OFFICIAL REPORT
AITHISG OIFIGEIL

COVID-19 Recovery Committee

Thursday 15 December 2022

Session 6

The Scottish Parliament
Pàrlamaid na h-Alba

Thursday 15 December 2022

CONTENTS

COVID-19 RECOVERY COMMITTEE
28th Meeting 2022, Session 6

CONVENER

*Siobhian Brown (Ayr) (SNP)

DEPUTY CONVENER

*Murdo Fraser (Mid Scotland and Fife) (Con)

COMMITTEE MEMBERS

*Jim Fairlie (Perthshire South and Kinross-shire) (SNP)
*John Mason (Glasgow Shettleston) (SNP)
Alex Rowley (Mid Scotland and Fife) (Lab)
Brian Whittle (South Scotland) (Con)

*attended

THE FOLLOWING ALSO PARTICIPATED:

Mike Gray (NHS Lothian)
Professor Rory Gunson (NHS Greater Glasgow and Clyde)
Dr Rachel Helliwell (Scotland's Centre of Expertise for Waters and the Hydro Nation International Centre)
Professor Matthew Holden (Public Health Scotland)
Professor Sharon Peacock CBE (COVID-19 Genomics UK Consortium)
George Ponton (Scottish Water)
Peter Singleton (Scottish Environment Protection Agency)
Dr Kate Templeton (NHS Lothian)

CLERK TO THE COMMITTEE

Sigrid Robinson

LOCATION

The David Livingstone Room (CR6)

Scottish Parliament

COVID-19 Recovery Committee

Thursday 15 December 2022

[The Deputy Convener opened the meeting at 09:11]

Decision on Taking Business in Private

The Deputy Convener (Murdo Fraser): Good morning, and welcome to the 28th meeting in 2022 of the COVID-19 Recovery Committee. We have received apologies from Brian Whittle MSP, and from our convener, Siobhan Brown, who has been unexpectedly detained but might be able to join us in the course of the meeting.

The first agenda item is to decide whether to take in private item 4, which is consideration of our approach to our inquiry into long Covid. Do members agree to take item 4 in private?

Members *indicated agreement.*

Covid-19 Surveillance

The Deputy Convener: We move on to item 2. The committee will hear from two panels of witnesses on Covid-19 surveillance.

The first panel will give evidence on waste water surveillance. I welcome to the meeting: Dr Rachel Helliwell, the director of the Centre of Expertise for Waters—CREW—and the Hydro Nation International Centre; George Ponton, head of research and innovation at Scottish Water; and Peter Singleton, research, innovation and evidence manager at the Scottish Environment Protection Agency. They all join us remotely.

I thank the witnesses for giving us their time and for their written submissions. We will allow an hour or so for the evidence session. I will start with some questions, then ask my colleagues to come in. If any of the witnesses would like to respond to a question that is not directed specifically to them, they should put an R in the chat box, then we will be able to bring them in. I am keen that everybody gets as much of an opportunity to speak as possible.

I ask each of the witnesses in turn, starting with Mr Ponton from Scottish Water, to tell us a little bit about their experience with waste water testing, how it worked in practice, what the challenges were and what they have learned from it for the future.

George Ponton (Scottish Water): Good morning, everybody. The waste water sampling programme was set up initially to support a piece of research that the Roslin institute wanted to instigate. We worked closely with Rachel Helliwell's team at CREW to set that up.

The experience of the programme was that, initially, a lot of risk assessments had to be set out. When the programme started, we were all in a bit of an information vacuum. We did not know what the transmissibility of Covid was and there was a lot of concern among our operatives as to whether there might be transmission from waste water. That was partly why we joined the research project with the Roslin institute.

09:15

Once we had carried out the necessary risk assessments, established that there was no risk and made sure that our operatives had the right protective equipment, sampling at the waste water treatment works was relatively straightforward. We already carry out operational self-monitoring and regulatory sampling at our waste water treatment works, so access to waste water at the inlet of the waste water treatment works—the area that we

targeted for the surveillance programme—was relatively easy to set up.

Once we had the programme up and running, and in discussion with some of the health boards, we started looking at the opportunity to sample in the networks. That was a little more challenging. The waste water networks are designed to drain foul and surface water from communities; they are not designed in a way that allows discrete sampling in communities.

We had discussions with some local authorities that wanted to get better information in areas where results from clinical or polymerase chain reaction testing were not coming through. That, too, was a little more challenging. There was a long lead time to set up that sampling programme. We had to do a lot of desk work to identify which areas drained into which parts of the network and which cross-flows were coming from other networks that were not under our surveillance.

There is also a health and safety aspect to sampling in sewers. We established that anything deeper than about 3m was unsafe. Anyone working on the surface is effectively working at height, so sampling anything deeper than about 3m became problematic.

We learned that there is a consistent flow at waste water treatment works. It is also possible to set up auto-sampling, in which you take a sample every 15 minutes or every hour to get a combined sample for a 24-hour period. That gives a better sample. In the network, you are dependent on what is flowing in the sewer at any given time because you are just taking a grab sample. When the sampler turns up and drops a container into the sewer flow, they get whatever is there; it is just a snapshot.

There were a number of challenges, but the programme worked well overall. I commend our staff across scientific services, waste water networks and operations for their efforts in challenging circumstances during the Covid pandemic.

The Deputy Convener: Thank you. Before I bring in the others, I have a couple of follow-up questions based on what you said.

How many test points were there across the country? What were the resourcing implications for Scottish Water in undertaking that work?

George Ponton: I cannot remember the exact number, but the initial programme covered 50 per cent of the population. SEPA identified target waste water treatment works that would give a representative sample of 50 per cent of the population. That was quite a small number of waste water treatment works initially.

I do not have the exact number to hand, but I can get it while you are asking other questions, then submit it afterwards.

The Deputy Convener: Would the number be in the hundreds or fewer than that?

George Ponton: No—it was fewer works than that, because some of them serve quite large areas of population. For example, Seafield in Edinburgh serves a population of more than 600,000.

We also sampled some of the smaller works in West Lothian, Tayside and Perth and Kinross. In the island and more remote communities, sampling a waste water treatment works almost tells us the level of infection in that local community. Some of the bigger urban systems drain quite large geographical areas. For example, the Dalmuir works drains almost the whole of the Kelvin valley—from Kilsyth, Cumbernauld and all the way down through that vicinity—so sampling that one site gives a very large population coverage. We were doing up to 300 samples a week.

With regard to resourcing, initially, because a lot of operational activity was stopped due to lockdown, we could utilise our existing sampling resource. However, as we got back to normal operational sampling and other activities, we had to recruit extra resource. In particular, when we were doing the network sampling, we were also utilising a couple of sewer network contractors—one in the west and one in the east—to do some of the sampling. That is no longer happening, because the network sampling is not included in the current surveillance programme, due to some of the challenges that I set out earlier.

The Deputy Convener: Okay. Thank you very much.

I will ask Peter Singleton a similar question to the original question that I put to Mr Ponton. What was your experience of the programme? What lessons have been learned from it for the future?

Peter Singleton (Scottish Environment Protection Agency): Good morning, everyone. The greatest lesson that I have learned from the programme was what we can do in an emergency. I have been involved in the business for 30-plus years and I have never seen the barriers between different organisations come down in the way that they did during that time. When people were asked whether they could do something, they responded by saying, “Yeah, we can do that”, and when people said that they did not have a bit of kit, that was okay because someone else would lend it to them. Across the board, it was an incredibly positive experience.

As George Ponton said, the programme grew out of worry about keeping Scottish Water staff safe. We quickly realised that we had all the kit that the Roslin institute was using, so we could mirror what it was doing as an academic exercise and use that to put in place a monitoring programme.

There is quite a big difference between putting a few samples through a lab and putting in place a monitoring programme. As George explained, we had the great opportunity that most of the kit was already in place, so the speed with which we could react was supported by the fact that we already had monitoring programmes in place. The Roslin institute had sampling kit in most of the right places, and we had a lab that was set up for putting multiple samples through it. If we had tried to do that from a standing start, it would have been a very different experience.

When we started in May 2021, we were doing 40 samples a week, at 24 or 28 sites, I think. That increased to just under 300 samples a week, and we are now back down to 200 samples a week from—I have just checked—120 sites. That gives us coverage of about 80 per cent of the sewered population, given that parts of Scotland have lots of private waste water systems.

The other thing that I learned is that there is an interesting opportunity in waste water-based epidemiology. I have sat on calls with various people from different walks of life with whom I would not normally interact. There is a data source in waste water. However, data for data's sake is no use, so the question that is always in the back of my mind is: how can we turn that information into something that helps people to do their jobs better or differently or to have knowledge that they do not have currently?

The Deputy Convener: Do you have a view on how valuable the exercise was to the Scottish Government and health advisers in formulating Covid policies?

Peter Singleton: I have often struggled with that. In effect, we crunched a bunch of numbers and stuck them on a website that was available to everybody who needed it. It was heartening to see the data going into things such as the Covid modelling reports. I could show my chief executive what we were doing and point to that information being used in a report to support decision making. It is really difficult to know whether decisions would have been made differently if that information had not been available.

It has been interesting to hear the anecdotal evidence as the world has returned to semi-normal and I have started to talk to people. At a conference, I bumped into someone who said that they had been using our data in Orkney to decide how many test and protect people to make available for the week. I was told that, if our data matched their data, broadly speaking, they assumed that they knew most of the people who had Covid. However, if our data had a spike and theirs did not, they guessed that they should do a bit more phoning round. I already knew that, because I had bumped into somebody who had been doing that job for six months.

The Deputy Convener: Thank you—that is really interesting.

I move on to you, Rachel Helliwell. As I did with the others, I ask you to reflect on your experience of the process.

Dr Rachel Helliwell (Scotland's Centre of Expertise for Waters and the Hydro Nation International Centre): Good morning. My role is to work at the science and policy interface. I work closely with the Scottish Government and its agencies. The centre of expertise provides that link to enable the Scottish research community to respond when there is an issue such as Covid that needs urgent attention.

I was asked to prioritise the waste water testing ahead of everything. I concur with George Ponton and Peter Singleton in that it is amazing that, when we have a crisis, everybody jumps on board to try to work together to find a way through the issues. CREW was fortunate because we had established relationships with the key partners who were required to address the pandemic and respond accordingly to the waste water surveillance.

We worked with SEPA and brought our understanding of the research community in Scotland who had the skills to come on board to respond. We had four projects in CREW that were related to waste water-based epidemiology and we were able to work with them efficiently. We had processes in place to ensure that projects could be set up and procurement could be followed quickly and effectively.

On the budget that we had for the work, we funded the first project entirely from our existing CREW funding. However, as the work progressed—as we could see that there was promise and that we had successes in identifying the virus in waste water—the Scottish Government provided more funding through CREW to support the activities.

It was a stressful and exciting time; everyone got a real buzz from working together and seeing what could be done. With no barriers—as Peter Singleton described—we really did work at pace, and it was very effective.

09:30

We also drew very much on staff at a United Kingdom level from the Department of Health and Social Care and the joint biosecurity centre. They engaged with the Scottish team, and shared protocols, learning and samples. That was crucial, and we all appreciated their input. In addition, through CREW, we connected internationally to other discussions. From my perspective, that was a very positive experience.

With regard to learning, communication with some sectors to help us to make decisions could have been improved. We were very keen that the outputs from the waste water surveillance should have an impact and make a change. From what George Ponton and Peter Singleton have both said, it is clear that there were changes as a result of that work.

There have definitely been a lot of discussions in the Scottish Government and more widely about process and practice, and about operations, which I think have been very beneficial. As we move forwards, the lessons learned are that we need to work, and bring interdisciplinary and cross-sector teams, more closely together, and have a more formal platform to enable us to liaise and collaborate.

That is a summary of where I am coming from. I really feel that the Centre of Expertise for Waters is the enabler: we bring people together and organise meetings, take actions and try to make a difference. I think that that was successfully achieved in this area.

The Deputy Convener: Thank you for that. Do you have any reflections on the value that your work has had in driving Government policy?

Dr Helliwell: As Peter Singleton said, that is a difficult question to answer. With regard to the value of our work, what has been delivered is incredibly important, and there have been changes in certain areas of Scottish policy.

Essentially, we provide the evidence and the information to help decision makers, and those decisions are made at a level above me. I know that there are all sorts of committees in the Scottish Government where the information from that work has been used and discussed to influence various policy areas. Within CREW, we are running a project to try to understand the impact of that information and what happens to some of the evidence once it leaves our area of responsibility and involvement.

I think that our work is influencing, and has influenced, change in how waste water surveillance is used and interpreted in various Government departments.

George Ponton: In response to the question about the value of our work, I would add only that, although I do not have visibility of how it has influenced policy, I know that, during the pandemic, the information that we provided through the programme helped health boards and local authorities with their planning for putting out the mobile testing facilities and units. It certainly drove some of that activity, so it was definitely valuable from that perspective.

Peter Singleton and I continue to be involved in a stakeholder group that is looking at some of the policy questions that you referred to. There is now a much broader discussion on what else waste water-based epidemiology can and cannot be used for, and our work has raised the visibility of what the potential might be for future policy.

Jim Fairlie (Perthshire South and Kinross-shire) (SNP): I find the stuff that you have all talked about really interesting. People have said that barriers have come down as a result of Covid, not only in your sector but across society. What bothers me, though, is that the barriers were there in the first place. Have you gone back into your silos? You have all said that there has been good co-operative working and that we should do that. Are you not still doing it? Have you all gone back to working independently of one other? I would have thought that that co-operation should be used across huge areas and many disciplines, whether that involves surveying for other diseases or all sorts of other public health issues. Where are you with co-operation now?

Peter Singleton: There are always slight barriers, are there not? SEPA regulates Scottish Water, and George Ponton and I are in effect our own heads of research, so there is less of a barrier between us, in a way, because we are looking at things in an innovative space.

Scotland was the first place in the UK to get the programme up and running, which reflected the fact that fewer people were involved—in SEPA, Scottish Water and the Scottish Government—so we could react more quickly. To be honest, the biggest barriers that came down were those across the UK. I have never had such positive conversations across the whole of the UK. The Department for Environment, Food and Rural Affairs set up a call with 40 folk on it, asking what we could do, and there was really open communication and learning.

There was also no barrier to do with resource. As George Ponton said, both organisations were pretty much in an emergency, mothballed state. I did not have to fight to find people who could do the work, because the laboratory was shut. We simply opened the lab to do the work, and that was it.

I definitely noticed the UK's barriers going back up as living in a pandemic became more normal. There was an issue with whether we had funding to do this or that, and people were slightly less open. Again, however, because we live in the research world, we were able to work our way around that successfully. We were allowed to have more open conversations than we would have been able to have if that had been seen as an permanent operational approach.

You are right to question why the barriers are there and to ask how we can live in a more open world than we perhaps did previously. It is also a little bit about relationships, is it not?

Jim Fairlie: Yes—that is probably an important part of it.

Dr Helliwell: I agree with Peter Singleton. With regard to where this work will go in the future, there are so many opportunities in this space. We have been developing methods to detect Covid in waste water, but waste water can be used for a range of other purposes. There are many applications, such as using it to detect community-wide use of illicit drugs or lifestyle chemicals such as nicotine, caffeine and alcohol. There are all sorts of possibilities. In the future, we will need to think about how we can work together more closely and re-engage.

Jim Fairlie is right to highlight the disengagement after the initial surge of activity. In my eyes, that perhaps happened after the last CREW project finished. I felt like I had become disengaged from the process just because the funding had stopped. It is awful that that should be the situation. We need to keep the dialogue going and keep getting the right people in the room to think more strategically about where we need to go in this space, because there are so many opportunities, and the resource and the sampling are in place. The hard work has almost been done, so let us think about the opportunities moving forward.

George Ponton: On the point about the barriers coming down and why they were there in the first place, I think that it depends on where one is sitting. It is clear—this came out in some earlier comments—that it is not so much that there are barriers; it is more about conflicting priorities. Covid was a slightly simpler time: there was only one priority and it was always survival, so everybody focused on the issue at hand. That meant that it was easier to get resources and to focus our time on the particular topic that we are discussing.

I have a very broad portfolio—as I am sure Peter Singleton does—of areas in which we are working, so it is sometimes difficult to carve out the time. However, picking up on Rachel Helliwell's point, I note that there is still on-going discussion and collaboration on waste water-based epidemiology. There is a group in the Scottish Government that is trying to lead the policy development in that space. It includes people from epidemiology, such as Kate Templeton, who I think will be in the room later, and from genomic sequencing; people from Public Health Scotland and various parts of the Scottish Government; and people from Scottish Water and SEPA. Collaboration is still going on, but it is now about focusing and agreeing on what the priorities are.

Jim Fairlie: Grand. Peter Singleton wants to comment, but I will put two more questions or thoughts to the witnesses before he does so.

First, do you now have a resource that can be upscaled if necessary? Secondly, I ask George Ponton to say how you get community sampling done. I am thinking of specific small communities. We have often heard that areas of deprivation were the hardest hit by Covid, and in some communities the uptake of vaccinations has not been high enough. Are you in a position to be able to go to specific areas to find out whether a community is in trouble or not?

I will bring in Peter Singleton first, and then the other witnesses can comment on those two points.

Peter Singleton: I will give you an example of co-operation that already existed. SEPA had access to Scottish Water's entire geographic information system—not only the network, but information on where it had sampling in place. We could therefore design the original sampling programme based on the equipment that we knew that Scottish Water had. We had already put that element of co-operation in place between the organisations, which is probably what allowed us to move faster than the rest of the UK. We literally built a tool that would allow us to design a network, and we have used that tool continuously to adapt the network as we go along.

To some extent, that allows me to answer your second question. The smallest community with a sewage works is about 2,000 people somewhere in the Borders. As George Ponton said, if we want to break out parts of Livingston or Glasgow, we will need their guys to go to their sewer network and break out housing estates or whatever. They did that really well, but it is not straightforward. Nowhere was built with that in mind, so they may get to a point where they discover that a sewer is not where they thought it was or they cannot get a sample because it is in the middle of a motorway.

09:45

Jim Fairlie: George, do you want to comment?

George Ponton: Yes—thanks. Given the resource that can be upscaled and the sampling of discrete smaller or deprived communities, the answer to the second question is yes. We have a nationwide resource that samples from the remotest islands in Orkney and Shetland to the biggest cities in Scotland, and our national logistics network transports those samples. On the drinking water side, that is well established, as it has operated for a number of years. More recently, we have moved to operator self-monitoring on the waste water side. There is an established sampler network, so we can sample at very small works across the country.

On the availability of resource that can be upscaled, this might sound slightly contradictory, but in some small or remote communities it is difficult to get people beyond our core operational team. As I think I said earlier, because the funding for the waste water programme comes in on only an annual basis, we are using additional agency and temporary resource, rather than our core resource, to do the waste water sampling. That is slightly more inefficient than it would be if we were using our core resource, through which sampling programmes could be combined.

In some of the more remote areas, particularly in the island communities, we find an issue with the availability of people to do the work. There are lots of vacancies in those areas and it becomes a little more challenging. By and large, however, the resource is there and we can upscale it. We demonstrated that during the pandemic, when we upscaled.

Jim Fairlie: We heard in an earlier session about how the personal protective equipment system was established. It was learned very quickly that people cannot stick PPE in a cupboard and wait for five years until they need it. There has to be a continuous rolling of stock. Collectively, how able are you to say to the Scottish Government that you need funding to keep that going and develop it?

The PPE system has grown to become almost an industry on its own. How do you collectively say, "We can provide this, this and this through the funding that you give us, and then we can use that if there is another emergency"? Do you see what I mean? I am trying to find the quid pro quo for keeping it going, because we might wait for 50 years for another pandemic, or we might wait for five years. We just do not know. How do you do that? Are you looking at it?

George Ponton: As I said, the Covid waste water monitoring programme is grant funded. It is not part of our core regulatory funding. We are having a conversation with the Scottish Government about the fact that, if funding was secured for, say, a rolling period of three years or five years, it would allow us to build the Covid waste water surveillance programme into our operational and other regulatory sampling programmes. That would mean that the resource was built more into business as usual.

At the moment, because the programme is almost ad hoc—it is additional to what we are required to do under normal operational conditions—it is run almost as a separate project. It is similar to our dealing with an incident or a capital delivery project for which we need additional resource. If additional funding was in place or there was a commitment to continue with the programme beyond a given financial year, it would bring an opportunity to drive innovation in the way that the samples are gathered and, perhaps, the way that the analysis is done.

At the moment, a sample is taken and it is transported to a central lab, where analysis is done on it. The water industry is working on how we can move some of that data gathering and analysis from the labs into the field. If there was a longer-term commitment, if the work was valued and if we wanted to do that in the future, it would create space for people to innovate. At the moment, people are reluctant to innovate because they cannot see the programme having longevity. They could develop an instrument today, but it could be decided that Covid is no longer an issue and that we will not bother with it.

Taking a longer-term view gives people opportunities to look at different things because they can see the benefit of doing so for the future.

Jim Fairlie: That answer has given me an idea for a question to ask the next panel.

Peter Singleton: That is the killer question. I agree with George Ponton: if people can see long-term funding coming in, it will allow them to establish a permanent solution and to innovate. I go back to what I said before: we need to have a pool from the user community. It does not seem terribly intelligent to keep doing what we are doing just in case. We have proved that we can ramp it up and that there is very conceivably some really useful information that would be useable day to day.

Doing that work would give us samples that could be analysed for anything. If we had a freezer full of two years' worth of samples, it could be used every so often when we got requests from either academics or PHS for samples from a certain sewage works in a certain month because somebody had reported something unusual. They could then go back and look at the samples. To do that, however, we need to have a pool from the user community.

I agree 100 per cent with George Ponton that the direction of travel should be to take analysis

into the field. Quite a lot of working is going on in relation to that.

Academics are now on the case, and waste water-based epidemiology is not going back in the bag. It is out, and academics will be working on it.

Jim Fairlie: Rachel, do you want to add anything?

Dr Helliwell: I do not think that there is anything for me to add. George Ponton and Peter Singleton have covered it.

Jim Fairlie: It sounds as if you should all have regular conversations with one other.

John Mason (Glasgow Shettleston) (SNP): The conversation has been really interesting. I have to say that I am not an expert on sewage or related matters.

I will start with a question for George Ponton. What waste water surveillance was going on before Covid, particularly on diseases? What were you actually looking for, and how much water surveillance was happening?

George Ponton: Scottish Water did not look for anything related to diseases, at all, because that is not part of our general analysis. Waste water analysis was going on for general sampling, regulatory compliance, to get an understanding of what is going into our waste water treatment works and to see how our waste water treatment works are performing, but Scottish Water was not doing any analysis in that space.

Samples were taken from a site in Glasgow as part of a UK-wide modelling programme for polio, but other than that, I am not aware that any other waste water epidemiology surveillance was going on. It is certainly not something that Scottish Water undertakes. Our role in the programme was to facilitate access to water so that others could do the analysis, and SEPA was doing that.

John Mason: Dr Helliwell, were other countries doing that? Did the idea of testing the water start with Covid?

Dr Helliwell: Scotland was leading in terms of how quickly and efficiently it mobilised its teams to respond to the crisis, but there have been projects internationally, including in the Netherlands and more widely, where research teams have developed methods and approaches to determine SARS-CoV-2 ribonucleic acid and viruses in general from waste water.

One activity that I was involved in with the chief scientific adviser at the time was to engage with the Rockefeller Center in the United States. We talked about international activities and partnerships in the area and consolidating progress and information on samples and protocols to try and move forward at pace. That work was not only on a practical level; it also drew on experiences of airport sampling of waste water to try and target new methods for detecting and sampling at airports to reduce spread and so on.

All sorts of different angles were taken in that international dimension. That is very much something that—[*Inaudible*.]—activity. The beauty of the work that happened in Scotland was that Scotland is relatively small, and those existing partnerships and networks allowed us to take a lead on how to work together from an environmental regulator and industry perspective. We also brought in public health, of course.

Peter Singleton: George Ponton is right that the UK has a polio programme. The World Health Organization monitors polio using waste water, but it uses quite old-fashioned technology—it cultures it. The big shift has been being able to use genomics as opposed to culture technology, so we can get a result much faster. To a large extent, it was a question of where the science was at the moment that the pandemic hit. Most other uses of waste water tend to involve chemical methods rather than looking for viruses and things, but now that we know what we can do, the world is our oyster.

John Mason: Seeing as you are there, I will ask you this. I do not totally understand some of the technical stuff that we were given. For example, a Scottish Government report on modelling the spread of Covid-19 says that, in November,

"wastewater Covid-19 levels were in the range of 21 to 32 million gene copies per person per day."

Can you or one of your colleagues explain even roughly what that means?

Peter Singleton: It literally means what it says, in the sense that it is the number of gene copies that we have measured. For a long period, we managed to match the results that we were getting out of the back end of our PCR machine with the case data that was being reported, so we had a very good relationship between the waste water data and the local case data. We did not worry too much about what our number meant; it was good and useful that it appeared to track the case data.

The real challenge with a Scottish waste-water system is that it is not only sewage in the pipe. There is a lot of run-off in the pipe, so if there has been a lot of rain, the signal is diluted by the fact that there is fresh water in the system and not just sewage. We needed some measure to show that if it has rained, we have adjusted that value because there has been some infiltration into the system.

10:00

John Mason: So, if there is less rain, the concentration will be greater, and it is effectively diluted if there is more rain.

Peter Singleton: Yes.

John Mason: That is an interesting point. Where I live, people are now trying to separate rainwater from sewage. Is that important? Would that be helpful?

Peter Singleton: It would be helpful, but we can work around that. We used ammonia as a signal for the proportion of sewage in the sample, which seemed to work really well. It is neater if the run-off stream and the foul stream are separate, because that makes it easier for Scottish Water to treat.

John Mason: You talked about a correlation regarding testing waste water and testing the samples that health boards were getting directly from people. When new variants came along, who was picking them up first? Was it you, or was that coming from testing?

Peter Singleton: It was the testing. The medics will keep me right. I hope that my understanding is correct. When you take a swab from a person, there is only one variant in that person.

John Mason: Right.

Peter Singleton: It is what it is. If you take a sample from sewage, that might have 200 people's Covid in it, so there will be multiple variants in the sewage. When we test sewage, we are always looking for known variants, whereas a sample from a human being allows us to look at the Covid and see what it is.

John Mason: Right, okay.

Peter Singleton: You need to know what you are looking for in sewage.

John Mason: That is helpful.

I think I picked up that we are currently testing 200 samples per week, which is less than previously. Can you, or Scottish Water, explain that number? Is that good or bad? Should we do more? How long should we keep testing 200 samples per week?

Peter Singleton: There was some negotiation or discussion in the group about the right level of resource to put into that, the throughput that the lab can handle and the infection levels that we are detecting. That seemed to be about the right number. It allowed us to maintain a sampling network for the 120 sewage works, but did not mean that our lab was concentrating solely on Covid.

John Mason: Thanks.

Dr Helliwell, do you want to add anything? We have said that polio can be detected and we have talked about alcohol and drugs. All those things can be analysed or sampled. Is it just a question of having the resources and political will to do those things?

Dr Helliwell: Yes, and there is also a public health requirement. As I said, the investment, infrastructure, methodology and resources are all there. The chemistry and biology of the samples give a diverse range of information. It is essential that we look at the wider applications.

The current figure of 200 samples is dictated by resourcing, finance and lab capacity How busy the labs are can change over time. All those things should be considered as part of any future strategy.

Antimicrobial resistance is one area where I think waste water-based epidemiology could make significant inroads. There are so many possibilities in that space. I have mentioned examples of illicit drugs and lifestyle chemicals, and waste water can be used to estimate prevalence of infectious diseases based on pharmaceutical usage. The opportunities are just vast.

Perhaps George Ponton or Peter Singleton might want to come back in on that. From my perspective, though, the future in that area is quite exciting.

John Mason: Perhaps I could ask you one more question, then if they want to come back in they can do so.

It has been suggested that we should have a chief scientist for public health. Have you a view on that? We already have a chief scientist for health and a chief medical officer. I would be reluctant for us to just keep creating more posts, but do you think that having such a position might be helpful?

Dr Helliwell: It was certainly a recommendation from the social science team involved in the CREW report. From the interviews that they carried out, it was clear that public health expertise spans a range of skills and expertise that is wider than those applying solely to human medicine. The recommendation to appoint a chief scientist for public health stems from the recognition that it would be beneficial to bring a greater breadth of knowledge and expertise into a complex and multifaceted policy area. The feedback from interviews that were conducted for the CREW project was quite clear. In the future, public health challenges will increasingly require a multidisciplinary approach that goes beyond an understanding of medicine and human health. That is more or less where that recommendation came from.

The report has definitely instigated in-depth discussion across departments within the Scottish Government. As you said, a number of chief scientists and advisers are already working at a senior level, but in order to implement change we need to get them working together more closely and engaging relatively regularly on subjects such as this.

John Mason: That is very helpful. Mr Ponton, do you want to add to that?

George Ponton: I go back to your earlier question about what else waste water-based epidemiology could be used for. Sometimes I try to be the voice of reason on that. There are lots of things that we can do, but the key factor is that there are practicalities about where we can do them in the waste water network.

One of the biggest learning points from the whole exercise, certainly from a sampling perspective, was that taking a sample from a waste water treatment works is relatively easy to set up and do, but taking it from the waste water network is a lot more challenging and resource intensive from a health and safety perspective. The way in which the network is configured does not always allow us to achieve our initial objective. That was clear from our discussions with the health boards when they were trying to obtain discrete samples from different parts of communities, which was a challenging exercise.

John Mason: That is very helpful.

The Deputy Convener: I welcome Siobhian Brown to the meeting.

The Convener (Siobhian Brown): Thank you, deputy convener. I apologise to everyone for my late arrival, which is due to my having to deal with another matter. I also apologise if I should repeat any questions.

I thank Dr Isabel Fletcher for her written evidence, which was based on research conducted by her and Professor Catherine Lyall. It noted some interesting things, such as:

"In crisis situations, people initially turn to their existing networks for assistance with unexpected and urgent tasks."

It also highlighted that

"the climate crisis will result in increasing threats to human health (including future pandemics) demanding responses that span public health, animal health and environment. This, in turn, will require more joined-up approaches with effective day-to-day working relationships"

with the Scottish Government and other agencies.

My colleague John Mason said that it was suggested that there would be benefit in creating a post of chief scientist for public health. Are there any other ways in which such approaches could be co-ordinated by the Government?

Dr Helliwell: The report mentioned a recommendation that a secretariat could be bought in at that level to help to co-ordinate responses. From my perspective, we need to consider some centre or secretariat, along the lines of the role that CREW has played in the past, to facilitate engagement, work with the Government to understand what the priorities are and think about how to enhance the resilience in that space.

Isabel Fletcher mentioned that, in climate change, there are all sorts of unknowns. The Government needs to have some kind of committee centre to plan, take action and work together to know who is operating in that space. One thing that was brought out was the lack of understanding of who is who in the Government departments, for example—who to draw on and bring into that space. Some register of experts, or whatever it might be, would be really helpful, just to understand who we need to engage with. I do not know whether that completely answers your question.

The Convener: That is helpful. Thank you.

Peter Singleton: It is an interesting and tricky space to unravel. As we said earlier, part of the success of what happened is that it was led from the research end of the businesses. In essence, therefore, two of our key contacts in the Government were the chief scientist for health and the chief scientist for the environment, because, in effect—to use shorthand—they were heads of research. We therefore did not need to understand or have the knowledge of the rest of the system that Rachel Helliwell was just explaining. We could just go to them. They had the understanding of which department in the Government was doing whatever, so they became our sales force, to an extent. That was definitely one of the success points.

It is much more difficult to work out the right solution for the future. I come back to the idea that it is all about pull. As an environmental scientist, for most of my life, I have been in a box, looking after the environment. However, over the past 10 to 15 years, there has been a much greater acknowledgement of the impact of the environment on human health. That is growing. There is now a much wider understanding of what people tend to call "one health". For example, we use a lot of the same drugs as in agriculture—veterinary medicines are not that dissimilar to human medicines. There is a wider acknowledgement of the overlap in that space.

The Convener: That is really helpful.

I know that I have missed most of the session, and I apologise for that. It has been fascinating to read in the papers all the work that has been going

on, and I commend you for that, because, in the dark cloud of Covid, there has been a silver lining in such ground-breaking work. Thank you.

The Deputy Convener: Thank you all. I appreciate your taking the time to come and speak to us. If you have any follow-up evidence to submit, please feel free to do so in writing.

There has been a lot of talk of sewage for so early in the day. I know that John Mason was delighted with that but, for the rest of us, it has been a bit of a challenge—but thank you very much.

We will have a brief suspension to allow a changeover of witnesses.

10:15

Meeting suspended.

10:20

On resuming—

The Convener: Good morning, and welcome back. I apologise again for being late this morning. We have received apologies from Alex Rowley.

We continue to take evidence on Covid-19 surveillance. Our second panel of witnesses will be giving evidence on genomic sequencing. I welcome to the meeting Professor Sharon Peacock CBE, executive director and chair of the COVID-19 Genomics UK Consortium, who joins us remotely; Mike Gray, service manager for laboratory medicine at NHS Lothian; who joins us in person; Dr Kate Templeton, head of molecular diagnostics in microbiology, virology and molecular pathology, and director of the sexually transmitted infections and viral genotyping reference laboratory at the royal infirmary of Edinburgh—that is a mouthful; Professor Rory Gunson, consultant clinical scientist, and virology clinical lead and laboratory director of the west of Scotland specialist virology centre at Glasgow royal infirmary, who joins us remotely too; and Professor Matthew Holden, COG-UK principal investigator at Public Health Scotland.

Welcome, everybody. I thank you for giving us your time this morning, and for your recent submissions. We estimate that the session will run up to about 11.20, and each member should have between 12 and 15 minutes to ask their questions of the panel.

For the witnesses who are attending remotely, if you would like to respond to an issue that is being discussed, you can just type an R in the chat box and I will try to bring you in. I am keen to ensure that everybody gets an opportunity to speak, but I apologise in advance in case, if time runs on too much, I have to interrupt members or witnesses in the interests of brevity.

I invite the witnesses to introduce themselves briefly, starting with Professor Sharon Peacock.

Professor Sharon Peacock CBE (COVID-19 Genomics UK Consortium): Good morning, everybody. I am professor of public health and microbiology at the University of Cambridge, and I am also the director of the COVID-19 Genomics UK Consortium, which was stood up in March 2020 to provide genome sequence data to the pandemic and public health agencies.

Mike Gray (NHS Lothian): I am the service manager for laboratory medicine in NHS Lothian, which is the organisation within which one of the Scottish systems sat. I am part scientist, part manager by trade.

Dr Kate Templeton (NHS Lothian): I am a consultant clinical scientist in Edinburgh. I was part of the COG-UK consortium, led by Sharon Peacock, which sequenced Covid-19 from March 2020, and I then transferred that service to NHS Lothian as part of the network with Rory Gunson and Matt Holden.

John Mason: You do not need to press your button for the microphone.

Dr Templeton: Do we not? Oh!

The Convener: No, it should be done for us.

Dr Templeton: Oh, I was so excited about that. [*Laughter*.]

The Convener: I will bring in Professor Rory Gunson.

Professor Rory Gunson (NHS Greater Glasgow and Clyde): Hi there. I am clinical lead for virology in NHS Greater Glasgow and Clyde. As Kate Templeton mentioned, I host the viral genotyping service for the west, which feeds into the service to which she and Matt Holden also contribute.

Professor Matthew Holden (Public Health Scotland): I am professor of pathogen genomics at the University of St Andrews, and I have been working as a genomics advisor in Public Health Scotland. Since the beginning of the pandemic, I have been seconded to Public Health Scotland, first to help it to work with COG-UK to integrate the data into the response, and latterly to help to establish and build up and the genome sequencing capacity.

The Convener: I will ask the first question, which is very simple. Will you explain how genomic sequencing works and what it is?

Professor Holden: I can begin, and others can chip in. Every living organism, including infectious

agents such as a virus, has genetic material inside it that is a blueprint for life and the instructions as to how it works. Genome sequencing effectively takes that, decodes it, and turns it into a genetic sequence.

Why do we want that information? Each genome has a set of instructions that gives us clues as to how it behaves—for example, it can say whether an organism will be resistant to an antibiotic or potentially cause a more severe disease. Each genome is also a historical record, because it comes from its ancestors. By comparing genomes, we can therefore understand whether two separate micro-organisms or viruses are very closely related and share a common ancestor, and then perhaps trace back to a transmission or an outbreak. We use genome sequencing to do that.

When genome sequencing, we take our organism or virus, harvest the genetic material from it in the laboratory—it is, in effect, a big polymer or chemical chain—use a series of molecular techniques to break it up into tiny fragments, and read the sequence of them using sequencing the technologies that are now in Kate Templeton's, Rory Gunson's and Sharon Peacock's labs in Cambridge. That decodes the bases—the Gs, Cs, As and Ts—which can be turned into digitised information that we can analyse with computers. We can decode and extract all that useful information about the template of the micro-organism, which gives us clues about how it behaves. We can also do genetic fingerprinting to help us understand the origins and spread of pathogens.

The Convener: Were you already working together as a team or were you brought together when Covid came in March 2020?

Dr Templeton: We were all working together, but we are definitely more of a team now than we were. There were a lot of different academic institutions in the COG-UK framework that perhaps would not necessarily have worked together before. Sharon Peacock can speak about that more.

We definitely all came together under that umbrella, but there has always been a close working relationship in Scotland among all the labs, and a pre-dating programme had already been set up within Public Health Scotland to do genomic sequencing for Neisseria meningitidis, salmonella, and Shiga toxin-producing E coli. That basis had already been set up, so there was already something in existence.

Professor Peacock: Back in March 2020, a large number of people, including universities and the four public health agencies, were capable of doing genome sequencing of pathogens. However, the system was not connected and we did not at that point have the scale that we needed in order to sequence the number of genomes that we anticipated that we would need to sequence to track the genetic changes that would occur over time.

In mid-March 2020, there was a coming together of 16 academic institutions and universities, the four public health agencies of the United Kingdom, and the Wellcome Sanger Institute. We got together in a meeting room at the Wellcome at Euston Road, and we decided that we would pool our ideas and develop a plan to provide the sequencing capability that was connected across the country. As the virus was going to travel across the country and not respect borders, it was key that there was a four-nations approach. That is why we set about creating a country-wide sequencing network. We were all familiar with each other, but we had never before had the opportunity to work together in such a cohesive way.

The Convener: That is really helpful.

I will move to my next question. Do you feel that Scotland is well placed at the moment for any future pandemics, as well as for any other threats, such as antimicrobial resistance?

10:30

Dr Templeton: The great thing is that, as a result of the money that we received from the Scottish Government to set up the sequencing service, we are now in the best possible position to sequence more pathogens. At the moment, funding is guaranteed only until March 2023; however, we have that legacy, ready to enact and evolve.

Although we have been focusing on Covid, I point out that we have also sequenced monkeypox within the period. There was an outbreak of monkeypox and we were able to sequence it using exactly the sort of techniques and templates that we had set up for Covid. The idea around the infrastructure with PHS and bioinformatics was to turn all the Gs and Cs that Matt Holden talked about into data that is understood. That is the key thing from all that we have set up.

Professor Holden: Following on from that, I note that, on the back of Covid, a lot of work has gone into upscaling and building capacity. As was nicely illustrated in the earlier session, Covid turbocharged what we could do, which has definitely had an impact on pathogenomics. Before Covid arrived, we were whole-genome sequencing in the reference labs, albeit that it was on a smaller scale and on a more limited budget. However, we managed to achieve capacity that

was responsive to the Covid pandemic that will contribute and will help, going forward.

Furthermore, it is not only about sequencing; it is about introducing whole-genome sequencing into what the organisation does and, alongside that, thinking about the other components that make genome sequencing effective, which is the really important consideration. We can sequence genomes, but if we cannot translate that into useful information on which people can take action and make decisions, it will, potentially, not be effective. A lot of work has been done to link data, to create databases and bioinformatic resources, and just to get genome data into the everyday vocabulary so that people—politicians and the public—understand it. The population has a detailed interest in genetic variants and variance because the subject has had such an impact on our lives and has become part of our understanding and consciousness.

Genome data is also now feeding through the organisation on a regular basis. That has given us an understanding of what we can do with genome sequencing. We are very well placed to capitalise on that and to apply it to other threats such as antimicrobial resistance, which the convener mentioned, and which is arguably the hidden pandemic in the background that is not going to go away.

We are well placed to capitalise not only on the investment, but on all the work that has gone on around it to support sequencing and to integrate it into public health, through the national health service and the Government.

Professor Gunson: Matt Holden has covered the point very eloquently. I was going to say that we are well placed, with all the infrastructure and with users who are aware of how to use the technology.

However, as Kate Templeton said, the biggest worry at the moment is funding, which is currently until March next year. If we are to build on what we have put in place, we really need the funding situation to be clarified.

Mike Gray: I will briefly come in to back up those points from an operational standpoint. Working in the healthcare system in Scotland, and given that the testing is being done within NHS boards, it is difficult to find oneself in a position in which the accumulated skill set that has been built over the past 18 months is on the precipice and might fall off the cliff.

Although it is a fairly standard trope to say so, we can talk about legacy all we like, but without the workforce and the skill set, and a sustainable plan for the future—if it all stopped tomorrow—it might take quite an effort to restart. That is always a fear that we hold in our systems, operationally.

The Convener: Thank you for that. I will bring in Murdo Fraser.

Murdo Fraser (Mid Scotland and Fife) (Con): Good morning. I want to follow up on the convener's last question. It sounds as though you have successfully and quickly been able to scale up your work to address issues and to provide the capacity that is required. You have identified the risk to that work continuing. How essential is it that we maintain that level of work? What are the risks to it, in terms of future funding?

Perhaps Mr Gray can go first, as he addressed that point previously.

Mike Gray: I will start from a non-scientific base, then I will hand over to my professorial colleagues.

From a basic workforce perspective, if we had put out an advert two years ago for genomic scientists or for the particular skill sets that we now use, we would have found that such skills did not really exist or were not out there in large numbers.

I will highlight one of the legacy benefits of what we have just been through. We should bear it in mind that we had a bit of hot start for sequencing, because we had already been in team mode for routine polymerase chain reaction testing for laboratories across Scotland and systems across the UK, so we were well versed in putting our operational team in, on the ground.

However, the endeavour that we are discussing today required a completely new skill set. Although it might now be easier to put out an advert and accumulate people, if the level of work dwindles, we will find that the marketplace to supply those people does not exist. With regard to pandemic preparedness, we want to avoid a peak-and-trough element with the workforce. Our workforce is currently a great asset with a great skill set, and is a true legacy.

On the science, I will pass over to Dr Templeton.

Dr Templeton: First, I will answer directly the question of what difference it would make with regard to Covid if that work were stopped.

Various reports are produced regularly that are used by, for example, our infection control team in NHS Lothian. There is something called a cluster report, which tells the infection control team where there are some cases that are not related on a ward, and where there are 10 cases on a ward that are all related. The team is then able to infer practice and policy around ensuring that we keep as many hospital beds open as possible. At this time—or probably any time—every bed that is open is crucial, so such reports are really valuable. Without sequencing, they would stop.

The other part of the data that we are producing is about understanding what is going on with Covid, which is informing vaccination policy. For example, it looks at how often we see reinfection. That is linked with the SIREN—SARS-CoV2 immunity and reinfection evaluation—study, which is another well-funded study from Scotland and is UK led. That, too, has hugely influenced and informed our vaccination policy; genomic sequencing on Covid is completely crucial in that regard. As we have all seen, vaccination is the reason why, although Covid remains, we are not all sitting here with masks on.

Those are the two main examples of regular reports that are produced weekly.

With regard to the legacy, we are always seeing new threats coming along. Right now, group A Strep has hit the headlines. There are all sorts of unknowns there; sequencing could absolutely be a tool to get us to a point at which we understand more about what is going on. Whenever there is an outbreak on a ward, our team in NHS Lothian tries to sequence it, and we always find out something new when we do so. Sequencing is a vital tool on the front line of the NHS, and it also improves our understanding on a legacy basis.

Professor Holden: Kate has eloquently set out examples to illustrate the point.

With regard to where we currently are on Covid, beyond the examples that Kate mentioned, our work provides intelligence so that we know what other variants are circulating in Scotland. As the committee is aware, Covid changes and new variants regularly emerge. The BQ1 variant, which has just appeared, has now effectively become the dominant strain in Scotland. As part of planning, understanding and responding, we need to know whether we have a new variant. We then need to be able to identify it so that we can look back at patient information and make assessments at population and public health levels of how it behaves. We can then make assessments of vaccine escape or severity of disease to help us to plan for the future.

Again, a lot of the data that we generate from genome sequencing is providing the genomic intelligence that goes into—as Kate said—the NHS response, and into future planning through modelling to project how such things will behave in the coming months, when the pressures on the NHS are greatest.

Murdo Fraser: Thank you for that.

As a follow-up, I will go back to funding. Is there funding in place to maintain the capacity that has been built up? Mr Gray suggested that there is not.

Dr Templeton: No.

Murdo Fraser: What needs to happen?

Dr Templeton: People in the Scottish Government are trying to source the funding, but there is currently no clarity on it.

Professor Holden: The funding that supported the expansion of genome sequencing was from the test and protect programme, I think. As members will be aware, budgets have changed as we have moved on. We had a year's budget from that source, but funding going forward is not part of a centralised core stream. There is therefore a need to identify a source of funding for the service as we shift from Covid response funding, and to look at the potential for longer-term funding.

As Mike Gray indicated, when we have funding that can keep the service going, we also need to be able to invest in skills and personnel and to offer contracts. It is very difficult to offer contracts when we do not have projected funding for the future. Our current funding will end at the end of March; colleagues can speak about the impact that that has had on staff retention because of uncertainty. We are working hard with colleagues in the Scottish Government and PHS, and in the labs. The funding element is very much on our minds at present, and it poses a potential threat for the future.

Murdo Fraser: Thank you. I think that Professor Peacock indicated that she wants to come in.

Professor Peacock: No. I am sorry—I think that it might have been Rory Gunson.

Professor Gunson: I want to follow on from what Matt Holden said, and to build on what Mike Gray said. In Glasgow, we have employed people and trained them. There was previously very little sequencing experience in the NHS, but we have got people up to quite a high level of experience that we can build on in the future. However, because of the temporary nature of the funding, they have jumped to permanent posts as we have neared the end of the contract. We need long-term funding so that we can build on that experience. Those people could then be used to do the sequencing.

They could also turn their attention to some of the other pathogens that Kate mentioned, or look at what we currently do and consider how we could do it better. We have a plan that has been in place for a while, but the funding needs to be aligned with that plan so that we can build on it, rather than having to start again in a few months, which is my current concern.

Jim Fairlie: Guys, your responses keep on throwing up more questions than answers.

I will come to Professor Holden first, if he does not mind. This has nothing to do with the committee's inquiry, but your comments sparked

some interest in me. You talked about ancestral genomes. What time range does that ancestry cover? Does it depend on the particular genome? That question is purely for my own interest.

Professor Holden: As you know, organisms evolve, and their genomes pick up mutations. We can use the rate at which they accumulate mutations almost like a clock to work backwards in time.

Colleagues can correct me if I am wrong, but something such as SARS-CoV-2, or severe acute respiratory syndrome coronavirus 2, mutates about—

Dr Templeton: Twice every eight weeks.

10:45

Professor Holden: Yes. There are two mutations every eight weeks; it is like a clock, so we can work backwards to its ancestry. When we sequence genomes, we can effectively build what we call phylogenies, or family trees, from which we can reconstruct the evolutionary history. Those are informative in identifying groups of very closely-related strains that might be part of an outbreak or a successful lineage. However, other organisms—

Jim Fairlie: Does that allow you to forward plan?

Professor Holden: There is information that we can get from the mutations that can tell us the potential evolutionary trajectory and how much scope there is for variation. At present, that raises an interesting question. We saw omicron come in, and it has, in effect, settled and become the dominant strain. However, in the way that omicron is now evolving—in contrast with the previous alpha, beta and delta variants, which were very different—it seems to be throwing off the smaller subvariants with mutations that are cropping up independently in the same population.

People are looking at that and asking whether it predicts what we are now going to face in terms of future threats. Will we see small reinventions of the same thing, or big jumps? To be frank, that is something for research. It is very difficult to use that information to plan effectively, because there is so much uncertainty. Nonetheless, we can use the information that we get from looking backwards to think about what is possible in the future.

Jim Fairlie: Okay.

Dr Templeton: Within a month, we can make predictions. For example, when we see a variant such as BQ1—which Matt Holden talked about—increasing, we can see the rate of change over one week: it suddenly pops up and is way in front of all the others. We have the epidemiological information on whether all those BQ1 cases are in intensive care units or are all hospitalised and requiring oxygen, and the epi team in PHS is able to add to that. If we see that happening in the first week, we know that in the next three or four weeks we will be hitting a time when we will have more ICU admissions.

Right now, that information is not a long-term tool, but it is a short-term prediction tool from which we are able to infer certain things.

Professor Holden: That is the basis for the variant technical reports that the UK Health Security Agency produces, to which Public Health Scotland contributes. They look at the current behaviour patterns of a new variant that seems to be on the way up, in order to make predictions about how potentially severe the infections will be or how the variant will escape vaccines.

Jim Fairlie: That can give you information to pass on to health boards to say, “This is what it looks like, and this is what we think is coming.”

Professor Holden: Yes.

Jim Fairlie: Fantastic.

I have a load of wee questions, so I ask you to bear with me. My first question is on working together. I put this to the previous panel; I do not know whether you heard it. Were you working in silos before, and are you now out of those silos? From the sound of it, you all had a reasonably good working relationship, which has grown into a team effort. However, as we heard earlier from the lad from SEPA, he is beginning to feel that the barriers are now coming back up at UK level. Do you have the same concern, or are you still working as a team?

Dr Templeton: We are absolutely still working as a team. Even in relation to COG-UK, there are still talks and things going on, so we are still connected. It has given us a fantastic connection with other academic groups for what we do as we move forward.

With regard to the link between Rory, me and Matt, we are basically going forward for accreditation as a single service. We might not all be in the same building, but we see ourselves as a single service working together.

Jim Fairlie: I am concerned by the fact that you have all talked about the lack of funding next year. As someone with a background in sheep farming, I know that antimicrobial resistance is a major problem in that sector, because of the overuse of antibiotics, wormers and all that stuff. What work are you doing on that? Is that the kind of thing that you could put to Government? I know that it sounds like you are selling something, but, in effect, that is what you are doing. Can you say to Government, “This is what we’re working on and, if

we can keep the genomic service going, we can put something more in place that will add value to what we're already doing"? I know that it sounds ridiculous to have to say that, but can you put something like that to Government to maintain your funding?

Professor Holden: Yes.

Mike Gray: Yes.

Jim Fairlie: Do you want to expand on that? [*Laughter.*]

Dr Templeton: Matt Holden and I recently had a PhD student who was working on an organism called VRE or vancomycin-resistant enterococcus, which shows its resistance in its very name—the "vancomycin-resistant" bit. Unfortunately, Scotland has the worst rates in the whole of Europe, but at the moment, we are not—

Jim Fairlie: What is it?

Dr Templeton: It is a bacterium.

Jim Fairlie: Right. What does it do?

Dr Templeton: It causes infection. It is not as bad as staph aureus or some other bacterial infections, but it can cause nasty infections in hospital. In particular, it gets into those areas where there are lots of plastics, so those kinds of units—units for haematology and cancer patients, for example, and other places with very vulnerable patients—are a problem.

For whatever reason, Scotland has the highest rate in Europe; we would like to be able to do a lot more work to understand why, and one of the ways of doing so is through whole-genome sequencing. At the moment, you can treat vancomycin-resistant bacteria with another drug called linezolid, but if that goes, you lose your last-line antibiotic for that infection. Matt Holden can say more about that, because he has been involved in that work, but it is an example of something that we are not doing anything about. It forms part of research projects at the moment, but it should be something that Scotland is doing something about.

Professor Holden: When we make the case for extending support and for future support, we are always making it clear that this technology is very applicable to other threats, such as AMR—in fact, particularly AMR. It can probably add more value than has so far been the case, because of the detail that you get from it.

I can illustrate that with reference to the work that Kate Templeton has mentioned. PHS has had a request to develop a service to deal with that issue, using existing capacity. We have a governance structure in place, and we are looking at developing a pathogen genomics strategy going forward and at expanding the service, utilising the capacity that we have already built. Moreover, a paper has been put forward for consideration and recommendation that looks at whether to develop a service to support the use of whole-genome sequencing in order to characterise all the strains that are coming from hospital-acquired infections and, as a result, get better intelligence on what is circulating in Scotland and how it is spreading.

Jim Fairlie: That is excellent. Professor Peacock, did you want to come in?

Professor Peacock: I just want to build on the AMR story and extend that to other areas where we definitely need sequencing.

I completely concur with colleagues about the importance of building our capacity with regard to the issue of antimicrobial resistance. By doing so, we will detect the emergence of new resistance and enable the tracking of it, as we have done with SARS-CoV-2. In particular, AMR can be very impactful on patient outcomes in hospitals when there are multidrug-resistant outbreaks. We have already heard that the capability to carry out outbreak investigations on multidrug-resistant pathogens in, say, intensive care units is not available in most places, but it is really important in trying to bring those outbreaks under control.

Other areas to think about with regard to having sustainable countrywide sequencing capability include food-borne pathogens and food-borne associated outbreaks. There is an increasing trend to automatically sequence all pathogens that could be associated with a food-borne outbreak and then use the sequence data to detect outbreaks, instead of doing it the other way round. In traditional food epidemiology, you would need to look at clusters of people with food-borne associated disease in an outbreak and then sequence the organism to see whether the cases were related.

However, that approach is now being flipped on its head, because we have found that, if we sequence all the pathogens, we can detect outbreaks really early and be guided by the genome data rather than the epidemiology. Given the food production processes that we have, food from a single source can be found across the country and, indeed, across the world, so the advantage of the genome data is that it can allow you to detect where the outbreak might be coming from.

There was a really good example of that a few years ago. An organism called listeria got into a food production process—in that case, sandwich preparation. The sandwiches were sent to hospitals across England, and it was only the sequencing that captured the fact that there was an outbreak—and it happened way before there was an exceedance in numbers. Colleagues might

want to expand on that, but the detection of food-borne outbreaks using sequencing as a very powerful detection tool is important.

Tuberculosis is another area of importance. Indeed, the UK developed one of the first sequencing capabilities for TB. There are a number of reasons why you would want to do that. First of all, sequencing can detect multidrug resistance in TB much faster than laboratory methodology; in fact, you can get to that answer in a day or so, whereas, with the culture methods, it can take weeks or months to detect that sort of thing. You will want to know whether TB is multidrug resistant before it starts to spread, and you can also look at how it is spreading in the community. As Matt Holden has said, you can connect two cases, because of the relatedness of the genome, and see whether an outbreak is occurring.

AMR is really important, but we need to think about the much wider piece and about where sequencing has already been established but really needs to be consolidated in the national service.

Jim Fairlie: With your reference to food-borne pathogens, you have just raised a whole new load of questions. That work is vital, given the global food supply chain. Indeed, a number of years ago, we had an E coli outbreak that killed quite a number of people. Are you doing any work on that in the food industry?

I have to say that you kind of confused me when you said that you were flipping the approach on its head. Where do you go to catch an outbreak in the first place, if you do not yet know that there is a problem?

Dr Templeton: All shiga toxin-producing E coli are already sequenced in Scotland, as are all the TB cases, and that is giving us a great opportunity to put people on the right drugs so that there is a full, linked-up, four-nations response in our TB work as well as our work on STEC. Salmonella is also sequenced in Scotland, as a result of the pre-existing work. Again, that is linked across the four nations; indeed, that has to be the case in order for us to understand it. However, there are gaps, and there is definitely a role to play in improving things and ensuring that we always connect all the dots, so we would like to build on that.

Professor Holden: Work is on-going to bring together the domains of clinical, animal and food health, and Public Health Scotland is leading on the gap analysis that is under way, with discussions involving stakeholders on where genome sequencing fits in and how we support that in recognition of the way in which the infrastructure works. For example, different labs do the microbiology work for the food, animal and clinical domains, so that is an area that could be developed.

With regard to what you said about flipping the process on its head, which goes back to a point made by Sharon Peacock, I would just point out that, in order to detect an outbreak, we are often reliant on looking at the numbers of cases and seeing whether there has been an increase. From that, we will investigate those cases, which will often involve looking for links between them—a common food source, for example—by carrying out an epidemiological investigation.

What Sharon is suggesting—at least, this is the aim—is that we routinely sequence all clinical isolates; if someone were to present with a salmonella infection, say, you would sequence it and automatically look at whether any samples were closely related. If you found that they were, you would know that they probably had a common source. Then, you could go straight in and investigate the epidemiology without waiting for the cases to pop up and somebody somewhere to say, “Hang on a minute—we’ve got 10 cases in Lanarkshire. We should do something about that.”

Jim Fairlie: That is excellent. Thank you.

11:00

John Mason: The session has been very interesting so far. Everyone has mentioned the issue of funding, but I have to say that we have not heard a lot of numbers. I do not know whether it is your area, Mr Gray, but would you like to put a figure on how much money we need?

Mike Gray: I will pass that over to the experts. What were the original and then the proposed bids?

Dr Templeton: The original bid was £14 million. That is what we originally asked for, but we have not actually spent anything like that, because we imagined that there would be a lot more Covid. We are closer to about £8 million—

John Mason: That is what you have actually spent.

Dr Templeton: Yes, although we are not at the end of the financial year. That figure was for the whole programme, not just for one year. We have been putting bids together, and the one that we would prefer is around the £5 million mark, I think.

John Mason: Is that per year?

Dr Templeton: Yes.

John Mason: And is that for Scotland?

Dr Templeton: Yes.

John Mason: You have all made the point that it has been good to work across the UK on this.

One would presume that there should be UK funding for work right across the UK, so perhaps some of this funding would come from Westminster.

Dr Templeton: I do not think so. After all, the whole of health is devolved in Scotland.

Mike Gray: It comes up the road and goes back down the road again. In other words, UK funding comes here, I think, and then decisions are made here to pass it out to the Scottish system. That is how we understand the system, but you guys will know more than we do.

John Mason: That is fair enough. I was just wondering about the financial side of things, because that is my background. Every part of this seems to work differently, but your response has been helpful and clarifies things a bit.

Professor Peacock, your report in particular was very glowing about how things went, and COG-UK seems to have been a total success. There is, in fact, nothing negative in the report at all. I think that RAND Europe did an overview, too, and everything that it said was also positive. Surely something went wrong. Could some things have been done better? For example, did people not join up as quickly as they should have done? Is there anything that did not go right?

Professor Peacock: You are right—the report was glowing, but that is because the response itself was largely glowing. It was quite remarkable for 21 different organisations to sign a legal agreement, have a data-sharing agreement and have everything working together.

Day to day, there were some bumps. First, we had to work in an imperfect situation, so we really had to focus on outcomes over process. People often likened it to trying to take off in an aeroplane before the wings had been fixed on. We were constantly working very hard to close any gaps.

At the same time, the system was changing very quickly. Overnight, we might realise that a whole new testing centre or a new Lighthouse lab had opened up, and we then had to connect that to our sequencing capability—which, I should say, is connected to 105 NHS testing labs and all of the Lighthouse labs that fed into our sequencing. I am not suggesting that it was altogether easy—it was really tough going—but, overall, it was a glowing response to the situation.

If I could have changed one thing from the very beginning, it would have been ensuring that we had better data connectivity and integration. It was a function of very large-scale testing being stood up across the country. Initially, the data flows from that were quite challenging, and we needed that limited amount of data. We needed to know where the sample had come from, what date it was taken and who gave it, because we needed to match it to that person's genome and provide that data to the public health agencies. The biggest problem that we faced constantly was data connectivity and integration and trying to make all that run smoothly.

Often, it was a barrier to getting the data available very quickly. We can sequence very quickly, but until we have connected it to the person's data, it is of no value to anybody. Data connectivity got faster, but it was quite problematic at the outset.

John Mason: Is that because we in the UK are too fanatical about privacy?

Professor Peacock: There are several reasons for it. The connectivity systems were not necessarily in place in the first instance, and that could have been partly driven by privacy issues. Another issue, however, was that the new systems that were being built from scratch had no data connectivity. For example, the major Lighthouse labs had to build their own data connectivity systems and then plug them into the rest of a highly complex data system. It was inevitable that, on the first day on which the Lighthouse labs were open, they had to start with someone collecting information on a piece of paper and then rapidly integrating that data into the wider UK picture.

Therefore, privacy was not the only issue. During the pandemic, we saw a lot of changes in how data could be shared, and those changes have really helped with data integration and sharing. It was largely a combination of the system that we had when we went into the pandemic and the fact that so many new things came in that were not connected to the original system.

John Mason: Okay. So far, we have mainly mentioned connectivity within the UK picture, but what about the international scene? How have other countries been doing with genome sequencing, and how are they planning to go forward? We tend to think of America as the leader on such matters. Where does it stand in all of this? What about the rest of Europe?

Professor Peacock: I can start to answer that, and then others might want to come in.

First, all our data was immediately shared with the Global Initiative on Sharing Avian Influenza Data—GISAID—international database. As soon as we had data we would share it, and we also had an open access policy on our methods and protocols. In many ways, therefore, we were leading on the analysis of genomes and developing methods by which people could analyse their own genomes. Everything was made public. At one point, the UK was producing 50 per cent of the genomes in that global database, so we were very much ahead of the curve.

Many other countries did an excellent job, too. For example, Canada had a similar initiative to ours, and many European countries such as Denmark undertook good sequencing. The US was hampered on the pace at which it stood up its genome sequencing because it is such a large country and every state has its own systems for sequencing and testing. Joining those up was quite a challenge.

Others on the panel might have something to say on the matter, too.

John Mason: The universities tend to have good relationships with others around the world. I wonder whether either Dr Templeton or Professor Gunson has experience of working internationally on this issue.

Dr Templeton: I mention monkeypox, which is a good example. The pathogen was known about, but the whole virus had not been sequenced at scale much before the outbreak arrived. We were able to connect with Yale University, which provided us with primer sequences. We then sequenced the virus by using the same techniques as we had there, and then we published our work. That all came about through connections that have developed from COG and beyond it, through which we are always trying to find out what other people are doing. The position has definitely been helped by having had connections built up from COG.

John Mason: How would developing countries cope? They were often slow to get vaccines. Would some of them have struggled in that area?

Dr Templeton: There have been various initiatives, again through COG. I have done various projects in Uganda. Through the Fleming fund of the University of Edinburgh we are trying to train up fellows in Uganda on AMR and are setting up processes in their labs. It is a UK-funded initiative through the Fleming fund programme. Through it there have been connections that have enabled them to be trained up on whole-genome sequencing as well.

The technique that we were using for Covid was first employed on Ebola in the 2014 outbreak. Most of the affected countries do not want samples to move outside them; instead, they want sequencing to be done locally. So, the beauty of the technique that we were using was that it could be done locally in the country. The ARTIC network's protocol for sequencing, which we used, is what was used for Ebola.

That approach requires scientists to go out and find funding, whether it be through the Fleming fund or others, which is difficult. With the money that we hope to get we focus on delivering the service that the Scottish Government has asked us to. If it were to involve having connections with other countries, that could be part of it. However, at the moment we are working with our academic or university hats on.

John Mason: Professor Gunson, have you anything to add on international relationships?

Professor Gunson: The position is very much as Kate Templeton has described it. I am aware of initiatives through the University of Glasgow, although I am not directly involved in its training of people and trying to push the technology back into those countries so that they can use them locally. I am also aware of the initiatives that Sharon Peacock alluded to concerning what COG-UK has done.

The sharing of data is probably the key element in all rapid responses. If people have complete access to what is going on in other countries they can respond much more quickly. That has been the great benefit from Covid and COG-UK, I have to say.

John Mason: Okay, thanks.

My final point concerns a question that I put to the earlier panel, which was about the desire to have a chief scientist for public health. Does any of you have an opinion on that?

Dr Templeton: The only thing that we find difficult is knowing who we should go to to ask for money, as Matt Holden has already alluded to. We would like to be able to go to one person whom we know is responsible for that and who has the hat of responsibility on their head. However, the current position is not clear, because the test and protect process has stopped. Various departments are involved, as is NHS National Services Scotland, which gets its funding through a different route. If having a chief scientist for public health would make the process easier, that would be good.

Mike Gray: I would probably advocate for having such a role. I will sound like a broken record, but if that job could start to make the connections on what workforce is required to deliver for Scotland, that would be beneficial. The UK is not a set of four equal countries as far as the development of healthcare science in England, Wales, Scotland and Northern Ireland is concerned. Scotland is fairly poorly apportioned for on the development of all healthcare science training posts.

If a chief scientist for public health were to be involved in conversations about sustainability and contingency planning, that would be helpful. Would you believe that while my colleagues were talking about antimicrobial resistance in sheep flocks and so on, I wrote down here the words "genomic fire brigade"?

If we think about it, there are two parts to this situation. When we ask for cash, are we adding value? Absolutely. The second part is about business continuity. We would not hire a fire brigade on a temporary contract, to be switched off in March. We do not know what the next issue coming over the horizon will be. Having even a small amount of money would allow us to develop a coherent workforce. If having a chief scientist for public health could help with that, it would be fabulous.

John Mason: I am tempted to get into a debate on some of that. As you will probably know, in the political field everyone wants the money to go into accident and emergency, to deal with the actual issues.

Mike Gray: Of course.

John Mason: What you are asking for would probably be seen as preventative spend, on which there is a bit of pressure.

Professor Peacock: I go back to your previous question about our involvement overseas. I will make two quick points. One is that COG-UK was very much plugged into the Foreign, Commonwealth and Development Office, which would often bring us into various meetings and interactions with people.

The second point is that there was huge inequity in access to sequencing capability, in the same way as there was with access to vaccines. Given that we had only a limited budget, we spun out a training arm called COG-Train, which developed online courses that took people through every step of how to do sequencing. It included virtual classrooms and train-the-trainer courses.

11:15

We felt that that training underpinned the work. We could not provide the funding or the equipment for countries to do sequencing, but we could provide support for training, so that is where we invested our time for the amount of money that we had, which we thought would give us the best outcome.

John Mason: That sounds very positive. Does Professor Gunson want to come in?

Professor Gunson: On the question of a chief scientist for public health, it would be a good idea if—and it is a big if—it were to bring together all the separate streams that currently seem to be working in silos. That includes pandemic planning, animals—which we have talked about—and food. If all that could be brought together under one strategy, and one person, it would make things a lot simpler. There is currently a lot of separate planning that does not seem to take account of what is happening elsewhere.

Mike Gray's point was clear. If we have a long-term strategy that brings all those things together, we can plan the staffing. At present, we know what we want to do, but there has not been any long-term planning around staffing for labs and the scientific side of things, or for bioinformatics analysis. All those things need to be built up alongside the lab plan to ensure that we can actually deliver at the end of the process.

As we have described, there is so much potential with this technology. We just need to ensure that we have the people in place to be able to deliver it.

John Mason: Thank you—that is helpful. I am sure that the Government is watching this session, but we can perhaps also raise some of those points with it.

The Convener: I will come in on one point. I know that there is currently no workforce development strategy in place. I take it from what you have said that genome sequencing is quite specialised. Would there be any challenges with training staff, or staffing issues, if you were to develop a future workforce strategy?

Dr Templeton: We have shown that we can do it. Over the past year or 18 months, we have recruited around 20 people in Edinburgh and trained them up to be able to deliver the big capacity that has been required.

If we got rid of that, all that would happen would be that, two years down the line, we would suddenly go back to square 1. I do not know whether we would find the same level of people—we probably would, but we would be going back and starting again.

There is also the train-the-trainers element; we would need the experts to train people. They may go and find some other role, so we would not have the expertise to be able to cascade the training down. It would not be impossible if we lost the funding, but that would definitely set us a long way back.

The Convener: I will bring in Professor Gunson. I am sorry, but we have only a couple more minutes before we have to finish.

Professor Gunson: I will be quick. As Kate said, we can train people. I would like to see the training built into some of the core preliminary training for biomedical and clinical scientist staff, so that we bring into laboratories more of those people who already have the experience that we can retain and then build on.

We also need to look at the management side—for example, how we manage the laboratories and address the quality process. In addition, we should not forget bioinformatics, which Matt Holden may want to speak to. There is also a need in that area

to develop people and have those positions available to recruit to.

We can definitely do it, but there needs to be additional funding for some of those core training groups.

The Convener: I will bring in Jim Fairlie, very quickly.

Jim Fairlie: To stick with Mike Gray's fire service analogy, are we looking for a retained fire service in the scientific community that can respond quickly and keep the information flowing? Is that effectively what you are asking for?

Mike Gray: In an absolute worst-case scenario, yes. We do not want to look at a worst-case scenario, however—we want what colleagues have described today, which is a well-trained workforce. If the question is, "If there was 50 quid left in the budget, what would you do?" the answer is that, yes, we would work towards some sort of business continuity. However, that would not deliver any of the benefits that we have talked about today.

Jim Fairlie: You said that Scotland is poorly served in terms of the workforce. Why?

Mike Gray: Clearly, healthcare is devolved. We can look at bare numbers for healthcare science across all the healthcare disciplines, such as physics, genomics, bacteriology, chemistry and so on. In England next year, there are 600 funded places; in Wales, there are 60 funded places; and in Scotland, there are four. That is based on information from NHS Education for Scotland.

Jim Fairlie: Okay—thank you.

The Convener: Thank you. That is us at time today. I thank all the witnesses for their evidence and for giving us their time this morning. If any of you would like to raise any further evidence with the committee, you can do so in writing; the clerks will be happy to liaise with you on how to do that.

The committee's next meeting will be in the new year, and the details will be published on our website in due course. That concludes the public part of our meeting this morning. We now move into private session.

11:21

Meeting continued in private until 11:29.

Published in Edinburgh by the Scottish Parliamentary Corporate Body, the Scottish Parliament, Edinburgh, EH99 1SP

All documents are available on
the Scottish Parliament website at:

www.parliament.scot

Information on non-endorsed print suppliers
is available here:

www.parliament.scot/documents

For information on the Scottish Parliament contact
Public Information on:

Telephone: 0131 348 5000
Textphone: 0800 092 7100
Email: sp.info@parliament.scot

The Scottish Parliament
Pàrlamaid na h-Alba