SCOTTISH HOSPITALS INQUIRY

Hearings Commencing
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CONTENTS

THE CHAIR: Good morning, everyone. Now, I think we're able to begin with Professor Leanord.

MR CONNAL: Indeed, my Lord.

THE CHAIR: Good morning, Professor Leanord.

THE WITNESS: Good morning

THE CHAIR: As you know, you're about to be asked questions by Mr Connal, who's sitting opposite to you. But first of all, I understand that you're willing to affirm?

THE WITNESS: I am.

Professor Alistair Leanord

Affirmed

THE CHAIR: Thank you, Professor. Now, your evidence is scheduled, I think, to go over the whole day. We will take our usual coffee break at about half past eleven, but if at any other stage you wish to take a break, just give me an indication and we can do that.

A Thank you.

THE CHAIR: Please feel that you're in control of the situation. Thank you. Now, Mr Connal.

Questioned by Mr Connal

Q I'm obliged, my Lord. Good morning, Professor Leanord. You have produced a witness statement and a supplementary statement and, subject to a point that I'll add in a minute, are you happy to adopt these documents as your evidence at the Inquiry?

A I am.

Q The point that I'm adding at your request, I think, is that there was there was one area where the phraseology that has been deployed you now think needs tidied up, if I can use that as a neutral phrase, and probably easiest if we simply pick that up at a convenient point when we go through the statement.

A That is correct, and thank you.

Q Now, I'll come and ask you about your current position just in a moment. Can I just ask you about one point of detail that's been raised with me? If we go to your witness statement at page 76-- and I'm using the electronic page numbers, which will appear on the screen. That's the supplemental statement there. It's the witness statement. No, still the wrong one. Thank you.

So, we go to page 76. It's a point of pure detail. In paragraph 14 on page 76, you say you were clinical lead for the HAI team at HPS. Now, it's been suggested to me that, in fact, Professor Jacqui Reilly was the clinical lead of that team. Could that be correct?

A Yes. I probably used NHS GGC nomenclature. I would have been the microbiologist for the antimicrobial

resistance in the HAI team.

Q So, the point that's been suggested to me – that Professor Jacqui Reilly was the clinical lead is correct – is that right?

A That's correct.

Q Thank you very much. In terms of your involvement, we know that you prepared what I'll call for short the "whole genome sequencing report". That's not the full title, but we won't bother repeating all of that. We'll find that later. It's, for the notes, in bundle 6, document 40 at page 1195, but we don't need to bring that on the screen at present. You were acting lead Infection Control doctor in NHS GGC from November 2019. Is that correct?

A Correct.

Q Now, I'm going to use-- As I think I've indicated to you in advance, I'm going to use your witness statement as a kind of guide to help us get through the evidence. It may not always mean that we have a logical sequence or a chronological sequence, but we'll do the best we can. Can I just ask you about something that crops up on page 78 of your statement in paragraph 26? This is following on you explaining a number of the roles that you had. You say there:

> "...the pressing piece of work was to develop a Standard operating Procedure that described patient placement, as per Infection Control requirements in the specialised [ventilation] pressure rooms."

Now, I think I'm right in saying that at various points of your statement you make the point that you don't regard yourself as any particular skills in hospital ventilation. Is that correct?

A That's correct.

Q I think it's mentioned at various places.

A I would say I've got a working understanding, but I would not call myself an expert in any way.

Q Would I be right in thinking – because we've had some evidence on this as you probably gather, in fact quite a lot of evidence about ventilation – that in order to create an SOP for patient placement, you would need to understand the ventilation properties of all the different rooms that were potentially available for placing a patient in?

A That's correct.

Q Can you help us at all as to why, as late as 2019, this issue was still outstanding?

A My understanding was that there was issues with the ventilation in various rooms. The rooms themselves were quite complicated; some had HEPA

filters, some didn't have HEPA filters, some had lobbies, some didn't have lobbies, and those issues were being worked through. It was very clear that this was a piece of work that needed to be done for-- well, to ensure patients were placed in the right place, either if they were infectious or if they needed protected.

I looked, and we had ventilation engineers looking at all these rooms when we started that piece of work around about September-- probably September or October of 2019, and we came up with a document that allowed us and clinical teams to put the patients in the safest possible place within the extant release date that we possibly could to ensure no risk to patients, staff or visitors.

Q As a matter of principle, when should that SOP have been available? At the opening perhaps?

A Ideally, yes, you should have a full understanding of your ventilation rooms, how they were operating, and I would have thought that the Infection Control team would have been able to use that information to develop an SOP in fairly short order.

A Can we go to page 82, because I just want to make sure that his Lordship has an understanding of what your current role means? You say, at the top of that page, your role is Chief of Medicine for Diagnostics, Glasgow, and then you say, "This is a medical management role," but help me, Professor, what's a medical management role?

A Well, a medical management role is a doctor who has got some management responsibilities and works closely with the clinical director or-- sorry, not the clinical director, the director of the diagnostic service, such that we can take issues that are requiring both management skills and financial skills, which would be our director, and clinical and medical skills, which would come through myself.

Q So, is it-- So far as that part of your post is concerned, is it mainly managing things rather than involved in anything clinical?

A That side of my role, yes. My clinical-- what's called DCCs, or direct clinical care, now come out of the reference lab for which I am the director. I do-- no longer do any out of hours on call for the Microbiology Team, and I don't do any duty room activity for the Microbiology Team.

A Yes. So, I think further down that page, you say that you cease doing what you might describe as Infection Control type work in 2023. Is that right?

A Yes. I demitted from leading-- lead Infection Control doctor in June ‘21.

Q But you were still doing duty hours and out of hours?

A I was still doing-- that was clinical microbiology and, occasionally, I do backfill for the Infection Control team because they're a small team, and so I will backfill on annual leave, but that's become less and less frequent as that team has grown.

Q Thank you. Well, we'll perhaps move on from that to the topic of the new hospital, which we touch on at page 84 of your witness statements. You're asked, there, a question I think almost everybody has been asked, which is, "What involvement did you have in the planning and design of the new hospital?" and the only involvement that you're noted as having was looking at the floor plans for the microbiology department. Is that right?

A That's correct.

Q Did you look at the ventilation requirements at all?

A In the microbiology block? No.

Q Okay, let's move on then. On page 85 of your statement, you say that when the new hospital opened, and I'm-- I'm generally, if I talk about the new hospital, I'm meaning the whole of the new hospital, I'm not going to say QEUH and RHC every time. When the new hospital opened, you were the clinical lead in microbiology and you set out various things that would be done at that time, and then on page 86 you say that the biggest concern you heard of from colleagues was that they had lost their offices, and I think this is something we heard from someone else that, traditionally, people are used to having their offices sort of close at hand and they're all put in a block somewhere else, basically, is that right?

A That's correct.

Q Now, is it not the case that in 2015 people like Dr Peters and Dr Redding and so on were reporting, or at least bringing you by way of copy, information about concerns that they had about the new hospital?

A I don't remember any specifics. I'm sure there's-- they would have if I got copied in. I would have taken that as a professional courtesy that I was to be-- was being informed. I wasn't directly involved in their concerns.

Q I'm just wondering because what-- you've picked up a point, as I say, that the other witnesses have talked about, the business about the offices, but you didn't mention there any concerns about the building or the ventilation in the building or anything of that kind?

A Certainly in 2015, I wasn't-- I was unaware of those concerns specifically.

Q And just so we can

understand, you were clinical lead in Microbiology, but prior to November '19, no Infection Control responsibilities. Is that right?

A That's correct.

Q I think that's what you say, just so we know where we've got to on page 88 of your witness statement. Now, we know then you did become involved in the Infection Control process, and we'll come to touch on at least some of the details of that later, but on page 90 of your witness statement, you're asked in question 90-- well, here you are, you arrived, you haven't had Infection Control responsibilities, "What support did you get to bring you up to speed?" And you say:

> "Support from within the IPCT from colleagues who had more experience and knowledge of issues in the hospital at that point than I did."

And who were they?

A Well, I reached out to Dr Inkster. I needed to try and understand, as much as I could, the background and the issues because they were still very much live. The-- Sandra Devine, who was the acting Infection Control manager, was very helpful as well, as were her team of Infection Control doctors who had a lot of experience in the RHC at the time, and there were other colleagues around me who were Infection Control doctors, not necessarily in the QEUH or RHC, that I asked for advice from as well, again, to get me up to speed, and as you can imagine, I then refreshed my memory of the National Infection Control Manual, which I hadn't looked at for years.

Q Any other doctors involved in Infection Control other than Teresa Inkster, or is that the name that comes to mind?

A I had-- So, Dr Peters would have been along the corridor from me. I can't specifically remember if I went to her but, again, Dr Peters would have had a-- or does have a lot of experience within the issues that I was now going to inherit.

Q So you can't remember it, but it's possible that you also talked to Dr Peters about what the issues were?

A Yes, and in fact, I do actually remember I also talked to-- not necessarily while I was in Infection Control, but while I was clinical lead towards the end, not 2015, but sometime round about just before Dr Redding retired, she was telling me that she had the concerns about the ventilation system.

Q Thank you. Another name that has cropped up and, in fact, the Inquiry has heard evidence from her is-- I think

it's Ms Harvey-Wood, because she doesn't want the title of doctor applied, Kathleen Harvey-Wood. Her name is raised with you at page 99 of your statement. You're asked, "Well, what concerns were raised by her?" Were you aware that she had concerns about the organisms that were being found in 2A and 2B in the RHC?

A Not at that time, and as I said, in 2018, I'd-- was-- whole time in the Glasgow Royal Infirmary.

Q The reason I mention it is, obviously, I mean, you know who she is, I take it?

A Oh, of course, yes.

Q And by the time she retired, she had about-- I think we heard about 40 years of microbiology experience, focused almost exclusively on paediatrics. A very experienced person in that field, and she seemed to have been concerned about what she was finding in 2018. You are aware of that generally, are you?

A I am aware of her background, yes.

Q One thing I did want to ask you about the point at which you became involved in the IMTs, paragraph 145 which appears on page 101, I'm going to be picky with you at the moment and just ask you about one word. In paragraph 145, you're talking about Dr Emilia Crighton, Dr Crighton being a Public Health doctor, and it says, "She was selected to replace Dr Inkster." Now, can I ask you first of all, what do you know about her selection to replace Dr Inkster?

A Nothing. That's a form of the words. You could actually-- The sense was that she was there to replace. I didn't know about the background at that time. I was essentially a jobbing microbiologist.

Q The point I want to ask you about is that Dr Inkster was removed as Chair, Dr Crighton appears, you appear on the scene around that time, and at points thereafter you chair various IMTs. There seems to have been an impression on the part of some of the clinicians that the whole approach of the IMTs changed almost coincidental to that event from-- prior to that, focusing on, "What's the problem, how can we solve it?" to, after that, "How do we prove it's nothing to do with the hospital?" Now, that's evidence that the Inquiry has had from Dr Murphy and Dr Chaudhury. Now, is that a correct impression?

A Having never been to the previous IMTs, I wouldn't be able to answer that.

Q But you could tell me whether the emphasis after the change was on trying to show that infections were not connected to the hospital?

A Okay, absolutely. So, I understand that. I think the-- I think that's correct. I think that the IMT was trying to put onto strong evidential basis some of the assumptions that-- and/or hypotheses that were previously postulated.

THE CHAIR: Which word do you prefer? Assumptions or hypotheses?

A Hypotheses----

THE CHAIR: Thank you.

A -- that were previously postulated. I also thought that there was a willingness to close down hypotheses that didn't stand or didn't have evidential basis.

MR CONNAL: I wonder if I can come back to the question because, given the evidence that we've had, I'm quite keen to get your take on it. If the approach of the IMT moved to a focus of trying to show that the problems were not connected to the hospital environment, would that not be the wrong question to be asking?

A In a sense, yes. However, if you're looking at a hypothesis that doesn't inform or there is no evidence for, at some point you're either trying to prove a negative or you have to drop that hypothesis.

Q I'm sorry to labour the point, but it may be important because I think the argument might well be, “If that's what your aim is, that's not you doing your job in the IMT properly. If you're trying to show it's not anything to do with the hospital, that's not what you should be doing.”

A That's not what I said. Sorry.

Q Well, I-- Please explain.

A Maybe I-- If you have a hypothesis that you have concerns about the hospital and that hypothesis cannot be shown to be correct or there's no evidential basis on which to structure or pursue that hypothesis, then I would say you're either looking at proving negative or you have to accept that that hypothesis does not bear muster.

THE CHAIR: When you say "no evidential basis," do you mean no evidential basis or do you mean insufficient evidential basis to persuade the person who is making the judgment?

A I would say a combination of both. I think both of them could be true. You can start off-- I would say an IMT is a safe space. It should be a safe space where everybody can contribute. We pull together relevant members for an IMT with different expertise. I believe – and when I've chaired – that any proposal or hypothesis should be-- or should be and is allowed to be postulated, and then it's up to the IMT, with input from the experts around the table, about what are the most likely, which ones they should pursue,

and how they would go about either proving or disproving that hypothesis.

THE CHAIR: Thank you.

MR CONNAL: In the next paragraph, whole genome sequencing starts to make an appearance and, as I indicated, I'm going to come back to that general topic later on, but if I can just-- I need to just touch on one or two things at the moment. At that point in time, when you're looking, you say, at Enterobacter and Klebsiella – and I will apologise in advance if I get the pronunciation of these things wrong – how much sequencing of Enterobacter did you do at that time?

A In 2019 for the IMT?

Q Yes.

A Not as much as is in the report.

Q Well, if we just stick to 2019 at the moment to try and get a picture.

A 2019. Yes, okay. So, this came out of the SBAR that Dr Peters and Dr Inkster presented to the IMT during Enterobacter increasing. I realised-- and I think it was my second or third meeting I realised that we had the ability within the reference lab, with both expertise and equipment, to try and show what was happening behind these bar graphs that were there, either to identify transmission or to show that transmission was not an issue.

Q I'm just trying at the moment to get some kind of flavour for, you know, how much did you do at that time, where from, and so on.

A So, we looked at-- We needed to do it at pace because we needed to-- I wanted to use it to reassure the clinicians. We looked at-- I would say it got chunked up into weeks. The first week we would have identified as many Enterobacteria as we could lay our hands on by interrogating the laboratory system, going into freezers, pulling out organisms. Week two would be growing the organisms, ensuring purity, extracting the DNA and sequencing. Week three would have been quality control of that sequencing output, and week four would have been the analysis and presentation at that time.

Q If you can't tell me at this distance, please just say so. Can you tell me how many samples of Enterobacter you sequenced at that time and whether these were from plates or from environmental samples?

A They were mostly from clinical samples at the time. I don't remember exactly how many isolates we managed to identify in that first week. I can give the Inquiry that information – it's on my laptop outwith this room – but it was very clearly an ad hoc analysis that was done quickly for a very specific reason.

Q I think the issue, as we know, is what significance you can draw from the various results. As I say, I'm going to come back to that in more general terms, but I think it might be worth pausing just here to ask this question. There seem to have been-- At least there appeared to be – and I'm using that phraseology specifically – an upsurge in these two organisms, and then they disappear later. Do you know why that is?

A Enterobacter and Klebsiella?

Q Yes.

A My own view is that when you look at the antibiotic use, I think that antibiotic-- broad-spectrum antibiotic use was a driver in the fact that we saw not necessarily only those organisms but other organisms as part of this outbreak. It's not the only reason, but I think there's multifactorial reasons. For Enterobacter and Klebsiella, I think there's a strong drive from antibiotic selective pressure.

THE CHAIR: Sorry, give me that again?

A From antibiotic selective pressure from the broad-spectrum antibiotics that were used in patients.

THE CHAIR: And the antibiotic is selective as to which organism it is?

A So, Klebsiella and Enterobacter and Stenotrophomonas-- I think there are signals in the data that will show that these, when you put somebody on a broad-spectrum antibiotic, you quite radically change their microbiome-- their gut microbiome, and if you have organisms that are resistant to that antibiotic, they will overgrow and predominate in that microbiome, and therefore you have a higher concentration of these organisms within the microbiome. When I mean microbiome, I'm talking about, essentially, your gut. Then those organisms would predominantly-- if there is gut translocation, would be able to enter the bloodstream and they would be the organisms by which you would see the infections occurring with.

THE CHAIR: Right. You'll have to excuse me for my rather ignorant approach to this. So, that-- If a patient group is receiving prophylaxis----?

A Possibly, or even treatment.

THE CHAIR: Or treatment by, I think you said a broad-spectrum antibiotic?

A Yes.

THE CHAIR: One would expect that that will be effective with-- in respect of some of the microorganisms in patients' biome, but not necessarily others, and therefore the others, unaffected by the antibiotic, will begin to predominate within the biome. Am I following this?

A Absolutely correct.

THE CHAIR: Right, and if you've got a larger number of particular microorganisms, then if there is transmission from the gut to the bloodstream, it is more likely that the transmission will be by these predominating microorganisms.

A Correct.

THE CHAIR: Right, okay. Thank you.

MR CONNAL: There is another part of your witness statement in which we deal with the same issue in the context of Stenotrophomonas, which we'll come to in due course----

A Correct.

Q -- but I just want to try and understand that proposition, because if this is all to do with the prescription of broad-spectrum antibiotics to a patient cohort, which we were dealing with here because this was 6A, which was the people who had had to move from another ward, would you not expect the pattern to continue?

A So, my supposition is it's not all to do with antibiotics, but I do believe antibiotics played a part. So, my view is that this is multifactorial. I think antibiotic stewardship played a part. I think the built environment played a part. I believe that possibly patient acuity played a part.

THE CHAIR: Sorry, patient----?

A Acuity, how sick your patient is. It's possible that patient numbers played a part, such that there was more activity, and also the way that the patients were cared for. I'm not saying any of them predominated, but all of them could have.

MR CONNAL: I'll leave my further questions on that until we come to Stenotrophomonas because of the twist with that one. Can I just ask you, when you were doing this at speed exercise, did you discuss these issues with, for instance, Dr Peters?

A No.

Q Any reason why not?

A I had no contact at that time with Dr Peters.

Q She was one of your clinical microbiology colleagues at that time, was she not?

A She was, but I was based in another hospital doing a different role.

Q Thank you.

THE CHAIR: Again, I apologise for my lack of understanding of these things. The first step in your four-week programme I've noted, possibly inaccurately, as pulling out the Enterobacter results. Now, I think you explained that these were largely or exclusively the results of blood sampling of patients. Am I right?

A At that time it would have been exclusively the sampling of blood sample-

- sorry, the blood sample patients. So, these patients would had an Enterobacter bacteremia.

THE CHAIR: Right, and these samples were recent samples?

A No, not necessarily. They would be stored samples. Normal procedure within the Microbiology departments is to store in -80 freezers all positive blood cultures, and we have an archive system that you can access and identify those samples, retrieve them, culture them and do whatever further testing you would like to do on them.

THE CHAIR: Right. So, because of the low temperature, the sample will be presumably maintained in its condition when it was for a sample?

A Absolutely, you take-- and it's also in a cryopreservative as well, and so the cells will sit there frozen and in a cryopreservative, and then you-- I was going to say, bring them back to life, but you re-- you culture them and, generally speaking, the re-culture rate is very high: 80/90 per cent.

THE CHAIR: When you talk about re-culture, it revivifies or becomes active?

A Absolutely.

THE CHAIR: Right. Now, you said that these were not exclusively recent. What sort of period of time?

A We would have looked from 2015 to the current date. The-- and it would be pure serendipity about what initial isolates the technician could put their hands on over that set period of time. We did a more extensive search laterally when we had fullness of time when we wanted to sequence a broader range of Enterobacter, and that did include some environmental samples but very few with Enterobacter.

THE CHAIR: Serendipity. Do I understand that not all samples from 2015 through to 2019 will have been archived in this way?

A Correct. You never get 100 per cent complete collection for whatever reasons. Either they've died, they haven't been put in the right place in the freezer or somebody has forgotten to follow the SOP and preserve them for potential further testing.

THE CHAIR: I appreciate that it's not a question that can be answered precisely, but what sort of proportion of the number of samples which were taken from patients in that period are archived?

A Mid-90 per cents.

THE CHAIR: Right. Okay. Thank you. Sorry. Sorry, Mr Connal.

MR CONNAL: While we're on this area, I've been asked to ask whether you're aware of the term "opportunistic plumbing pathogens". Is that one you've come across?

A Only through this Inquiry.

Q The question is whether the two organisms we're looking at here, Enterobacter and Klebsiella, are within that group.

A They are, but throughout this outbreak they have been exclusively placed within that category, whereas I have always understood these organisms to be enteric.

Q Just tell me what the difference is, then.

A Well, if you have an infection with either of these two organisms, you could either plate the-- their source could be from the plumbing, as you've described, with an OPPS, or a PPP, or they could be from the patient's own endogenous flora. Throughout all the analysis I've seen from this during this Inquiry, both those organisms have been placed within the environmental/enteric group, and I've never seen any suggestion that these were looked at individually to try and ascertain whether they have come from the environment or whether they have come from the patient themselves.

THE CHAIR: Right. My fault entirely. Can I just-- I should have got this immediately, but I didn't quite hear Mr Connal's description. The two microorganisms that we're discussing at the moment are----?

A Enterobacter.

THE CHAIR: Right, and that's the whole genus?

A The whole genus.

THE CHAIR: Right.

A And Klebsiella.

THE CHAIR: And Klebsiella.

A The whole genus.

THE CHAIR: Do I understand-- Again, if I'm following things, the source of both these genera may be environmental or may be enteric.

A Correct.

THE CHAIR: All right. Thank you. I just want to make sure that I'm keeping up. Mr Connal.

MR CONNAL: If they're enteric, can they then potentially enter the drainage system and cause infection to others?

A Of course, and that's how the environment itself would get propagated with these organisms.

Q Thank you. Now, if we could move on, I want to ask you about a slightly more general point. I was going to move on to page 104, but in fact-- I'll do that anyway, but I'm not sure the point necessarily relates to that precise moment in time. I suspect it's a much earlier point that I should have asked you about.

The suggestion's been made that a relatively early stage of Dr Peters' involvement in Infection Control at the

new hospital, she was in conversation with you, because you were her clinical lead, or whatever the right phrase is, and she was explaining some of her concerns about the building and what was going on in Infection Control. Now, first of all, do you remember having a conversation about these topics with her?

A I do not.

Q The suggestion then is-- and I need to ask you about it, nevertheless. The suggestion then is that in the course of that conversation-- and I'll say immediately it's explained, without any apparent ill intent, you said something to her along the lines of, "Why put your head above the parapet?" Do you have any recollection of saying that?

A No. However, it wasn't unusual for colleagues to have conversations with me. I would have taken that as almost like a pastoral conversation, where at that time a junior consultant, not that such a thing exists, was having a conversation with myself, who was slightly longer in the tooth, and I may have said – not that I do, but I can imagine myself saying that – "You do realise that this will not be an easy path to tread," or words to that effect.

Q I don't think that-- As you have no direct recollection of the conversation, it may not matter. The phrase "pipe down" or "you'll find things tough or things hard", something along these lines was suggested as a possible communication, and you recognise that as a conversation you may have had?

A Yes, but that particular phrase is an instruction, and I wasn't in the business or the place to instruct anybody, certainly not a consultant colleague, about what they thought best to do.

Q Yes. I think it was, at least as it was explained to us, it was taken not as a threat or an instruction but simply as an indication that “If you keep raising concerns, that could be a difficult road.”

A I don't dispute Dr Peters' recollection of that at all on that basis.

Q Thank you. Well, I think I can move on, then, to another issue that predates your Infection Control lead role in the IMTs, because I think the suggestion is that there were quite a few problems – or said to be quite a few problems – with the way Infection Control was being run in the new hospital, and this was concerning those who were involved with it.

Now, the first question I've been asked to put to you is, as soon as you got to learn about this, is that not something you could have sorted out from one of your previous positions, for instance, the HAI policy group, if there was some problem over, for instance, clarity of roles for ICDs?

A Whilst I was in the Scottish government?

Q Yes.

A I was involved in work in the Scottish government about trying to define that very point, the clarity of roles within an ICD, and we went round-- So, we had a number of meetings with what was called the Infection Control Network at the time. There was a paper developed at the time, but it never came to fruition. I'm not quite sure why, or either I left before it did come to fruition. I give this information to inform the Inquiry that that thinking had occurred at the Scottish government, and a piece of work was progressed along those lines.

Q Do you remember attending a meeting with all of the consultants in Infection Control with Mr Gardiner in September of 2019?

A Yes.

Q Now, I'll put the notes up just in a minute. It's dealt with in your witness statement at page 105. I suppose the general question I have, you know, given what you were hearing, did this bother you?

A Did it bother me at the meeting, or----?

A Well, was this a matter that concerned you once you heard about it?

A Of course. I took it very seriously.

A What did you do about that, then?

A Well, first off, I listened. I needed to understand exactly what the concerns were. I've seen the notes of a colleague in the bundle, and they more or less match my contemporaneous notes at the time. I've got no issue that what was discussed was discussed. I recognised that, as clinical director at the time, I had a responsibility, along with others, to try and see whether we could fix this. I use that term loosely, but there was a problem.

It was very clear what the problems were. It was to do with complexity of the workload, the scale of the workload, the feeling that there was not the skills within the full team to deal with the issues that the QE and RHC were throwing up, that there was a disconnect between the Infection Control team, IPCT – and by that I meant some of the nursing staff – and the ICDs.

There were concerns about accuracy of information, and there were also concerns about pressure to sign off workload, and the most fundamental issue that struck me was that my microbiology colleagues had resigned their Infection Control sessions, such that there was no effective Infection Control cover for that campus. Not only that, but two of our most experienced and well-

versed colleagues, Dr Inkster and Dr Peters, had demitted office, and so we were going to lose a wealth of experience and corporate knowledge about the issues at stake.

MR CONNAL: I think, in fairness and because it may help the way the Inquiry is recording the evidence, I'll just put up the note if you don't mind. This is in bundle 27, volume 4, page 354. Now, I think you've indicated you've seen this before. You've no issue with it. It broadly matches your own notes. That's your evidence today.

A Absolutely.

Q Yes. I tried to have a look to see what your contribution was, Professor Leanord. I think there's one reference on 355, because you're "AL" where you're saying, "The ICD role definition was never defined," and one or two other comments there including reference to some of the specialist areas that you're now encountering. Then on 358 I think there's another one or two comments.

Interestingly, near the top of the page, you say, "There's obviously an issue with the built environment. We're in a new area of how we deal with environment." Then you say you're not entirely convinced that what's in the environment is what you see in patients. It's possible.

So, that was possibly the start of an exchange on that topic back then?

A Yeah, possibly. I was certainly in active listening mode during those meetings.

Q Thank you. I think we can leave that minute, thank you very much. If we can just go to another point? Some of these, I'm afraid, by the nature that we're jumping around a little from topic to topic-- 107 in the witness statement. Now, what we're dealing with there is a decision on the safety of Ward 6A, which you touch on in paragraph 170. Now, what's said there is you're:

> "...asked by the Inquiry what view Professor Jones and I reached on the safety of Ward 6A from a microbiological perspective."

And you answer that by dealing with water testing results. Now, I suppose the question is does reviewing water testing results allow you to say whether the ward itself is safe?

A No, and you're absolutely right to point that out, but from a microbiological perspective, I was saying that the water was safe. I could not opine on anything else at that meeting as I had no data or information around about, for instance, the other hypothesis that was still in play at that point, which was the chilled beam units. I had no experience

of them. In fact, I've never even seen a chilled beam unit. I wouldn't know what it looks like, and I certainly didn't have any data on that. So, specifically, I was giving opinion on the safety or the wholesomeness of the water.

Q Did you visit the ward to help you form a view?

A Not at that time, but I had visited the ward.

Q But not for the purpose of this discussion?

A Not for the purpose of that discussion and, in fact, the information I would need would not necessarily-- for water safety would not necessarily be there.

Q As you say in this paragraph, one of the issues was that point of use filters had been fitted in that ward. So, whatever was in the water, if there was anything in the water, it wasn't going to reach beyond that.

A Absolutely. There were 0.2 micron filters. They were the last mechanical barrier to anything bypassing either the chlorine dioxide or the water management system that was there in place.

Q If we move on to 109, paragraph 177, when we're discussing what was or was not happening, you say, but halfway through 177:

> "My recollection is that the same environmental organisms were seen in infected patients in Yorkhill as was being seen in the RHC."

This is partly why I asked you about Dr Harvey-Wood earlier, because her evidence was very much to the contrary, that she was seeing very different things in the new hospital to what she saw in Yorkhill. That seemed to be what clinicians were saying as well. Do you have any views on that?

A So, they were broadly similar. We saw, if you like, the big-ticket organisms were there.

Q Just so we understand what you mean by that----

A So a-- Sorry, Enterobacter, Klebsiella, Stenotrophomonas for instance, were on both sites. I have seen in the bundle Dr Harvey-Wood's-- oh, sorry, Ms Harvey-Wood's data. That is count data. I've got no reason to have any concerns about that. The data is what the data is. The only thing I would say is that between periods from the old Yorkhill to the new Yorkhill-- or, sorry, to RHC, or between 2013 and now, we changed the way we identified organisms to a far more specific methodology, and although the methodology has not changed, there have been software upgrades between those periods which

could have allowed for better identification to genus and species level than we previously had.

Q As a matter of generality, if you're looking between, you know-- We know that, for instance, that what became Ward 2A moved from Yorkhill sort of lock, stock, and barrel. At least, that was a theory. Is it right to compare the brand-new flagship super-duper hospital with old Yorkhill?

A Yes, because that's all you have got to compare if you are looking at whether there was a change for better or for worse.

Q Was water testing done in Yorkhill, do you know?

A I'm sorry, I don't know.

Q Okay. If we look at the next couple of paragraphs, in 179 you say you think "...the idea that water in areas contaminated is a misconception." You make the point that water is not sterile. Is it correct that when you're dealing with immunocompromised patients you have to pay particular attention to the extent to which there are organisms in the water?

A I would say that water would be a risk, and therefore you would.

THE CHAIR: I wonder if I could ask you about this, Professor. Would I be right to read your statement as challenging the whole concept of contamination, or are you saying something else?

A I've got a very specific definition of contamination. Contamination is something within wholesome water that either pollutes it or makes it toxic or dangerous such that it cannot be ingested. That's what I would take as-- and that could be either by chemical agents or in some cases, organisms. There's a level down from that where I would accept that aquatic organisms that you would normally see – for instance, Legionella and Pseudomonas – because they have got an infective potential within humans and are maintained partly by engineering controls, I would also say that's contaminated.

What I don't think-- The harder definition is when you have normal aquatic organisms that go about their aquatic business in buildings probably like this and in healthcare buildings, at what level does too many of them become a “contamination”, or even can it be called contamination or is it an out of specification? And I think there is no criteria set that I'm aware of, or that the authorising engineers have let us be aware of, that would set a level that would be deemed-- that would tip you from unsafe-- sorry, from safe to unsafe with these aquatic organisms.

And then we get into the risk profiles

of the patients themselves, and that's where the risk comes from; as well as potentially some of these organisms might not all be the same in terms of the potential to cause infection, and we might touch on that later with the sequencing.

THE CHAIR: Right, what I'm taking from that is that water, for example, containing microorganisms which have pathogenic potential – in other words, which may be the source of infection in certain populations of patients – you would accept, as a concept, that a high level of such microorganisms might allow the water to be described as contaminated, but you point to the absence of hard definitions of where, on one hand, the water is as you expect it to be and, on the other hand, because of the high concentration of potentially pathogenic microorganisms, it could be described as contaminated, or am I wrong about that?

A I think water can be a risk dependent on the patient risk factors. You could have a very low concentration of a pathogen in-- sorry, not a pathogen, an organism in the water, but you could have very significant breakdowns in standard Infection Control procedure such that that pathogen-- sorry, the organism is transferred to the patient, who is then susceptible.

There still has to be a link for transmission from the water into the patient, and the concentration could be important. I don't know the evidence for that, but poor practice would be just as important, as would patient susceptibility to infections. So, I don't know that I could actually-- and maybe this is the issue why no one can say: when does a water system that's got normal aquatic organisms in it tip from being safe to unsafe?

THE CHAIR: I've noted down – because it seems to me a very important statement from someone who is an expert in the area – that the concentration of microorganisms could be a factor, but you don't know the evidence for that. Now, to the ignorant layman, that's surprising, but that is the expert position, is it?

A I would say that I can imagine circumstances where low concentration of water could infect a patient depending on what the chain of transmission is. You would logically think that a higher concentration of organisms would be easier to transfer along a train of-- a chain of transmission, but that's not necessarily the case. If somebody's practice-- their infection control practice or standard infection control precautions is poor, then it doesn't matter about the concentration because you've still got a link-- a possible link of transmission.

THE CHAIR: I can see that-- or at least I think I can see that one has to have regard to various steps along the potential pathway between the organism and the patient, but (break in recording).

A -- where concentration is a factor for water.

THE CHAIR: Right. As you recognise, that, to the ignorant, that's counterintuitive.

A Yes.

THE CHAIR: Right, and, to the ignorant, the fact that total viable count-- I appreciate this is a very rough and ready indication and it's not specific to organisms but, to the ignorant, the fact that, for example, as a definition of wholesome water, total viable count, if I understand things correctly, is of relevance-- If concentration is not or has not been shown by the science to be a factor, why are we interested, for example, in total viable count?

A So total viable counts is a very useful surrogate for the health of a water system, but in one of the documents that this Inquiry has from Dominique Chaput, who is one of the Infection Control clinical scientists. When you look at TVCs, you will find that organism growth will occur in 50 per cent of the samples, approximately 50 per cent of the samples that are-- have passed a TVC threshold. So TVCs do not tell you, when you're looking at named organisms, whether those named organisms are present in the water or not.

The value of TVCs are they will-- it's a trend value. One of TVCs do not help you, and you watch a trend in a system and you will see TVCs increasing when the water system is poorly performing, but it's not a marker for whether aquatic organisms are there, because even those who are below threshold-- you will still have those aquatic organisms.

Now, I will put a big health statement on that if I can. The way that Glasgow measure TVCs and organisms are different. TVCs are defined as a number of organisms per mil. When we're looking for named organisms, Cupriavidus , for instance, Sphingomonas, Delftias, Acidovorax, and the A to Z of environmental organisms, we take 100 times that concentration and we filter that down, and we find however many organisms that are there, and it may only be handfuls. It may be five or ten or six. So if you were actually to look at that by per mil, as a way that you measure TVCs, you would not see these organisms. So, we have taken a two log increase in the concentration-- sorry, in the volume of water that we use to try and identify these organisms.

THE CHAIR: Right, so, what's the bottom line on that particular? I

introduced TVCs to-- really to disclose that I-- you're the expert, I'm not. To the layman, the fact that one is interested in a count – even if the count is indiscriminate in the sense that it's everything – as an indicator of the wholesomeness of water suggests to the ignorant person that the concentration of microorganisms is of importance. Now, if I've noted you correctly, you say that is not supported by the science and that is-- I want to make sure I've got your evidence correctly.

A So, TVCs are a marker of system health, and they're measured per mil and we have got break points or-- where an out of specification becomes important, and you would do something about that. When we're looking at aquatic organisms, we are taking 100 times more volume and we are actually going hunting. We are searching for these organisms, and you might have-- For the sake of argument, you've filtered down 100 mils of water and you might have five Cupriavidus on your filter plate. Now, if you were to take 1 mil of that, your probability of having one Cupriavidus in that is-- Well, we can do some fast maths, but I can't at the moment, but you would not find these organisms if you took smaller volumes of water.

The reason we take high volumes of water is because that's what you do when you look for pseudomonas, etc, which have got significant problems if they're in your system. So when I'm talking about high concentrations, we're talking about quite low numbers would still be deemed to be high concentrations because you've taken a larger volume of water. So it would be low absolute numbers would still be in a system that could be contaminated, depending on how you define contamination.

THE CHAIR: All right. Well, thank you. Mr Connal, I'll leave that there.

MR CONNAL: If I'm picking that up correctly, one of the reasons why you're hunting for these is because the kind of things you're hunting for can have adverse effects if they get into the patient system. Is that right?

A Correct.

Q And therefore you want to know, “Are they there and how much of it is there?”, if you can.

A Indeed, and does it explain some of the infections that we could be seeing in the patients.

Q I assume that's why organisations like NHS GGC has a very stringent water policy about the amount of bacteria that's acceptable on various kinds. Is that right?

A Yes, and that was-- that's been in place since Ian Powrie and Dr Inkster came up with definitions, and when I took

over as lead, I saw no reason to change them, recognising them-- that they are very stringent and far in excess of what would be industry standard normal and probably far in excess for what other health boards are doing.

Q And is one of that-- is one possible explanation for that, that a lot of the issues that arose-- in the new hospital arose around wards which were occupied by particularly vulnerable patients to avoid getting into a debate about what's neutropenic or not?

A Yes, I don't-- I agree with that.

Q Yes, and that's presumably also why the water system in a building as complex as the new hospital was designed to have a lot of checks, balances, precautions and so on ,in order to avoid organisms growing that could be detrimental to health. Is that right?

A That's right. You want good system health.

Q I just ask-- Almost everybody's been asked about this, whether they were there at the time or not. Are you aware of the findings of what's been called the DMA report of 2015?

A I was not.

Q This is a slightly different question, but am I right in understanding at the time you're working on the Infection Control team, the dosing of the system with chlorine dioxide had started?

A It had. I believe it started at the beginning of '19, so it had been active for a period of nine months.

Q Do you know whether that's a process which selectively gets rid of some bugs but perhaps thus encourages others?

A We do know, because of the recommissioning of 2A, that there are chlorine-resistant organisms, which we found when we were doing recommissioning work. Off the top of my head, I think they were Sphingomonas, Acidivorax, and Delftia, are all chlorine resistant-- or more chlorine resistant, I should say.

Q So the effect of chlorine dioxide dosing is not immediately to eliminate everything, because some things are more resistant to being eliminated than others?

A Yes, but what I don't know is, although it may not eliminate, it may significantly decrease the bio-burden within the system, and you have the persisters who are chlorine-resistant, still residual there.

Q And are some of the residual organisms ones that are capable of causing illness in vulnerable patients?

A I guess any organism potentially could. I can't remember if Sphingomonas was one of the organisms that got looked at as part of the case note

review. I don't think we've-- I would have-- I'm sorry, I'd have to check to see if what-- if any of those organisms have been seen in patients. If they have, it's a handful, but I don't know the answer to your question off the top of my head. Sorry.

Q I'm not so much concerned with whether they, in fact, infected a patient, but----

A Oh, could they? Yes, any organism in a system could.

Q I'm going to come back to your whole genome sequencing proposition later, but as we happen to be, as it were, passing it at this stage of your statement, can I just ask you a couple things at page 110? You've talked about Cupriavidus, and then in 181 when you talk about gene sequencing, you say you know there's a stable population. Can you help us understand what you mean by "stable population"?

A They were-- Cupriavidus forms into-- well, all organisms basically, when you're sequencing, fall into what we call clades, which are-- think of them, in lay terms, as a family, and there are clades or families of Cupriavidus that are resident in the water system in RHC that are closely genetically related or have been there for the period that we tested them – so, that would be a three-year period – and are distinct from two other

families that sit within the hospital system as well, who, of course, are genetically related and so forth.

Q When you did the sequencing exercise that led to the report that we've got before this Inquiry, was that just done in the-- we called it a lab, just to use layman's terms, that you were using, or did you get it checked by anyone else?

A So, the sequencing report in this Inquiry has not gone to peer review. I don't think it could go to peer review in its present form. It was done by a very experienced clinical scientist with myself inputting.

Q No, it was just a factual question.

A Oh, sorry.

Q I just wanted to know what the answer was, and that's very helpful. Thank you. I think just while I'm touching around Yorkhill, do you know what steps had been taken in Yorkhill to deal with things like Pseudomonas and so forth?

A I'm sorry. I have no knowledge of Yorkhill at all.

Q Okay. If we just stick to Cupriavidius for the moment, you say in paragraph 183 that there's no agreed level, and that's something that you've been touching upon with his Lordship. So, would I be right in understanding from the answers you've already given that we don't know what level of Cupriavidus

could cause infection in an immunocompromised patient?

A Theoretically, it could be one organism, but that would have to have a perfect chain of transmission, but we don't know what the infective dose is and we don't know what the concentration in the water would look like that would be considered fundamental risk. We also don't know if all these organisms are the same. We've got a signature in Stenotrophomonas that some of these organisms are more capable of causing human infections, and some don't. Some are environmental. They do not have the requisite genes within them that allow them to invade and sit and fight against our immune host system. So, for Cupriavidus, I would say we don't know enough. We're starting that journey on trying to understand these organisms, but I wouldn't be able to say anything more than that. It's very early.

Q It's not-- or wasn't a particularly common organism to find. Is that right?

A Well, it is, it's in-- It's not very common, because people have never looked for it, but if you look at a piece of work that came out of Glasgow, every city building that had tankage has Cupriavidus in it. When you look at other hospitals – again, a piece of work which was done by Dr Inkster – 63 per cent of other hospitals had-- or samples from ten other hospitals had these types of organisms within them.

Q If you're trying to protect, in that state of knowledge, a potential patient cohort which is more vulnerable than the average, you would need, presumably, to try and prevent them, if possible, having contact with anything with Cupriavidus in it, because you don't know how much is going to cause a risk. Is that right?

A I would agree.

Q Can we move on a little? We know there's a report by Dr Kennedy, and I'm not going to ask you about that. Dr Kennedy to speak to that report we've heard already. So, if we move on to page 112 of your witness statement, Dr Kennedy produced some information about the water incident – or what we're calling the water incident – in March 2018. In paragraph 191, you say that the peak in a particular curve was most likely multifactorial, but you thought the likely source of infections with Klebsiella and Enterobacter was due to translocation of the organisms from the bowel, so not from the environment at all. Is that what you're saying there?

A So, I've thought about this. We haven't found either Klebsiella or Entrobacter in the water system apart from six or four organisms, so they are not in the potable water. If they're in the

environment, the theory would be they come from the drains. With drains, as soon as you wash your hands or your body, that drain will then become colonised with those organisms, your own flora. Then we've got the issue of directionality. How would I-- How do you differentiate between the drain, the organism in the drain getting into the person, or the organism from the person getting into the drain?

So, if we were to say that-- to do a thought experiment and stated-- Let's assume that the drain is being colonised by the organism from patient A. Patient A is not going to get infected by that organism; it's their organism. So, patient B now needs to come in and there needs to be some transfer from the drain into patient B through a chain transmission. The alternative is you have these organisms within your own body, and they can translocate and cause an infection in a place that they shouldn't be. Now, if you apply Occam's razor where the simplest explanation is usually the best, I would state that it would be easier to understand how you have got a large concentration of these organisms already within your body rather than stating that it has to go outside your body, into a drain, out of a drain, through a chain of transmission, back into your body. So, on that basis and the basis that the

Enterobacter sequencing, to my mind, does not show any-- shows sporadic infections, I think – and it's my opinion – that these organisms are translocating through the bowel and, in some cases, have got, as a result of two things, their treatment-- a potential antibiotic selection as a result of either treatment of infection or prophylaxis.

Q If these are processes that are naturally occurring, they would happen all the time, wouldn't they? If this is just something that comes from the patient's gut, you wouldn't get variations because unless you get a very odd patient cohort, you get roughly the same results all the time, would you not?

A If the same selective pressures were there constantly, but there is information in front of this Inquiry that shows that that's not the case.

Q What do you mean by that?

A If you look at the antibiotic use over the quarters, the last two quarters of 2017 and the first quarter of 2018, the DDDs, which is a measure of direct dose, goes over two and a half-- increases two and a half fold. At that period, Meropenem increases two-fold. It all falls down. That increase of antibiotic correlates clearly with the peak of infections in the autumn of '17 and spring of '18 and, in fact, it's actually evident in Dr Harvey-Wood's data as well.

THE CHAIR: Right, I didn't get a note of that.

MR CONNAL: Let's make sure we're understanding it. If I understand it, what you're basically saying is the cause of all the problems that we've been looking at has been the prescription of antibiotics?

A No, and I'm not saying, “all the problems”. I'm saying that can be-- played part of the problem. I think it's multifactorial and that would be some of the explanation but not all of the explanation.

THE CHAIR: I don't know if you're in a position to provide it, Mr Connal, but I will need the source of what Professor Leanord referred to as much for my notes as anything else.

MR CONNAL: Can you give us that bit again, a bit about the rates that were noted with the link to 2017 and 2018? If you just give it a little bit more slowly-- So, it may be important, so his Lordship needs to note it.

A Okay. So, the question was, “If this is happening all the time”-- sorry, “If this is happening, it should happen all the time.” My opinion is that it hasn't been happening all the time and there has been selective pressure. When you look at some of the broad-spectrum antibiotic use, in quarters three and four of 2017 and quarter one of 2018, you will see a two-and-a-half-fold increase in the broad-spectrum antibiotic Tazocin – or Piperacillin/Tazobactam for its proper name – and in the first quarter of 2018, a two-fold increase in Meropenem use. Both those antibiotics are capable of, as we've talked about, changing the microbiome and selecting out resistant strains of which Klebsiella, Enterobacter, and Stenotrophomonas could be selected out – especially Stenotrophomonas after Carbapenem use-- sorry, after Meropenem use. This is not all but part of the picture that we see.

THE CHAIR: Now, it's for us to find the references, but where should we be looking for the data which allows you to draw these-- the conclusions about the increasing use of antibiotics?

A So, they are from-- I have that information, which is from Ysobel Gourlay, who is our antimicrobial pharmacist, but also graph 12 of Ms Harvey-Wood's presentation shows some of that information as well.

THE CHAIR: Right, and, I mean, you said this is information that's in front of the Inquiry. Is this a document that----

A Well, it was Dr Harvey-Wood's-- I'm not sure it was----

MR CONNAL: We've got Dr Harvey-Wood's presentation. I think it's the other one we're checking for.

A So, the other one would be the

reference for the Meropenem use and an increase in of Stenotrophomonas. Well, it's well-known. Professor Dancer has already mentioned it to this Inquiry, but I think the reference is there. I can get the exact reference to you and give it to you----

THE CHAIR: Right. So, this may not be a document that we have yet?

A No, sorry, not-- This would be in the published literature. The document I was referring to was Dr Harvey-Wood's document, graph 12.

THE CHAIR: Right. Right.

MR CONNAL: Did you refer to a document produced by Ms Gourlay?

A No, that's data that I have, but is in-- Some of that information will be in Dr Harvey-Wood's graph 12.

THE CHAIR: Right. Could we ask that, possibly with the good offices of CLO, if-- at an appropriate moment you ensure that either we get the reference or, if it's an additional document or an additional journal article, we get that?

A I will do.

THE CHAIR: Right. Thank you. Would this be a moment to----

MR CONNAL: Yes.

THE CHAIR: --take our coffee break?

MR CONNAL: Of course, yes.

THE CHAIR: I'm not suggesting you need to do this over the coffee break, but if we get this information in (break in recording) fairly soon. Could I ask you to be back for twelve o'clock, if that's all right?

A Absolutely.

(Short break)

THE CHAIR: Mr Connal?

MR CONNAL: Thank you, my Lord. Can I just go back on one point that you mentioned earlier? We were talking about patient A having an infection in their gut and they can't get it. It goes into the drains and possibly infects somebody else if you can provide a route for that to happen. Is it not the case that patient A can be infected with something that comes from their gut?

A Yes, indeed, if it's translocated, yes.

Q That's why we wash our hands, isn't it?

A Yeah.

Q One of the reasons.

A No, actually, you wash your hands after-- That's altruistic. You are ensuring that your organisms don't go onto any of the sanitary wear so that the next person that picks it up----

Q But also they don't go into your mouth if you happen to----

A But then you would----

Q -- pick something up.

A But they're already in your gut. All you do is have a nasty experience in your mouth. It's not-- You wouldn't-- You can't reinfect yourself with your own organisms unless there's a breach in your anatomical barriers.

THE CHAIR: That's an interesting insight that washing your hands is altruistic as opposed to selfish. I'm interested. Sorry, Mr Connal.

MR CONNAL: The other thing I've been asked to put to you is talking about antibiotic prescription. The antibiotic is not being prescribed because people were getting all these infections. They were getting infections because of the antibiotics that were being prescribed to deal with the fact that patients were getting infections?

A Absolutely, but it doesn't remove the selective pressure, and also a lot of these antibiotics that were being prescribed are prescribed empirically because in this patient cohort you have neutropenic sepsis, and you do not know what the organism is, if there's an organism. If you take blood cultures, you'll get that result 48 hours later if it is positive. In many cases it's not positive, and you will find, for us-- Certainly in the case of Stenototrophomonas, you will find colonisation and selection of that organism as a result of your broad spectrum empirical antibiotics that you started because of a neutropenic sepsis, for instance.

Q I'm going to come to Stenotrophomonas in a minute, because I'm going to suggest it's in a slightly different category to Klebsiella and Enterobacter.

A I agree.

Q Just looking at this idea of translocation as the-- Well, you say it's multifactorial, so it's not the whole answer, it's only one of the answers. Is that right?

A So, antibiotics selection pressure – or antibiotic stewardship, as I would say – is one of the potential answers, yes.

Q If you're looking at this idea that an infection, say with Enterobacter, has been caused by translocation from the gut, presumably you could test that by taking a fecal sample and subjecting to whole genome sequencing, and then determining whether you get a close enough link?

A You could. One of the challenges of that is the high bacterial concentration in faeces. You've got a hundred million-- is that a US billion organisms per gram of wet faeces? A gram of wet faeces is roughly something around about the size of a peanut. So, you would need a reliable way of screening for that organism and a reliable

way of testing for it, so you could validate it. So, every time it was there, you got it, so you didn't miss it.

The other difficulty is that we do carry multiple strains of organisms within our gut, so you may select-- you may have one on your petri dish that you're going to test, and it might not be the one that is actually doing the infection. But the concept, as you describe it, is correct.

Q Did you do any such testing?

A No.

Q Can I just ask you then, just so we understand what you've been referring to earlier, to look at Dr Harvey-Wood's graphs and then you can tell us which one you're looking at and what you take from it? This, I'm told, we should find in her PowerPoint presentation, which is bundle 27, volume 6, page 103.

Now, that doesn't seem to be the correct reference. That's the reference I've been given? Oh, there we are. Right, now, we know we have a series of graphs coming. Did you say it was graph 12?

A I think it was graph 12. It's beautifully multi-coloured. Not that one. Not that one. Not that one. That one.

Q That one? So, this is prepared in 2018, and what do you say that we should take from that that's helpful?

A So, there's four lines to look at. The first line is the solid yellow line with triangles----

Q Mm-hmm.

A -- which is Meropenem use, and then we'll take this with-- and then the next one is yellow lines with dots, which is Meropenem-resistant environmental gram-negatives, which-- and so you can see that, from a DDD point in the fourth quarter of 2015, you can see a steady rise of over 150 DDDs into the first quarter of 2017, and attendant with that rise, you'll see an increase in the little yellow dotted line from 0 at 2016 in the first quarter, slowly rising up to the fourth quarter in 2016, and then going quite-- going up to 5 in the second quarter of 2017 and the third quarter in 2017, just after the peak in Meropenem has gone up to the first quarter in 21.

Then it drops down again, and then Meropenem goes back up from about 220 DDDs above 400 – so it's almost doubled – and you see a consequent increase in the first quarter of 2018 and the second quarter of 2018 in Meropenem-resistant organisms, so that it's four and five. When you look at these numbers such that they're at the rate of five in the second quarter in ‘17 and the third quarter in ‘17 out of a total of 13 organisms, that then takes-- that's well over 30 per cent. Almost 40 per cent of your organisms are within that graph, and

then if you look at the second quarter, i.e. the last bar in 2018, it's at five and that's of 16, so that's about 30 per cent of your organisms.

So, somewhere between 30 and 40 per cent of your organisms are Meropenem-resistant environmental gram-negatives, and my opinion is that that's driven by the increased use of Meropenem as a result-- selecting these organisms out, and I would guess-- I don't know what the organisms are, but I would have guessed that they're all Stenotrophomonas. So, that's for Meropenem.

The next graphic is Tazocin, and you'll-- following the blue line, the solid blue line, and then there's a dotted blue line, and you can see from the fourth quarter of 2016 Tazocin antibiotics is at 200 DDDs, and then it rises in the third quarter of 2017 up to above 500, so it's more than doubled. It's two and a half times what it was in a 12-month period, and you can see the dotted line-- you can see in the second quarter of 2017 from a standing start of zero to the third quarter of 2017, the wee-- Well, the dotted line-- the blue dotted line goes up to five organisms, and they are the Tazocin resistant environmental gram-negatives, and then it drops down again once Tazocin use comes down.

So I would guess that that's either

going to be Enterobacter or Klebsiella, and so that's four organisms out of-- in the third quarter of 2017. So, that then-- to my mind then, the total in 2017 is 13 organisms. We can attribute five, possibly, to selection out of Meropenem; four because of selection out because of Tazocin. So, of those 13, we can remove-- we can maybe have an explanation for seven of them. So, over 50 per cent of that increase, I think, can be explained by the use of antibiotics.

The other 50 per cent could be other things, but I think this is clear to me and has been written in the literature-- and it wasn't- I looked it up while I was in recess and it's Aitken(?) in 2021 describes this, and I'm happy to share that paper.

MR CONNAL: I think that would be helpful, but the-- Is it right to say that the cohort of patients in the Paediatric Haemato-Oncology unit tend to have a high proportion of Meropenen anyway?

A They do.

Q Because of the nature of, you know, resistance and allergies and all kinds of other things?

A Absolutely, and that's one of the-- So, that-- Yes. So, when you use these antibiotics, you will-- because of their powerful nature and their ability to kill a lot of these bacteria, you will be left with the survivors, which-- and you will

select these organisms out, and it's known in literature. We've done audits on it. Audits throughout-- in GGC would give you a 30 per cent increase in Stenotrophomonas.

Post-Carbapenem use, the-- We've looked at this patient cohort through a root course analysis, and we've found 60 per cent of the Stenotrophomonas in this cohort have had prior Carbapenems. So it's well-recognised and is actually occurring.

Q Well, if we can move to Stenotrophomonas, Stenotrophomonas isn't an enteric organism, is it?

A No.

Q So it has to come from somewhere?

A Yes.

Q And is the question not, "Where did it come from?"

A It will come from aquatic sources, and when you use Carbapenems, the area it gets-- you find colonisation isn't the gut; it's the oropharynx. So it makes sense that you've ingested water with Stenotrophomonas in it, they reside in your oropharynx, and when you use the Carbapenem, you will get selection and increased growth of those organisms within your oropharynx.

THE CHAIR: Sorry, just give me that again. Stenotrophomonas is not

enteric, therefore a source is ingested water. Now, it's the relationship-- Have I got the antibiotic noted correctly, and that's Carbapenem?

A Absolutely. A Carbapenem is a class description, and that would-- and it would encompass a number of antibiotic agents in that. Meropenem is one of them, and the most used one. There are others, but Carbapenem is like describing it like a Penicillin, but all of them-- all the-- that class has got the ability because of their broad spectrum of activity of creating that selective pressure, and the importance of that is that Carbapenems are really the antibiotics of-- were the antibiotics of last resort. There's newer agents in the market, but there was concern that we were seeing a lot of resistance developing in that agent or those agents.

THE CHAIR: Now, the-- I think which I did not follow was the-- the-- what you would regard as the selective impact of Carbapenem, a prescription in relation to Steno----

A Stenotrophomonas.

THE CHAIR: -- Stenotrophomonas.

A So, Stenotrophomonas are inherently resistant to Carbapenems.

THE CHAIR: Right.

A So, they've done nothing clever. They just are, and so as soon as you give that agent, Stenotrophomonas is

capable of surviving.

THE CHAIR: Right. Okay. I've got that, thank you.

MR CONNAL: So, can I just go back again to the question-- I want to ask you about Meropenen in a minute, but if Stenotrophomonas is not enteric, it must enter the-- and somebody has suffered from that-- It must enter the patient via some route, and I think you said water. Is that right?

A Mm-hmm.

Q So the source of the infection remains water?

A Ingested water, yes. But what we don't know is what duration-- what period-- what duration we can carry Stenotrophomonas.

Q In paragraph 192 of your witness statement where you're dealing with Stenotrophomonas, if we can go back to that, you talk about a GGC review of cases-- yes, sorry. Paragraph 192, page 112, and do you see that? You talk about GGC review of cases.

A Yes.

Q Is that something the Inquiry has?

A I'm not sure. I don't think so. This was a review done by Pamela Joannidis on 99 cases, and it's a "Root cause analysis" is what it's titled, but the striking thing from that is that two thirds of case-- of Stenotrophomonas cases had had prior Carbapenem up to 119 days prior. The duration of the agent prior I don't think is important. We know that antibiotic resistance will be extant in somebody's body up to a year after an agent is given, and we know it's up to a year only because the trial guillotined-- or stopped after that period of time. So it is possible that we carry these eight antibiotic resistance organisms within ourselves for long durations of time.

Q Where were these cases? Do you know? In one particular ward or one particular hospital or generally?

A It was in the RHC/QEUH as far as I'm aware. I don't know the breakdown in terms of wards, but that data's available, if required.

Q Well, I think, given I didn't know where it was----

A Yes.

Q -- that may be my fault because no one's given me it, but it may simply be that we haven't got it.

A It may be. I'm more than----

Q And those listening from the CLO will take steps to find out where it is and, if we haven't got it, to provide it to us at another stage so we can actually have a have a look at it, because it's not entirely satisfactory to discuss it in the abstract without it being present, as you can appreciate.

With Meropenen, in effect, you're

saying that one of the factors for somebody getting an illness is the prescription of Meropenen?

A With a specific organism, yes. Actually, could I-- They still have risk factors. The risk factors for translocation, it's not-- I wouldn't want to give the impression that if you take Meropenem – you or I take Meropenem – I'm going to come down with a Stenotrophomonas bacteremia. That's not the case. The risk factors for the bacteremia still exist within the patient cohort because of their immune suppression and the treatment that they are being put under. It's just that Meropenem is the opportunistic pathogen that takes advantage of that scenario as a result of being selected out through----

Q Not Meropenem. Meropenem's the antibiotic.

A Sorry, Steno-- Thank you very much. Stenotrophomonas takes the opportunity of causing the infection as a result of either current or previous Meropenem use.

Q Yes. So, you're still looking to prevent Stenotrophomonas entering the systems of these individuals?

A If you can. I mean, it's-- Stenotrophomonas is ubiquitous in the environment. It will-- If you were to test domestic water, you will find it, so you have that paradoxical situation where we

live in an environment where organisms are abundant everywhere and yet we have to try our best to ensure that the health-- where we treat these patients are as safe as possible. There are still-- We can only control one side of – or one part – a certain area in terms of infection potential. Once they're outside that area – and when I mean that, I mean the hospital and specialist areas in that hospital – then they would be susceptible to any environmental organism that they may encounter.

MR CONNAL: But while they're in the hospital, you're seeking to prevent them encountering it?

A Absolutely.

Q Just before I forget about it, in 191 at the end of that paragraph, you said there there could be issues of central venous catheter care. Do you have any evidence for criticising the central venous catheter care when you make that statement?

A No, it was a general statement. I know that there was a very excellent piece of work led by one of the senior nurses in paediatric hospital looking at central line bloodstream infections. They set themselves a very challenging target: best in class. They achieved it, and it was just-- As a call to improvement piece of work, it was fantastic. It was recognised, and it was only to suggest

that we should be looking at every aspect of care and improving it as best we can, and I thought that was a good example. I'm not suggesting that that's the case. It's just an example.

Q Thank you. Can we just move on to page 113? I'm possibly just picking up a few bits and pieces in some of these cases because, with your proposition that one of the factors in people becoming ill is antibiotic use, we've got a little diverted.

I mean, I just wondered if I could just put that to you. I don't think anyone else has suggested to this Inquiry that a factor in the issues encountered in the new hospital can be explained by reference to antibiotic use.

A I'll take this as a safe space. I would take this as if there was an IMT. I would make that suggestion if it was an IMT. I would suggest it as a hypothesis, and I would like that hypothesis to be tested.

Q Okay, going on to 113 just for a minute because we'll start to lose track of where we are in the chronological sequence, what the section under “Hypothesis” is dealing with is, I think, a hypothesis of infections found and discussed at an IMT in relation to 6A. I think you say here, "One of the two hypotheses was exposure to unfiltered water outwith Ward 6A," and I think at

places where there were not point-of-use filters is probably the point there. Is that correct?

A Yes, sorry, yes.

Q What you go on to say is efforts were made to see if it was possible to ensure that when patients, who were otherwise in 6A, had to go elsewhere, that pass-away was covered by point-of-use filters if at all possible.

A That's correct.

Q That's what you understood was done.

A Yes.

Q But you're surmising that the exposure to unfiltered water did seem to make sense in 197.

A It does make sense.

Q Yes. So the likely cause of-- or a possible cause-- I don't want to get into a debate about the correct use of "likely" or "possible" with you, but a possible cause of the infections seen at that time was unfiltered water which happened to have been encountered not through a point-of-use filter.

A That's possible.

Q You said that seemed to make sense?

A It does.

Q So, that infection wasn't endogenous. That was due to exposure to unfiltered water, or seemed to be-- make sense----

A You don't do that for certain.

Q No.

A You're trying to mitigate as many risks as possible. It's already been identified as a risk in other areas, and so it makes perfect sense to ensure that that risk is removed, because it's part of your hypothesis, wherever it possibly can be.

Q Yes. Now, I'm not going to ask you about biofilm. I'm going to ask you about that later. We'll touch on biofilms a little later on, and I know you say you're not an expert in biofilms, so it won't be a very long session----

A Thank you.

Q -- but we'll pick it up later on. It's just that you mention it in some of the succeeding paragraphs here. Moving now to page 122 of your witness statement, just really to get clear what we're saying here, we're dealing with the section under the heading "Microbiology Report", and another organism has made its appearance, Delftia acidovorans. You say:

> "I'm asked by the Inquiry why it's an unusual organism. [You say] It's unusual to see it cause a clinical infection."

So, this was an oddity again.

A Indeed.

Q Okay, bear with me a second. Now, I'm going to move on. I'm going to ask you another question about biofilm, but I'll ask them all in one batch. You weren't an expert in chilled beams, so I'm not going to ask you about chilled beams----

A No, thank you.

Q -- you'll be very pleased to know. So, we can move on. Can I then go to-- I'm not quite sure how this fits in the sequence, so I'll just ask you it generally. One of the criticisms that Dr Peters had was that the communications from IMTs to the clinical microbiologists was not good at all, and when you and Professor Jones were involved, you weren't really discussing the hypotheses with the clinical microbiology teams, although they were people who might have to do, for instance, out of hours cover. Now, do you recognise that criticism?

A Not really, no. I would say that the communication-- So, it depends what level of detail is required to ensure that you can do your job safely. Out of hours, you are performing what I would call reactive infection control. You are not involved in longer pieces of work which have got possibly many moving parts, some of which may be fruitful and some of them may not be. So until you have certainty, you're exploring all avenues. I would say that there was enough information to ensure that a

microbiologist could operate effectively between the hours of five o'clock and nine o'clock the next morning. If there was any issues that came up within that clinical area, then that would be reactive infection control. By that I mean immediate infection control; actions that have to be taken to either ensure patient safety, staff safety, etc. So, where do you put the patient? What should you do? That is what is required to be done in an out-of-hours situation. It's not----

Q I think the criticism, assuming it is a criticism, is probably that here you had a very experienced microbiologist in Dr Peters with a lot of experience in infection control, and she seems to think that when you and Professor Jones were involved, you really weren't discussing with her what was going on and bringing her up to date.

A I don't recognise that as an issue. I do recognise that myself and Professor Jones had a role to play in the IMT. We had that job to do. Where it was important that people knew what was happening, I think we would have communicated that to a level of detail that was required to ensure that patient safety wasn't compromised.

Q Well, that may be quite a nuanced distinction. I want to make sure I understand it. So, it's a question of communicating the information someone needs so that they can do the cover that they may be asked to do, as opposed to engaging in a discussion about what the issues are, what the hypotheses are, and what's going on?

A Correct.

Q These are two different things?

A Indeed.

Q And you would say you did the latter but not the former? Have I got that right?

A No, I think it was the other way around.

Q Other way round, yes.

A Mm-hmm.

Q You provided the information but didn't have the discussion.

A Because if that was the case that we had to do that, there's 19 microbiologists within GGC. We would potentially have to have that conversation 19 times.

Q Let's move on. 128, please. You'll be pleased to know I'm not about to ask you a lot of technical questions about HEPA filters because we've confirmed your position on ventilation, and what you say here is, "Well, they might do some good, don't know whether disrupt airflow or not and they cause a bit of noise," but you think they might be helpful?

A Yes, I see them as win-wins. They're cheap. I don't know how effective they are. A lot more information

came out during COVID about how they could or couldn't be used. They're effectively scrubbers, but I don't think-- There's nothing dangerous about them.

Q So better than not having them?

A Agreed.

Q But presumably not as good as HEPA-filtering the air before it enters the patient space.

A Absolutely agreed.

Q Thank you. Now, I think we're possibly starting to head to a point where we can get your little clarification into the narrative, because in paragraph 272, which is on the same page, we start to identify some areas where you had a difference with Annette Rankin, who I think at that time was with a difference of views. I'm not suggesting you had a stand up argument. I'm----

A Yes, maybe-- I mean, I've used Annette Rankin's name. I haven't got a difference of opinion with Annette Rankin. Annette Rankin was there as the representative of HPS, as it was at the time, and I think that was where the difference of views lay.

Q You appear to have attributed, at least, to her the statement----

A Yes, well, she was there----

Q -- that we were looking at unique organisms, and you say, no, we weren't.

A And indeed.

Q Did you understand that clinicians thought these were either unique or certainly highly unusual that you were looking at at the time.

A Yes.

Q Did you agree with that view?

A From the clinician point of view, yes, but from a microbiologist point of view, we know these organisms are there. When you do lookbacks, as we have a ten-year lookback over these organisms from GGC, we will find these-- we know these organisms are there in small numbers, handfuls, ones, two, threes, gaps of years, but the A to Z of the environmental organisms have been there. As microbiologists, we know about them.

The tricky thing for us is understanding what they are. They're always-- Well, they're unusual to us insofar as their taxonomy changes, and you always know you've got an unusual organism when you have to Google it because-- and then you find out it used to be called something else which you understand as-- So, yes, I would think that my level of clinical knowledge is different from the clinicians, and the clinician's level of microbiological knowledge is different from my own.

THE CHAIR: I think I can understand why that might be so. Could I

just maybe backtrack and see-- tease that out a little. The proposition was put to you that clinicians seem to have recognised unusual infections. Now, as a layman, I don't necessarily immediately understand what that might mean, but it indicates that the clinicians do not come across them commonly. Now, were you saying that the experience of a microbiologist might be different?

A Yes, because we will see these organisms coming from across every specialty and across a number of hospitals. The clinician will see these organisms as they relate to that particular specialty and that particular patient group. So, they don't have that breadth of vision that we would have.

They, for instance, in Hospital Y or another hospital in the GGC estate, we will see an unusual organism one year, and they've got no knowledge of it but we do. We will see-- We test over a million samples in any one year, and out of those million we will see some of these organisms coming through, not necessarily on the same place.

THE CHAIR: And were-- The data, as it were, that's available to both the clinicians and the microbiologist is blood sampling. Is that right, or is it----

A That's the easiest one to look at, yes.

THE CHAIR: I'm just wondering if the clinicians, on one hand, and the microbiologists are looking at the same data sets.

A No, they're not, because the clinicians wouldn't have the ability or the interest in interrogating GGC's data set for these environmental organisms. They would be more interested in the organisms that they would see, which would be a subset and a small fraction of that, and so that would be the difference.

We would-- Just because your denominator is so much smaller, you would-- you wouldn't see these organisms quite so frequently, if at all, in this patient group, whereas within-- across the whole five acute hospitals in GGC, we would.

THE CHAIR: But – and again I apologise for my pedestrian approach – we are talking about blood samples as opposed to environmental samples?

A Yes. Yes.

THE CHAIR: Yes, but I do see that clinicians in a particular area will be interested in their particular patients. Right. Thank you.

MR CONNAL: So, it's entirely possible, if I follow this narrative through, that clinicians dealing with, say, paediatric hemo-oncology – because that's obviously one of the main areas we've been looking at – might say, "Well, we've never seen this before in our

experience," and I think we know that a number of the clinicians have very extensive experience in that area and, combined, they probably have a huge amount of experience.

A Yes.

Q And you wouldn't necessarily say that they've got that wrong. It's just that somewhere, somewhere else, at some other point in some other ward or some other hospital, someone may have encountered the same thing?

A Correct.

Q Right. Let me move on to another label for you: “pseudo-outbreak”. You knew I was going to ask you about that, didn't you----

A Yeah, I did.

Q -- because you've headed it off, as it were, in your witness statement, and I'm going to take it backwards in terms of how you've set it out. A pseudo-outbreak-- and you correct me if I'm wrong, because you're the expert and I'm not. A pseudo-outbreak, properly understood, the standard usage of that term is where there has been some contamination from some external source in the lab or in the handling or something like that. So, in fact, what you think you're doing is looking at an outbreak, but it's nothing to do with that. It's somewhere in the processing system the infection had entered.

A Correct.

Q That's a pseudo-outbreak, because somebody at the end result gets results which suggest the problem, but in fact it's contamination in between.

A Yes.

Q You, I think, came under some challenge at least for using the phrase "pseudo-outbreak" in the context of IMT discussions, and as I understand it, what you've set out in your witness statement now is you didn't actually mean a pseudo-outbreak in its standard form at all? You meant something different.

A So, I used the term quite deliberately, really to try and captivate or engage the clinicians in an opinion that I had that I felt that the outbreak definition was very broad, thus making it not specific. By-- I mean, not specific, I mean in the sense that you will get false positives, and so infections that arise will be attributed to an outbreak when they are not, and thus you're in the potential situation of having an unending perpetual outbreak because what you're actually describing is the natural infectivity-- epidemiology within this patient cohort, and I deliberately used that to try and see if we could engender a discussion within the IMT such that we could tease that out as a concept. I'm not sure it actually happened. I think I----

Q I'm just a bit puzzled by it,

because if somebody knew the meaning of "pseudo-outbreak" as meaning a situation isn't an infection in the patient at all, it's come through some contaminated route, why would you deliberately use that phrase in discussion, knowing it was not correct?

A Because I didn't know that there was any other way I could actually describe what my opinion was without using something akin to that terminology. I didn't use it-- "pseudo-outbreak" in isolation. I gave the contextualisation that the outbreak definition was so broad, that we were in danger of perpetuating an outbreak because of a non-specific outbreak definition that was capturing all.

Q This is perhaps where we better get to the correction that you wanted to make to your statement. As I understand it, what you were saying in your statement was you were criticising the use of all gram-negatives as a group that were being adopted, but you don't think, on reflection, that phraseology is what you intended to use. Is that right?

A That's right. That was a transfer from a previous version of my statement. So, I understand the-- then, as now, it was organisms from water and soil that were associated with 6A or pathways within that. So, that was my error. What I would say is, like, mentally, we are talking about gram-negatives, because that's the group of organisms that these environmental organisms are, plus the enterics are gram-negatives as well, so it was an effective shorthand, mental shorthand.

THE CHAIR: Is there a particular passage in the statement you would wish to take me to, Mr Connal, so I could reflect that correction?

MR CONNAL: Yes, my Lord.

A If I can help, I think it's----

THE CHAIR: Please do, yes.

A --paragraph 233, 278 and 325.

THE CHAIR: Right, if you just give me those again. 233?

A 233, 278 and 325.

THE CHAIR: Okay, but I will check-- Let's just go to page 129, first of all, please, because that's where we get 278, and then if we-- it starts at the foot, where you say you used-- with its normal usage, and then on 130 this is where you pick up this point.

A Yes.

Q Is that right?

A Yes.

Q And instead of "all gram-negatives", I'm not quite sure where you say that directly, but what you accept is that----

THE CHAIR: I mean, that expression is found at the very bottom of page 129. Yes.

MR CONNAL: Yes. No one was

actually saying all gram-negatives. It was gram-negatives associated with soil and----

A Water.

Q Water.

A Yes, that's correct.

Q So, what you were objecting to was people looking for gram-negative infections associated with soil and water as a group, as opposed to any particular one or more of these?

A No, what I was trying to highlight was that the enteric organisms, Klebsiella and Enterobacter, were, by default, being put into an environmental basket and not into an enteric basket-- or they were being analysed both within environmental and enteric, but not enteric and gram-negatives. So, there was no differentiation between any of those organisms in terms of their source, either endogenous or exogenous. They were all assumed to be exogenous.

Q Although, in two cases, they can also be endogenous?

A Of course, but there was never any differentiation, as I could see, whereby they tried to-- the IMT tried to work out where the actual ultimate source was, and it was assumed, in every instance, that it was exogenous, even though these are endogenous organisms.

Q But they can also be exogenous?

A And they can also be exogenous.

Q Yes.

Q So, if-- if I get this-- if I can strip that down, your objection was that by including in a collection of gram-negative organisms associated with soil and water, two organisms which could also be found in the patient's body naturally occurring. That was causing a problem?

A Sorry, causing a problem within the patient or causing a problem to me or causing a problem to the data?

Q Well, causing a problem to the process that you were undertaking at the time.

A I don't know if it would cause a problem. It's just an observation that I felt that there wasn't enough stringency in highlighting or trying to delineate where those two organisms, Klebsiella and Enterobacter, were coming from, and they were always assumed to be coming from outwith the patient, and we know that's not the case.

Q Was that not what you were trying to establish, where they were coming from? Because the point of the IMT, if you go back to the discussion we had earlier today, if you're not looking to exclude the hospital as the source, if you go back to the old approach, which is try and find out what the problem is and how

to fix it, you're trying to find out where organisms of concern may be coming from.

A Yes, but I don't think that process occurred. The assumption was they were always environmental.

Q And were you assuming they weren't?

A I wasn't assuming anything. All I was saying is that the assumption throughout the IMT was that they were all environmental.

Q Part of the history we've got of what happened in the new hospital is of people making investigations, trying to work out where something's coming from, and possibly intervening in some way. Let's just say, to oversimplify it, some of these suggestions, “It might be the drinking water. Right. No more drinking water from the taps. Let's have bottled water,” and the infections then go down. Now, if-- and then they recur for some other reason, but just sticking at that point, if they go down after an intervention of that kind, then the initial hypothesis seems at least to be tenable.

A It would be tenable. It might not be right.

Q If they were getting the infection not from the water but from some other means, you would need to be able to work out what that alternative was.

A Correct.

Q Because that's one of the debates that you'll probably be aware has circulated, that it's all very well saying it wasn't the environment, but you have to show where-- another route for the infection to happen.

A And you do try, and you're not always successful. I have been in IMTs over my career where you do not get to the source of-- a proven source of where the infection came from and, ultimately, the infection goes away. The issue-- You've put in a number of mitigations. You don't know which one's worked. Everyone's very thankful that the problem's gone, but if you were to actually point to one mitigation or one source, you might not be able to say that's what done it, and that's just the nature of trying to deal with infections in complex systems, and this was a very complex, long, drawn-out investigative process, and I'm afraid that's just what happens sometimes.

Q Well, thank you for making the point that you don't always find a source because that's one that a number of people have made. Do you get any indications as to what the source might be by the success of the interventions you make?

A If they were done one by one, in terms of an actual experiment, you

could, but that's not the nature of an IMT. You do every mitigat-- You prioritise your hypothesis. You look at how you're going to investigate them, how you're going to potentially mitigate them. You put all the mitigations in place as fast and as efficiently as you can, and then you watch and wait or you refine your hypothesis from new information that comes through.

So, you don't have that ability to do a actual experiment and wait and see for an effect. For instance, an effect may be months down the line if we're talking about water systems. Let's say, for instance, you thought that chlorine dioxide was the key mitigation you needed. It would take months. The engineers will tell you it can now take two years to clear a system. You can't wait that long. This all has to be done the very next day.

So, in theory, yes, but in practice, I don't know how you would be able to do that. That's why, in some cases, you never know what the source is because you can't then say the mitigation at that point affected that source because it all happened quickly.

Even if-- When you come down to it, as I said, the situation is multifactorial. Even within that, there's smaller subsets within the large Venn diagram of the infection that, if somebody's practice isn't great, that will affect what the potential

source is. So, by that I mean that you still need a chain of transmission, a link between what you think the potential source is and how that potential pathogen or that organism gets into the patient's body.

Q So, your point, quite properly, is you can't say, "Well, let's not bother stopping them drinking the water. We'll do something else, but we won't do that, and if they still get ill, then we'll know it might be the drinking water," because you can't take that risk with the patient.

A Absolutely.

Q On the other hand, if all of the steps you took were focused on excluding potential routes for non-filtered water being encountered by the patient and the infection stopped, you might think reasonably that that had been the source.

A If that was your only mitigation, but it wouldn't be your only mitigation. The other mitigations would be look at practice; you would look at antibiotic prophylaxis; you would look at potential— I was going to say mechanical devices, for instance, catheter hubs, line care, etc. So there will be a number of things that you'll look at, but you're right: if you did one thing and one thing only, you would be able to identify that source, but that's a very, very high risk strategy, because if it's not that source, you have unwittingly allowed infections to continue.

Q Can we just pick up before we break another of the references that we want to make sure we've corrected? I think it's in paragraph 325, which appears on 140. Have I got the number right?

A Yes, that's correct.

Q So, where you say at the start of that paragraph:

> "Annette Rankin is absolutely right. Her definition of the outbreak was all gram-negatives,"

But it wasn't, actually.

A It wasn't, no, and that's-- I can only apologise to the Inquiry.

Q I might just ask you a slightly different question before we finish. Could we have-- Don't bring it up at the moment. One of the issues that has arisen for discussion is whether one has or should have background rates of particular organism. Some people are taking the view you should be aiming not to have background rates, others are taking a different view. At an earlier stage, a table was produced by Dr Kennedy with a whole range of organisms, and I wonder, will you just look at this? It's bundle 6, page 121. Now, there's a great long list of organisms. You may or may not be able to help us. Can you tell us, though, whether in your view any or all of these should have a background rate as it's been described?

A I don't think I can be specific because a background rate would be the rate of infections that you would see in a patient population as a result of their potential risk factors rather than because of the organism themselves. The risk factors in the patient are the things that will dictate whether they're susceptible to infections or not. We live in an environment of organisms. The back of your hand, every square centimetre, will have 100,000 organisms on it. That's the level. I could swab this desk and there will be organisms on it. Your keyboard that people are using, we know there's organisms on there. We live in that environment, so it's a risk profile of the patient rather than the organisms themselves.

Now, the difference with these organisms are they're usually recognised as of low pathogenic potential. The reason for that is they have been selectively driven towards having a gene set that will allow them to survive in a low nutrient environment and might not necessarily have the genes that they require to infect an immunocompetent person, but an immunocompromised person, I believe, is potentially capable of being infected by any organism by nature of their risk.

Q Thank you. We'll just leave

that. I'll ask two further questions, if I may, and, with his Lordship's permission, I'll just do that now. Apparently, you prepared something called an environmental sampling policy in 2020, and Dr Peters was asked to give feedback on it. First of all, do you recall doing that?

A No. Is this an Infection Control SOP?

Q I assume so. The point is simply that it has been suggested that you prepared the policy. She didn't think it was fit for purpose and gave you that feedback. Do you recall that at all?

A No, I don't.

Q Just one about behaviours, if I may, straying a little bit from the kind of topics we've been discussing this morning. After the Scottish government were involved in matters at the Board, we've had some evidence that a psychologist appeared on the scene, somebody called Jenny Copeland. Do you remember her?

A Yes.

Q There was somebody called Angela Wallace also involved.

A Yes.

A The suggestion is that there were things called "buzz meetings," at which both of these would be present----

A Yes.

Q -- as well as Dr Peters. Now, the suggestion is that you tended to laugh every time Dr Peters spoke and had to be stopped from both doing that and speaking over her. Do you have any recollection of that?

A I have a recollection of, once, I forgot myself on a Teams meeting in a back bedroom, and I would say it was more of a wry smile. To say it was a laugh was an embellishment, and I didn't deliberately talk over Dr Peters, but sometimes it's difficult on a Teams meeting to know when somebody has stopped talking and I may have inadvertently come in too soon.

Q Thank you. I think that might be an appropriate point, my Lord.

THE CHAIR: Yes. We'll take our lunch break now, Professor, and if you could be back for two o'clock. Thank you.

(Short break)

THE CHAIR: Good afternoon, Professor. Mr Connal?

MR CONNAL: Thank you, my Lord. During the lunch break, Professor, we've been trying to find out what the GGC review of cases that you mentioned in paragraph 192 of your witness statement might be. We weren't sure whether we had it or whether we didn't have it. We think it might be a document I'm about to show you. So, can we have bundle 4,

page 190, please? This, I believe, is a document primarily organised by Pamela Joannidis. Is this the document you were referring to that's got several pages?

A No.

Q No?

A The document I was referring to was a root cause analysis of 99 cases, which was done by Pamela Joannidis after she had retired, and there was discussion at the time about how useful it would be for the Inquiry, because it had a lot of information that was thought to be-- you had prior, so it may be that you haven't been sent it.

Q Right, because this appears to be a root cause analysis----

A Yes.

Q -- or at least that's what it's called, and then about halfway down that first page, we see, "This analysis still requires the input from microbiology and expert clinician."

A Mm-hmm.

Q So, the authors, who I think may be Ms Joannidis and some-- with assistance with some others, seemed to think it was a sort of provisional document. So, this is not something that----

A No. The other one is more comprehensive, and as I say, the title's got 99 cases on it. I'll-- I can point CLO to it, or our CLO will know this document well.

Q Right, and in any event, it's a document that was known to exist but was thought not necessarily to be helpful to the Inquiry. Is that right?

A Indeed, until I quoted it.

Q Yes. It's another point while we're at it. Can I have bundle 1, page 325? It's just that you were critical, I think, of IMTs always looking for a source in the environment, and I've been referred to this IMT minute, which as you'll see was one chaired by Dr Inkster. At the foot of that page, near enough, we see of the two (inaudible) cases. I assume one is possible gut source. So, it would appear, at least under the chairmanship of Dr Inkster, the IMTs were looking at both environmental and gut sources.

A It looks like that.

Q Thank you. The other thing before I move on that I need just to ask you about: in the course of your evidence, you've provided – initially without referring to it, then when we unearthed it – the graph prepared by Ms Harvey-Wood. Well, it's actually Ms Harvey-Wood and Dr Peters. There's no discussion of that graph, I don't think, in your witness statement.

A There's not. I wasn't aware of that graph until it was put into my bundle last night or yesterday.

Q So, that's the first time that it

occurred to you to comment on it?

A It's the first time I'd seen it.

Q It's just that no one has previously suggested the issues that you've raised with it at any earlier stage of the Inquiry, so we wondered where it had emerged from.

A My head.

Q Yes, just you thought of it last night?

A No, I thought of it before, but the evidence was there before me to point to.

Q Right. Now, we'll try to work out how to deal with the fact that no one else has had a chance to look at that point that you've just raised. Can I ask you about some other matters? Hopefully not too many before we get to the whole genome sequencing issue.

I just wanted to ask you briefly about Cryptococcus, acknowledging, of course, that I'm not going to ask you questions about ventilation ducts and so on, because that's not your sphere of expertise. You did have an involvement in an IMT on 2 July 2020 where there was suggestion of Cryptococcus as a cause of an infection in an individual. Was that right?

A That's right. I chaired that IMT.

Q Yes. Now, one of the issues here, I think, is that you think it was a false positive that had been found in the

case of this individual. Is that right?

A That's correct.

Q According to the material we have, Dr Sastry, who was the treating clinician, disagreed with that conclusion and in fact went on and treated the individual for Cryptococcus successfully. So, could you be wrong about it?

A No.

Q No, he's wrong?

A No. So, you never take a diagnostic test without the context. During the IMT, the clinician that was present was Dermot Murphy, who said that there's no evidence that this patient had Cryptococcus/was being treated as such. The risk benefit of having a positive antigen test, Cryptococcal antigen test, with a patient who did have a fever is such that you would use antifungal treatment while the diagnosis was being settled upon.

Q And there had been some initial positive tests. Is that right?

A The Cryptococcal antigen test was positive. It was positive at “neat”, as we would say. So, that means-- What you would normally do is then you would dilute, i.e. you would teeter out the antigen, such that you would find out at what teeter you no longer get reactivity. Now, in an invasive Cryptococcal illness, you'll be able to teeter the antigen out several hundred fold, at least 10/50, if--

Cryptococcal meningitis, sometimes even 2,000 fold.

Now, that's a surrogate marker about how much Cryptococcus is within the system. In this case, the latex antigen agglutination test did not teeter. So, what we had is a positive antigen test that could not be teetered out. So, if there was Cryptococcus there, it was at a very low level. Invasive cryptococcus does not generally-- and if you look at the literature, it's all HIV literature, but an invasive Cryptococcal illness will have an antigenemia that will teeter somewhere between, at its lowest, somewhere between 10 and 50. That would be for an asymptomatic cryptococcal antigenemia.

In disease, that's much higher. So, that's where we were in terms of that patient. The patient came in with a neutropenic sepsis of unknown origin and was given broad spectrum antibiotics. The inflammatory markers that you look for in a patient is called a CRP. The CRP at that time was high, and then over a four-day period, without antifungal treatment, it dropped down to near normal. After that-- At the time of antifungal treatment, the CRP had dropped from over 100 down to 17. Above 10-- Sorry, below 10 is described as being normal.

Invasive Cryptococcal disease or infection is not a self-limiting infection, and yet this patient improved, biochemically improved, on a background of no clinical condition showing Cryptococcal illness despite having no antifungal treatments. They had broad-spectrum antimicrobials, but no antifungals. The antifungals were started after a period where this patient had improved biochemically and was showing no clinical signs of cryptococcal illness. No other test that I'm aware of, the CSF, nor cryptococcal DNA analysis showed any evidence of Cryptococcus.

Q So, if Dr Sastry's evidence is that this patient was showing signs of Cryptococcus, was treated for it and recovered, he's wrong?

A Well, there's a difference of opinion.

Q Are you aware of more recent cases of Cryptococcus at the hospital?

A No.

Q It's been suggested there are at least four with possible connections to the hospital environment. Do you know anything about that?

A I don't.

Q Should you know anything about it in your capacity?

A No. That will go through an Infection Control route.

Q I want to take you to one final part of your witness statement before we look at some other things. Page 170 of

the witness statement, please. It's an issue that's cropped up with another witness, so I wanted to ask you about it. You can see in paragraph 449, where you say:

> "The Scottish government is keen that [ICDs] with experience or expertise in the built environment are part of the planning process."

Now, just leaving that hanging shot of the practicalities for the moment, would you agree that that's a good idea?

A If the Infection Control doctors are going to be embedded into the building process, yes, they need the skills and expertise to inform that process adequately.

Q Turning it the other way around: if you're building a hospital which may contain many of the most vulnerable patients, should you not have Infection Control at the heart of that process?

A Yeah, I agree.

Q Your point is essentially that there aren't that many of them about at the moment?

A There aren't, and not many of them are willing to take up the role at the moment.

Q Let me just now leave your witness statement. I'm not going to take you to your supplementary statement, you'll be pleased to know. Can we just look briefly at your sequencing report? I'm not going to ask you about the technical details of all the technology that goes into producing a whole genome sequencing, otherwise we might be here for some time going through the technology. We find this at bundle 6 at page 1195.

That's obviously just the heading. Just so I'm quite clear, usually with a medical paper that you see, say, in publications, the first named person is, as it were, the lead author, and the others are the contributors. Did you tell me earlier, and correct me if I've got it wrong, that in this case, Mr Brown did most of the work, and you contributed?

A Yes. I have no analytical skills in terms of sequencing. I deal-- I deal with the outputs. Mr Brown has nearly 30 years of experience of manipulating DNA and the expertise to put it all back together again.

Q Had the lab any experience of sequencing these three organisms before this?

A No.

Q Thank you, and I'm right in thinking that when the materials were being gathered to do the exercise, some isolates were taken from other hospitals as well, a small number. Is that right?

A That's correct, just to try and add context.

Q Now, can we just look at 1198, and it may be, given what you've just told us, that you can't help us with this. At 1198, under the general heading of, "Laboratory methods," subheading, "Subculture and storage," the end of that first paragraph there, "A single colony was taken from the purity plate and inoculated into," and then there's a description of what was done next. Now, is a single colony enough, or do you not know?

A Yes, a single colony is enough. There is a narrative, which I've never heard before until this Inquiry, that you need 30 picks. That is something that our-- my clinical scientists have never heard before. We went back to the originator of that statement and asked for a reference, and the originator of that statement clearly said that this was a statistical analysis given to her by a statistician from HBA. HBA hasn't been in existence for 13 years. She has no longer any of the calculations and couldn't remember the assumptions that were made on it, and it was only for Legionella.

If that assumption was true, it's not confirmed by the data in this piece of work, such that I would reference-- If it was 1 in 30, I'd reference clade 6 in the Stenotrophomonas, where we have got seven closely clustered

Stenotrophomonas from the basement water tanks, which are genetically quite close. If the statement that you need 30 picks to show any association was true, then that seven-clade grouping is a one in 21 billion chance of happening, which is 30 to the power of seven, and that is not reasonable.

Q I think I understand the general point that you're making. I think the question is really focused around if you'd simply take one, should you not take a number? Whether it's 20 or 30 or 10 or 6, it probably doesn't matter.

A So we looked at that, and within the sequencing report we sequenced all of the organisms. In this report we did Stenotrophomonas, but we've done exactly the same with Cupriavidus – it's just we did that after this report was written – and we show that those organisms, when they come out from a single outlet or a single sample, are clonal, and so that in itself is why I'm very comfortable that one pick is enough.

The other thing is if you need more picks, this is very expensive and quite complex technology. If you were to exponentially increase that by however multiple you want to have, first off, it becomes unwieldy. It becomes very costly and difficult to do. Lastly, every whole genome sequence study I know

has always taken one pick. If you need more than one pick, it invalidates almost a whole literature base based on no evidence that I'm aware of, no reference that I'm aware of that you need that, except for the assertion that that be the case.

Q On page 1211-- and I've not much more to ask about this. You've got here-- You're talking about Enterobacter, which was one of the organisms. In fact, I think pseudomonas, there wasn't enough material to form a view. That's why it's three organisms rather than four. Is that right?

A Indeed.

Q But here, in terms of Enterobacter, you've got 42 isolates, 7 clinical isolates, 6 environmental isolates, 2018, 2019.

A 29 clinical isolates, is that not in line two?

Q Sorry, the first seven was from GRI, you're quite right. That's from a different hospital.

A Yes, indeed, sorry.

Q And 29 from 24 patients. Looking at the environmental isolates, given the issues that we've been hearing about the water system, is six environmental isolates enough to say you've got something representative?

A Oh, no, no, and very clearly we say that in the limitations of this report. We do not see Enterobacter in the potable water. I think there's six isolations in over 10,000 samplings over a five-year period, so it's not in there. If it's in the environment, it would be drain associated, and there is no samples or very few samples, and for the reasons I think I might-- were in the supplementary report, where we don't have those isolates.

What the pattern does show you is it shows you that there's no point source for Enterobacter. It shows you that there is no successful clone that has, i.e. a superbug, a super Enterobacter in the system, and all the organisms are roughly around about 5,000 snips different equidistance, and so, to my mind, that looks like sporadic infections, and that's about all you can say without actually gearing down and then doing like for like for Enterobactors.

I'm just going to say, in defence of this work, this is-- this has never been done before. When we put the first-- not Enterobactor, but when we put the first ten Stenotrophomonas that we sequenced into the UK data set, we almost doubled the sequenced data set in the UK, and it's one of the biggest pieces of sequencing work I know within a water system thus far.

Q Well, let's see if we can come now to the issues that have come from

this report because, as you quite rightly say, we're not having a debate about whether the Illumina machine is a good machine or otherwise. We're talking about what use you make of the materials, because the proposition that you argue for, as I understand it, is that if you don't find a sufficiently close genetic link between environmental samples and the patient sample, then you can exclude the environment as a source?

A So you haven't proved causality.

Q Well, that's not the question I asked.

A Well, I don't-- so you can----

Q Let me just rephrase it----

A Yes.

Q -- because I think there may be two different questions. If you're looking-- Whole genome sequencing is a fantastic idea, particularly if you're to find something, "Is bug x in, you know, that glass of water?" or whatever.

A Agreed.

Q And you do your whole genome sequencing and, lo and behold, there it is, tick. The question then is, I would suggest to you, what you do if you don't get that nice, simplistic answer? Because one possibility – and I think this is just about what you said – was you have not proved definitively that there was a link between source A or B or C or D, or A, B, C or D, it doesn't matter, and the sample-- So it is simply you haven't proved it, or as I think it's been suggested, your work supports you can exclude the sources as a source of the infection found in the patient, so it's a slightly more nuanced question. So, is it, "You just haven't proved it, we'll stop," or is it, "You can use that evidence to exclude the environment as a source"?

A You can use-- It's the latter, I believe, because you can see there are-- So, sequencing can be used in many ways. So, you've got-- exactly as you've said, you're actually looking for direct causality in terms of there's a perfect match, or however you define a perfect match, and we defined it as less than 25 SNPs, was we would say that was evidence of transmission. So, you can look at a transmission chain and, as you say, if it's there, Eureka, that's it proved. If it's not, then you don't know much-- you can't say much about it. Then you're into how to prove a negative.

The other thing that sequencing can do is it can show you the relationships between organisms, because you're actually sequencing fathers, sisters, mothers, cousins, effectively, of bacterial progeny, and you can see whether there is – and I referred to them earlier – a family. So you can actually see bacterial relationships within that, and I would say

that my expectation when I first sequenced Enterobacter, was I was completely surprised at what we-- what I-- what we found. I was expecting to see a super clone, a clone that was very successful, that had come early using the graphics from Dr Inkster and Dr Peters that had then multiplied within the water system and was an apex predator, if you like, that survived within that water system, and that's not what we saw. We saw a different relationship such that you can't-- there was no commonality and they all looked sporadic. So you can actually infer how-- what those relationships are like.

And not only that, you can put times on things and how quickly those relationships will change. There's a lot of things you can do with sequencing apart from just that causality, and I would be saying, and I would concur, that if there were close families that were reasonably close and you hadn't actually hit the one bug combination that shows causality, I'd say you can't exclude it.

But what we have is we have a massively heterogeneous-- well, they're different. Enterobacter, we've got a massively heterogeneous population that looks sporadic. Stenotrophomonas, we've got a massively heterogeneous population that closes down into what looks exactly like nature. If you're a

Stenotrophomonas outside the hospital or Stenotrophomonas inside the hospital, the world looks exactly the same to you, and for Cupriavidus, you've got families, and you've clades, and they look stable.

So, they're very different, so you can actually look at the relationships of these organisms. They can't be put into one homogeneous basket and say, "They're all behaving similarly." What you have to do is-- or what you can do, sorry, with whole genome sequencing is you can drop new infections into the context of what you have as a background.

And one of the key limitations to whole genome sequencing is the very first time you see an organism and you sequence it, it's meaningless data. You've got nothing to compare it with. It's just a sequence. Then you get two. Now, they're either going to be the same or very different, and as you build up your library of sequences, then you can start contextualising where these organisms sit and also how they might be-- you can look at the molecular-- or you can try and understand the molecular epidemiology a lot better. So the more sequences you have, the more background information you have, the more useful it is to you. So I think-- I'll answer your question. I think you can exclude the environment if you don't see those kind of parameters that

you might expect to see, as well as not seeing causality.

THE CHAIR: I'll just see if I've understood this. You point to the heterogeneous character of-- are we talking about the samples from blood or samples from blood and samples from the environment?

A Both. They all fall within the same dendrogram, if you like, the same population.

THE CHAIR: Now, I think I heard you saying that that is a situation that you would find in the wider environment, the domestic situation in a building in Glasgow.

A So, for many of these organisms, yes. For Stenotrophomonas, which has got the most comprehensive data set, the world of Stenotrophomonas is exactly the world in the QE of your Stenotrophomonas. We see the same subtypes. Every single subtype that has been globally recognised, we can recognise in the QE. Every subtype that has been able to form clinical infections, we can see the same subtypes with patient data within them. Every subtype where you see exclusively environmental organisms but no clinical cases in the world literature, you see in the QE in exactly the same way. It is a smaller mirror image and a smaller microcosm.

THE CHAIR: Right, so, I did hear you say that. I mean, is this based on knowledge of the literature, knowledge of the subtypes of Stenotrophomonas that have been identified and matching that with the subtypes that you found in the study which is the subject of your report?

A Yes.

THE CHAIR: I mean, I take it there has – because I can't immediately see the purpose of it – there has been no whole genome sequencing of the general Glasgow or Scottish environment.

A Not that I'm aware of, but we know that those organisms are there. It's just that level of detailed sequencing work has not been done. I think this is one of the key questions that I would have is that what proportion or what-- yes, let's say proportion. I've forgotten the word I wanted to say, but the proportion of these organisms you would be exposed to outside in your own domestic water source or any other domestic water source or water source within a large building that you may exposed to, and we all possibly are exposed to, outwith the healthcare environment.

Now, if you're Stenotrophomonas, I believe it would be-- they're ubiquitous. If it's Cupriavidus, we know for a fact they're in buildings and they are ubiquitous. Enterobacters, it depends where you look. Klebsiellas, I would say it depends where you look. When I say it

depends where you look, it depends if you're going down your shower drain, or your handwash basin, or your potable water source, but we know that both Cupriavidus and Stenotrophomonas are in the mains water.

THE CHAIR: You contrast what you've found with what you thought you might find, which was a more closely related group of subtypes.

A For Enterobacters, yes, I fully expected to see a super aggressive, well-adapted key pathogen-- key organism that had got a selective growth advantage against its competitors in the environment it was in, and it grew and there was a colonial expansion of that population. In some ways, that would be much easier if it was the case, because we would then-- So, you don't want to be sequencing every single organism, so you'd look at this super apex pathogen, if you like, and you'd say, "What is its attributes? Has it got something that we can recognise within the diagnostic laboratory, i.e. an antibiotic resistance,"-- which we can argue about whether that's appropriate or not, or a test or-- and I'm going back years, when we had MRSA in the Western Infirmary; I'm going back to the 90s. We could tell just by looking at it because it grew slightly differently, so we got very attuned to it. If you saw that and you knew that you were seeing that particular clue in patients, then it would inform decisions that you could make about your response – i.e. this is one that we need to take very seriously, we know this has got a propensity to transmit and to cause infection, and so we have to take quite aggressive interventions to prevent that happening. We didn't see that. We saw a homogeneous, heterogeneous population that seems to a different organism infects – and I'm talking about Enterobacter – a single person at a time, and they're genetically very different through a homogeneous and heterogeneous background.

THE CHAIR: Do-- If we take the example of Stenotrophomonas, do different subtypes have a different propensity to infect?

A It looks like that's the case. That's certainly what the literature will suggest, and we have seen that in our own data set as well. So, not all Stenotrophomonas are the same. Some look like they have got genes or the adaptive ability that when they enter the body can survive, multiply, and cause infections. Others don't seem to have that ability. This-- Oh, sorry.

THE CHAIR: No, no. Carry on.

A So, the second question that you would ask of that data set, if you wanted to research it, is then you'd look at a whole genome sequence analysis

where you would find the genes of your environmental organism, your infective organisms, see what genes are different and see whether you can actually explain – it's called GWAS – but see if you can explain in terms of the genes and whether they carry virulence characteristics that allow one to infect more so than the other, and then you can get quite sophisticated about – and I'm going into university academic departments here – about why that might be the case.

So, there's many years of research that you could do with this. We've seen it with Stenotrophomonas, I've got no reason to believe that that wouldn't be the same, or potentially the same, for any other environmental organism that could infect a patient because they need the machinery, the genetic machinery, to allow them to do it.

THE CHAIR: Would I be right in thinking there's no necessary relationship between the more infective subtype and the frequency that you encounter the subtype? I don't know if I'm making my question clear.

A I know exactly what you mean. I know that they're independent, but unfortunately the most frequent subtype, SM6(sic), in the world literature is also the most frequent subtype in the QE, and that is one of the infective families. So, it's the most prevalent, although every one of the 23 subtypes of Stenotrophomonas are representative in the QE.

THE CHAIR: You designated that MS6?

A MS6 is its designation. Yes, my Lord.

THE CHAIR: Thank you.

MR CONNAL: In the way that things tend to do, phrases emerge from scientific documents, which are expressed in much more lay language. The phrase that seems to emerge from your work is, "Nothing was going on." I just want-- I think you mentioned that in the context of one of the IMTs where you say you wanted to do some work to show that nothing was going on, and that phrase has been repeated elsewhere. So, I want to give you the opportunity of understanding what you're saying by that.

A Okay, so, I wanted to do the work to see if there was transmission and if there was transmission, what that transmission would look like. The sequencing work does not confirm that there is evidence of direct transmission from the environment to the patient, and that's as far as you can take the sequence. I wouldn't say that there was nothing going on. We know that if you take the antibiotic stewardship proposal, something's going on, because we are

selecting out, by use of antibiotics, these organisms. It doesn't mean to say that these organisms-- There is no direct evidence that these organisms are coming from the environment except for they are in the environment and the assumption that has been made is that because they're in the environment and they're in the patient, they are the same organisms.

That is not what the evidence shows. In fact, in no instance where we have done any sequence in those three organisms is there any evidence apart from one case, which is called the 2016 aseptic unit case, that there is evidence of direct transmission from the environment to the patient. Now, either we've missed it from all the, despite the tens of thousands of water samples we've taken, or it doesn't happen as described.

Q That's why the long version of "nothing was going on" that you've just given us has been promulgated, because the effect of what you're saying is that all these concerns about the environment at the Queen Elizabeth, the water and so on, the things that stopped when interventions were taken, none of that matters, because you haven't been able to prove any link.

A I'm not sure that none of it matters. I don't think-- I wouldn't put it that way. I would state that where you have evidential data that would show whether there's transmission or no transmission, the data shows that there is no evidence of transmission as it stands within that data set. I wouldn't be quite so-- I wouldn't say that there's nothing going on, or I'm saying that the data shows that there's no evidence of direct transmission between the environment and the patient.

Q That's helpful. Can I ask you about biofilms?

A Yes, yes.

Q I know why you make a face, because you made comments on them and I'm simply trying-- I'm going to ask you about them now to avoid picking them up in very various bits of your evidence----

THE CHAIR: Before we go on to what sounds like a slightly different topic, I just really wonder if I've taken an accurate note of what Professor Leanord said. Talking about the absence of match, I've noted you as saying either it doesn't happen or we haven't found it. Now, I just wondered if I got that right. Did you say it doesn't happen or did you say it hasn't happened?

A It hasn't happened within this data set----

THE CHAIR: Right, it's----

A --and so-- but at some point, you are trying to prove a negative, and at

some point, if your hypothesis is not-- if there's no data to support your hypothesis, you either have to keep going, so you're into the land of diminishing returns, or you have to question whether your hypothesis was right in the first place.

THE CHAIR: Yes, you're not saying that an environmental-- a potential pathogen, of which there are many examples within the water system in the hospital somehow cannot be a source. What you're saying is your work has not demonstrated that it has been a source.

A For these three organisms, and that's another caveat. Some of the organisms, for instance, Elizabethkingia, I think there were three cases. We haven't seen-- We never saw that in the water system, but the value of sequencing that is limited because you could get three sporadic sequence pieces of data and, as mentioned before, that was exactly the reason why we can't make any inferences out of pseudomonas except for, “They were different,” but we can't say anything further than that. That would be overstretching the interpretation of the data.

THE CHAIR: Thank you.

MR CONNAL: So, the data relates to the three organisms that we've talked about?

A That's-- Absolutely.

Q Yes. Well, that leads me nicely into biofilms. Now, I'm going to-- where I've picked up what you've said about it, I'm going to give the passages-- I'm going to quote the page numbers and so on, so that the records have that. It'll make life easier for anyone reading them later, and the first thing-- you say you're not an expert on biofilms, which is at para 285 on page 131. Is that correct?

A That's-- That's-- Yes, I'm not an expert on biofilms.

Q And-- but would you accept, generally speaking, that they can be complex communities?

A I-- That's my understanding, yes.

Q And would it therefore follow that what may or may not have built up in a water system, which we've had some evidence wasn't dealt with in the way that would ideally have been done over a period of possibly four years, you couldn't tell us what kind of systems-- biofilms may have built up in that over that period?

A No, unfortunately not, although I've got a fridge full of pipework that is to be looked at to see if we can answer that question.

Q What you do say in your witness statement is you say: "This serious contamination of a water system would produce a range of biofilms."

That's at para 289 on page 132. So, I mean, I-- I think I've got the quote almost exactly right. So, that's your position?

A If-- I think the direct question to me and my question answer was, "What would a serious contamination of a water system look like?" and it would-- to my mind, it would-- these organisms would live in biofilms there. They-- That's what they do.

Q The reason I think you were asked about that is that there may be a difference between, perhaps, you know, the kind of biofilm that builds up in an individual tap near the exit to the tap, where you have a debate about organisms that need oxygen and so on and so forth, and what may or may not have built up in the depths of a complex system over a period of years. Is that a fair point?

A Yes, I can't disagree.

Q Yes, and even if you're dealing with an individual tap, one of the points you make in your statement is that sometimes you can have a predominant organism, but different things may be shared at different times, so you can get more than one organism from one source.

A Yes, you might, but it's also clear that-- from the Stenotrophomonas data that where you get a resident strain, that resident strain looks like it's got primacy within that outlet and it stays there for weeks, if not----

Q I was simply quoting from paragraph 207 of page 115.

A Oh yes, no, no. Absolutely, and there's many things that can happen with biofilms.

Q Yes. Now, if we then move from biofilms to some of the issues that arise when you're doing environmental sampling generally? If you're taking, for instance-- As you suggested you could, you could swab this desk or computer – I hate to think – computer-type set, you have to get-- your aim is to transfer the biological content onto a swab, and we've had some evidence that you're unlikely to get the whole biological content of what's on the surface onto the swab. Is that fair?

A Yeah, Nobles' Rule of Tenths.

Q Sorry, what was that?

A It's called Nobles' Rule of Tenths.

Q Right, and what----

A So, you'll get a tenth-- Every time you use that swab, you'll get a tenfold reduction in the bacteria. So, if you swab the desk-- So, if there's 1,000 bacteria in your area that you swab, you'll pick up 100 in your swab, and then you take that swab and you put it onto your agar plate, you'll get 10. It's a rule of thumb called Noble's Rule of Tenths.

Q Noble's Rule of-- Well, thank you very much, and presumably if you're trying to make sense of a complex water system, like we've been told the Queen Elizabeth hospital has, you can only have a-- it is a true question of sampling. You're taking some water samples from a particular location, but you don't know how they relate to anywhere else, other than perhaps if you're taking them from a tank which is stationary.

A Either tank will-- yeah, or push-flush sampling will sample water that's further into the system. So, there is a way of doing that rather than just pre-flush.

Q So, can-- So his Lordship understands, what process you're just telling us about, can you just explain what that is?

A So, there's standard SOPs that are used by our water contractors on how to take a sample. You can do what's called a pre-flush, which means that you're really just using-- you have to take the tap out of-- or the outlet out of use for a couple of hours, the idea being that if there's any organisms within the mechanism, the tap, they will be there, and then you take your sample, and that tells you what's in that water sample quite close to the outlet.

I think-- I'm no expert in this, but the authorised-- the engineers will tell you

that that will be approximately the last-- the first-- sorry, the last two metres of your outlet. The alternative way of doing it is that you flush the tap and you let the water run through, and you stop the tap, and that's got rid of any, if you like, localised organisms, and then you then test the water that has been further into the system, because you've let a significant water come-- draw through, and that tells you the health of the system per se, if you like, and so that's one of the fundamental differences about how to test the water.

THE CHAIR: Does the rule of 10 apply to samples taken from water?

A No.

THE CHAIR: No.

A Because you've captured them within your-- whatever volume you've taken, and the way water testing occurs is that you then take that water and put it through a vacuum of which there is a filter. The vacuum draws all the water through that filter and the organisms are then deposited on the filter and you culture that filter and so everything that would be in whatever volume it is – 1ml or 100ml – would be captured. So, Noble's Rule only applies to either hard surfaces, or it-- well, it only applies to where you're using a swab.

THE CHAIR: Thank you.

MR CONNAL: When you were

doing the process of gathering the material for your WGS report, I think the phrase that's used in the report is "serendipity", which we've come across already today. There was, to some extent, it was a question of luck and what you could actually find.

A Yes. Yes.

Q Is that right?

A It's more than luck. It's-- and that's one of the limitations of a retrospective piece of work like this. You would never design this as a fully funded grant study. You would have a number of other things going on. It's only-- you can only sequence what has been stored. So, again, in terms of serendipity, there's-- if it hasn't been stored, we can't sequence it. We find that with Enterobacter, for instance.

It doesn't mean to say it completely invalidates some of our conclusions, but that's the nature of a retrospective study. The advantage of having this data set is that, going forwards in the future, if there are-- or in any data set, if there are future infections, you can contextualise them about where they sit within the molecular epidemiology of these organisms.

Q And, in fact, as a matter of routine housekeeping, many environmental swabs and so on are discarded, because otherwise the labs would be overwhelmed by the need for storage.

A Absolutely, and that's the nature of microbiology labs.

Q Yes. I'm-- When I'm going through this exercise, I'm acknowledging, just so it's clear to you, that – and I won't call it up on the screen – at page 1230 of the actual report that the heading, "Limitations of the Analysis" in which many of these points are acknowledged and, in fact, that was one of the issues, that a lot of the environmental samples have not been saved.

A Yes, and-- but I will give credit to Dr Inkster insofar as, in March 2018, she asked the environmental lab to save-- well, to do two things, which I think was very prescient, which was to identify all gram-negatives, not just the target ones, because we would look for a target pathogen, but all gram-negatives were to be identified and saved and-- from the water samples.

So, from then on, we had an excellent repository archive, if you like, to go back and do this work. Without that piece of foresight, this work wouldn't have been possible.

Q And one of the other issues that arises, as I understand it, is that when a sample is taken, it's then grown on, but generally, only a single colonic, a single item, is then retained so that at the time when you're doing your exercise you

don't know what else grew on the plate.

A Exactly. Yes. I mean, although if there were three pathogens on that plate, they would save the three pathogens, but then we get back into the "Do you need Multiplex or not?", which we've discussed.

Q So, I have to come back to some general points. We still have a situation in which a group of very highly respected clinicians are saying, "We ain't seen this before. You know, this is very different to our experience." You know, clinicians who were otherwise not being subject to any criticism, as far as I'm aware, in this Inquiry to date, very highly regarded people, and you're getting similar reactions.

For instance, Dr Maddocks, who gave evidence to the Inquiry earlier, said this was quite different from any experience he'd ever encountered, and that's a view shared by some others as well. So, these are all people who are identifying something unusual, something that is outwith their extensive experience. Dr Harvey-Wood was the same. She'd had 40 years. She'd never seen some of these things. I'm not quite sure the extent to which you're saying they're all wrong.

A I'm not saying they're wrong. What I'm saying is that the data doesn't support an evidential link of direct transmission from the hospital

environment to the patient.

Q For the three organisms?

A For the three organisms.

Q I suppose it still raises the question: if you've got a very experienced group who spend all their time, particularly the clinicians, looking for infections because they're terrified of them – I don't mean that in a pejorative sense, but they're worried about them because of patient safety – why are they suddenly encountering this if it's not explicable in some way? Are you able to help us?

A So-- I'll just go back to-- I think this is multifactorial. I think there's elements here that will explain some of that. I don't think you can completely-- and I don't discount the built environment as an issue. I have got no data on some of the organisms that are less frequent. I've mentioned Elizabethkingia, for instance, and I can't definitively give you an answer to the question you've raised.

What I can say is that when you look at the organisms that have got the highest number and therefore the greatest defect in any epi curve – Stenotrophomonas, Klebsiella-- No, it's not-- Klebsiella, we haven't seen but Enterobactor and Cupriavidis, which caused an issue – there's no direct evidence that came from that building. They can still be environmental. We

know that these are ubiquitous environmental organisms, but that's not what the data shows.

Q I think your suggested root for much of this infection is endogenous?

A I-- For some of the organisms, yes.

Q I suppose the question then is, if what was being seen was a burst of endogenously originated infections, first of all, would the clinicians not recognise that? Secondly, would they not have seen it regularly?

A Yeah, and my supposition is that it's not-- that's not what-- that only explains part of this, and I think that one of the conundrums about this occurrence is that we may never know what the sources or source was, and we've talked about this earlier, that sometimes you just do not know, and I cannot give you a definitive answer. If I could, we may not be sitting here.

Q I suppose that the other possibility which I need to ask you about – leaving aside the idea that if it was endogenous, it would be a constant, subject to your point about antibiotic spikes – is that we know from investigations done by an expert group on the water system, including people within GGC, people outwith GGC, and so on and so forth, that widespread contamination of the whole water system was found and drastic action was taken to deal with that at the same time as these issues are arising. Does that not suggest a possible link between the two rather than a coincidence?

A I don't think-- There is-- You would have to investigate that that is a possible link, and that's exactly what GGC did. And this work here was trying to understand what that link might look like from a molecular point of view.

Q Just coming back to the study for a moment. If you have an organism of concern-- Let's leave aside for the moment the analysis of whether each clade is capable of causing infection or not. If you have a series of samples which show-- from the environment, which show an organism of concern, let's say you have a number of these, but the sample from the patient isn't closely connected genetically by the definition you use, you say that – notwithstanding the existence of all these organisms of concern – there is no connection, and that's that, end of investigation.

A So, I would go back to say that I would try and-- I would use the tools that we have to try and understand where that-- the context of that organism. I don't think that you would say-- So, the unknown in this-- I'll go back. The unknown in this is what, if any, contribution does the normal

environmental organisms outwith healthcare play in infections that are identified?

One of the things that we don't know and we touched on it – and I'll raise it with Stenotrophomonas – is that you said, "You ingest it." Yes, well, we do because-- and that's why when you select it out that's why it's in your oropharynx. What we don't know is at what level it's there, if it's in us. Every single time I take a drink of water, do I reacquire Stenotrophomonas and it does me no harm because I'm not immunosuppressed, or if I have one of these organisms, if it stays with me and becomes part of my, if you like, normal flora, certainly in the oropharynx, where you get some of the highest densities of bacteria in your body-- We do not know or fully understand that.

We talked about the microbiome. We're starting to understand that a wee bit more. So, I can't answer your question definitively because I don't think the data's out there to help us answer that question. You would say there's an association, but there's not causality.

Q I think in the kind of example that I gave you, someone like Professor Dancer would say, "No, you don't assume since there's no link in the samples you found, therefore there's no connection." You might keep looking.

A And I agree. You might keep looking, and you might never find.

Q I think we probably have an easy consensus that if you're trying to find an organism, and you do whole genome sequencing, tick the box, that's fine. You get-- find the organism.

A Agreed.

Q I think the question is how far you use the failure to find the link as excluding, as opposed to simply saying that it's not being proved.

A So, I agree with that supposition as well. What-- In that situation, you're not relying wholly on whole genome sequencing. What you're relying on is your sampling structure before the whole genome sequencing. Your sampling structure would, in effect, be your net that you would catch those organisms within that would then allow you to sequence and give you a yes/no answer. If you've got either a very narrow sampling structure, you have got the potential to miss something, and I mean narrow, both in terms of geographical, either time, geography or what you define it as.

GGC is one of the most sampled healthcare systems that I am aware of with tens of thousands of samples over-- Well, we're talking about five years, but now seven years that we've had that really-- It's been under scrutiny like no

other system before. As far as-- In my opinion, that is a very wide net to spread. If there was organisms there, they're not difficult to grow.

They would grow, and we would then sequence the outputs of that growth and come to some sort of conclusion about whether it was valid to state that that organism came from that building and that water system or not, and did it look like that organism in that patient that was in that building or not? So it's not the sequencing that would give you that answer. It's your surveillance structure and your sampling structure prior to the sequencing.

Q I'm just wondering – and maybe you can help me with this – if you adopt the approach that you're suggesting, which is you're looking for this causal connection-- If you don't find it, nothing to do with the environment. Does that impact on the steps that might be taken by, for instance, an IMT trying to look at something? Because we've already had examples of where somebody has taken precaution x or precautions x, y, and z, as you would say, and, lo and behold, things improve.

A So, no, I think the IMT would take exactly the same-- exactly the same precautions. Another limitation of whole genome sequencing is that whole genome sequencing is effectively after the fact. So, unless you-- So, even if you gave me a bug today, I wouldn't give you an answer for four weeks, and that's just the nature. Well, two weeks is the best we can do, but if your bug was in a freezer, that's four weeks.

So, and the first organism and even the second and the third and the fourth don't give much information. What gives you the information is the background, your library, your archive of sequences. So, you really need-- Once you have that archive of sequences, you can build up a molecular epidemiological narrative. So, it doesn't help you at the initial part of an IMT unless you have your archived sequences to relate back to when you get an organism.

In many ways that's going to be impractical. If you've got-- and I'll go back to the three-- Elizabethkingia, I don't know how many years that would take to collect that archive. You can get national and international repositories, so you can compare them, but it doesn't look like your home molecular epidemiology. So, that's an issue. It's no accident that we have taken the big numbers here, because that's the ones that we knew would be there and we can actually make some inferences, imperfect as they may be, on the molecular epidemiology to within the hospital.

Q The use of the absence of

genetic closeness to exclude as opposed to simply say not proved-- Are you-- Can you help us? Is there any other published material we should look at, which supports that proposition?

A For Stenotrophomonas in cystics, I know of one paper that looked at, I think, 90-odd Stenotrophomonas types and compared environmental-- Well, it was 90 environmental and I can't remember how many patients, and they concluded exactly that. There was no linkage, despite it looking like an outbreak had occurred in the same way as we're having a discussion here. Now, that's unusual because there is publication bias in the journals where a journal will take a piece of work that gives an affirmative answer more readily than a piece of work that takes a non-affirmative answer, and that's recognised.

So, there's a publishing bias, and there's also the authorship bias. If you've shown nothing, it's harder to write your paper and say nothing was shown and to get that accepted, but I know of one case. I don't know the literature-- I haven't gone through the literature systematically, but if it helps this Inquiry, we can dig that reference out. I don't even know of it. I'm familiar with it. I'm not an expert on it.

Q I don't think I have any further questions at this stage for this witness, my Lord.

THE CHAIR: Professor Leanord, what I must do is discover if there are other questions in the room. So I'll ask you to go back to the witness room, maybe 10 minutes or thereabouts, and I'll be able to tell you whether there's more questioning.

A Thank you.

(Short break)

THE CHAIR: Mr Connal?

MR CONNAL: My Lord, a number of issues have arisen from this evidence, but none give rise to questions to be asked today.

THE CHAIR: Right. I understand, Professor, there are no further questions for you this afternoon, and that means you're free to go, but before you go, can I thank you for your attendance today, but can I also thank you the work that has gone into preparing for that evidence, including the preparation of the witness statement? I'm grateful for that, and thank you for that, but as I say, you're now free to go. Thank you.

A Thank you, your Lordship.

THE CHAIR: Right. You say there's things arising from the evidence, but nothing that needs to be----

MR CONNAL: Done now.

THE CHAIR: -- done-- done at present?

MR CONNAL: No. No.

THE CHAIR: Well, we shall resume tomorrow at ten o'clock, I think, with the evidence of Dr Armstrong.

MR CONNAL: Dr Armstrong.

THE CHAIR: Yes.

(Session ends)