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Coronavirus Standards Working Group Meeting Summary

Dear Colleagues –

Thanks so much for another lively and interactive meeting on genomic surveillance this morning -- thanks to Brian Krueger for sharing the super work he's led at LabCorp to build a system for "at-scale" genomic surveillance. Pandemic-scale means they've done more than 40M PCR tests and sequenced more than 70000 SARS-CoV-2 genomes since last March.

I started us off with a update on the Viral RNA Harmonization Study, summarizing the data we've received so far ([see my slides linked here](#)) and the logistical dashboard, I briefly reviewed the recent progress considering the Serology Harmonization Study, and noted that Jack Collins of the NCI FNL is moving forward to lead development of a set of SARS-CoV-2 Genome Reference Samples -- we will work with Jack's team to help! The RNA Harmonization Study team will have an open, focused follow-up to review preliminary analysis of the Viral RNA Harmonization results together.

[Brian's slide deck is linked here](#) -- thanks to LabCorp for their leadership and for presenting their work so openly in our working group!

As so many of our presenters have brought to us, we got a front-line review of the challenges of operating a lab in the pandemic. Brian showed us LabCorp's experience with the supply-chain logistical challenges, and how they met those through innovation and systematic processes to cover their bases. There are definitely lessons to bank to prepare for next time.

Brian reviewed the overall approach of high throughput robotics to "cherry-pick" residual extractions from positive samples and developing a system to get those sequenced in high-throughput on a PacBio Sequel II system using the "HiFi" circular consensus mode --

this yields Q50 sequence data that can be reliably analyzed for variant calling. The system has been optimized over the past year to yield turn-around-times of a few days, a key performance metric if genomic surveillance is going to support public-health in real-time. They can sequence 3500 samples/week, and have deposited more than 30000 samples in GISAID since January '21.

There are many more details in Brian's slides, including some animations that will be available in the deck on the JIMB website in the next few days -- linked in this email is the PDF version. I recommend watching Brian's talk on our recording if you missed it this morning!

[The meeting recording is here](#), and there is a transcript of the audio, and the chat is downloadable.

Troy Kemp will present on developing the US SARS-CoV-2 Serology Standard next week!

Cheers and stay safe!

Marc

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