[MUSIC PLAYING]

So obviously, over the last two years, we've learned a huge amount. And how do you think that's going to help inform what happens the next time a dangerous pathogen enters the population?

All the lessons that we've learnt so far are going to contribute towards handling a pandemic in the future. And now that sequencing has become so ubiquitous in hospital settings, it's going to be much easier to monitor pandemics and kind of preempt these health issues in the future.

I think it will be a lot easier to roll out as well. I think coming from a hospital perspective, there's been a lot of advancement in understanding of genomics data. So originally when we first started giving out data to the clinicians, they were like, oh, what's this, what can I do with this? Whereas now they understand variants, they understand what that means when you're saying that this links to this particular one. And I think it definitely will be an easier uptake with that learning early on. So it's not just learning from us as scientists, but it's learning for those people who are wanting to use that data as well.

And I think that's probably true for the population at large. I think everybody now knows what you mean when you say about a variant. So understanding how viruses mutate, that just has a huge impact just having that brief understanding and knowing the benefits that sequencing can have on helping to monitor it in almost real time, which is essentially what we've been doing.

This virus has changed considerably since November 2019. And yet, we've used that information to help design the vaccine. We've helped use that information to identify new drugs that can help people that have caught it. When you think about what's happened over the last two years, it's really quite amazing.

What would you say are the biggest lessons you've learned throughout this process are?

That's a really difficult one. I don't think, if we knew what we knew now, we'd have done things in the same way. I think everything would happen differently. I think we did the best that we could with the information that we had at the time. And that information changed and improved, and we went through and everything was developed. I think the next time we will be far more prepared to set something up to set up surveillance operations, and as Sharon has already said, understand the benefits that can have in a clinical context.

But I think if I was going to give myself one piece of advice thinking ahead to the future, it would be making sure to build in redundancy to the system. I was very scared through most of the work that we were doing because most of the work we only really had one bioinformatician on the team, which was myself. So I was very conscious that if anything was to happen to me, that would really cause a problem for the whole system because nobody else was really in a position to be able to analyse that data. So really, redundancy, I think, is essential, along with the infrastructure that we've now put a lot of effort into building up. But how about yourself?

For me, I would say don't be afraid to make mistakes. When I started I didn't have loads of experience, but I learned a lot along the way. And then from the lab side of things, definitely having those single-use aliquots with unique batch numbers really helped us to prevent contamination when it did occur in the lab and to find it.

I think my take-home message is that you don't need a lot of samples or a lot of data to make a big impact. Those first few runs that we did, those first few weeks, we were providing data to our clinicians to sort of help with management of patients and potentially dealing with a potential outbreak.

So even in those first 20 to 24 patients, a lot of that information that came out was really useful. So you don't need to be running thousands of samples with a huge team and a huge lab team. We started out with barely anything. We started out with, in fact, borrowing and stealing from across the hospital in the University. We were using class II hoods instead of PCR hoods. We were clambering with just using single channel pipettes rather than multichannel pipettes. You can still do a lot with a small team and small amounts of equipment and still achieve a lot.

Well, thank you very much. Angie, Sharon, it's been absolutely fantastic reminiscing over how the past two years has really gone for this project. And I hope it's has been very interesting for you, too, to hear about how we've gone from a very small start to having a very large impact through the COG-UK Consortium. And if you have any specific comments or questions, please do put them below in the forum. Thank you.