are being observed in the wastewater from sequencing. Then also from the RNA sequencing, we can even see viral pathogens inclusive of norovirus and Aichi virus.

Slide 12

In addition to that, we can see antimicrobial resistance genes. We found that they were significantly higher and more diverse in the hospital wastewater compared to the wastewater treatment plant. As you go downstream, through the sewer system, we're seeing lower levels and less diversity.

Slide 13

We've also teamed up with a group called Phase genomics and Phase genomics has a very unique technology where they can provide host attribution to AMR genes. So, for example, the host of the bacterial host of Prevotella there's two antimicrobial genes that are shown by the blue stripes here. Those two AMR genes are found in the genomic structure of the bacteria.

Slide 14

Our next steps are focusing on targets beyond SARS-CoV-2 and we're looking at air and surface sampling as well as wastewater. We're very excited about the sequencing and the target agnostic analysis provided by sequencing. The big challenge is how do we interpret all of this information that we're getting from wastewater - getting the clinical data to match up to the wastewater so we can know what it all means? This is one of the challenges in putting this information together. Then, of course, data simulation - trying to put the wastewater data with the human health data automatically so that reports can be generated in a faster fashion.

Slide 15

And that I'd just like to say thank you. My email is here if you have any questions. We have our publications shown here as well. Thank you.