[MUSIC PLAYING]

My name is Dr. Catherine Ludden. I am director of operations for COG-UK. Prior to joining COG-UK, I worked at the European Centre for Disease Prevention and Control, where I designed and developed genomic surveillance systems for antimicrobial-resistant pathogens. In addition, I received a fellowship from the Wellcome Trust. It was a Sir Henry Wellcome Fellowship, where I looked at the transmission dynamics of antimicrobial-resistance pathogens from a One Health perspective.

At the beginning, we needed to sequence as much as we could from as wide a geographical region as possible. And that was based on the capacity that we had for sequencing. Every country has different capacities for sequencing. So you need to think about what you have available and what you can address with that capacity.

So when we started COG-UK, we started off with much lower sequencing capacity than we have right now. And we focused on that broad, random sampling and tried also to capture samples from the hospitals from the severely ill patients. Now, as time has evolved, we split our sequencing capacity into different priorities. However, we've always tried to maintain a minimum of 50% of our sequencing capacity from random surveillance of community and hospital samples.

And the other 50% has been split across other priorities, such as the severely ill patients-- and that's for those in intensive care units-- also for national core studies, so we can look at how the virus is spreading and how it changes in different populations such as care homes and different populations in hospital, also in prisons and other groups population. It's really important that we don't just focus on hospital samples. Yes, we want to understand what virus is circulating in the hospitals and how it's affecting the patients. But we need to be able to spot what's also circulating in the community.

If we want to detect new variants that are circulating in low frequency, we need to be sampling a random sampling set of individuals from the community so we can spot those new samples at low frequency and be able to respond as quickly as possible. We are now at the stage where we have an algorithm where we can select samples at random from the community for sequencing. And this means that we can see a random representation of what's circulating in the community. And this helps us spot new variants that may be circulating at low frequency.

This is what we've always wanted to achieve. It's difficult to get there at the beginning. But I think it's what we should all be working towards. So there's a huge amount of questions that we can answer with genomics. But we really need to consider what capacity we have available and what is the key questions you need to address in your country at that time.

And it's also important to always have a little bit of contingency. You don't know what's coming around the corner. And you don't want to be maxed out every week. You want to have that little bit left aside.

So if a sample needs repeat sequencing or if you get a new outbreak or there's a new investigation of border samples, that you have that contingency, so that you can do that sequencing rapidly while it also means that you have the staff available that can respond. Because we need to build a sustainable system for the future of infectious disease genomics.