Vol II (Mar 2)

F/CR/17/90

IN THE COURT OF QUEEN'S BENCH OF NEW BRUNSWICK

TRIAL DIVISION

JUDICIAL DISTRICT OF FREDERICTON

HER MAJESTY, THE QUEEN

- and -

ALLAN JOSEPH LEGER

A TRIAL HELD BEFORE THE HONOURABLE MR. JUSTICE DAVID M. DICKSON, JUDGE OF THE COURT OF QUEEN'S BENCH OF NEW BRUNSWICK, AT THE BURTON COURTHOUSE, BURTON, NEW BRUNSWICK, ON THE 1ST AND 2ND DAYF OF MAY, A.D. 1991

- TRANSCRIPT OF EVIDENCE AND PROCEEDINGS -

EVIDENCE OF DR. JOHN WAYE ON VOIR DIRE

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APPEARANCES:

Anthony Allman, Esq., Graham SIeeth, Esq.and John Walsh, Esq., Solicitors for the Attorney General of New Brunswick

Weldon Furlotte, Esq. and Michael Ryan, Esq., Solicitors for the Accused, Allan Joseph Legere

MR. FURLOTTE: That was last evening, yes.

THE COURT: And said he would be -- he'd try to get along this afternoon if he could. But it doesn't -- he suggested it wouldn't affect your case, you were handling this end of it.

MR. FURLOTTE: Yes.

THE COURT: Now, you were on your direct examination of Dr. Waye. Would you continue with that, Mr. Walsh.

MR. WALSH: Yes, my lord.

DR. JOHN WAYE, still under oath, continued to testify:

DIRECT EXAMINATION CONTINUED BY MR. WALSH:

Q. Dr. Waye, you finished up by referring to the final schematic, it was not a schematic it was the chart, I believe, Mr. Clerk, it was VD-45 was the last item marked yesterday.

THE COURT: 45.

Q. And you were explaining inclusion, exclusion inclusion in relation to band. At this point in time, doctor, I am going to ask you if you could we get into the area of how you actually get into the interpretation of an autorad, an x-ray that's made. Do you have a schematic that would assist you in that regard?

A. I have a slide.

Q. Yes, a slide?

A. Yes.

MR. WALSH: My lord, at this time I am going to show the doctor this particular paper reproduction --

THE COURT: Just before we come to that, are these charts that are on display, the larger charts, they're just reproductions of the earlier ones but are they going -- you're not putting those in in evidence, are you?

MR. WALSH: No, in fact the purpose behind the paper reproductions, my lord, would be that whatever is on the slide or on the charts is in the paper reproduction, it would be unnecessary for the clerk to handle them unless you would wish him to.

THE COURT: Why don't you, you needn't do it right now but later for convenience write on the top of those things in three places the corresponding numbers and put copy of VD-30, VD-40 on the left hand or whatever and if you're using them again, it would be -- remind you of what the numbers are, okay.

Q. I'll show you this paper reproduction, is this an accurate depiction of the next slide?

A. Yes, it is.

THE COURT: And this would be VD-46.

MR. WALSH: Perhaps if we could have the lights.

Q. Pardon.

A. I don't have my laser.

Q. Oh yes.

MR. WALSH: If I may have a moment, my lord, the doctor, he requires that laser pointer, if I could just have a second.

Q. Okay, doctor, perhaps the question I could commence with this morning is what interpretation of the autorad that you produce is done and what is the purpose behind such an interpretation?

A. Again, with a forensic case, you're asking the question could this evidence material as which is shown in Lane B, could this material have come from the victim which is shown in Lane A or two people accused of this crime. And at the end of the experiment, you will have one or two bands, in this particular case the victim as a two banded pattern, as does the evidence, a blood stain and the blood standards from the two accused. They all have two banded patterns.

The one thing that is on this example and it wasn't on the example yesterday, are the marker lanes, the flanking marker lanes. They will show up on the autorad as well. And these are fragments of known size. We know the precise base pair size of this fragment and this fragment and this fragment and this fragment all the way down. See, the reference points, much like the scale on a ruler. Again the interpretation is the fragments, the distances from the origin is a function of their base pair size. In this particular case it's two banded pattern, the bands migrated further, both of them migrated further than the two bands in the victim. So the evidence sample could not have come from the victim. Again, the pattern is quite distinct

from the pattern of Suspect 2. So the evidence could not have from Supect No. 2.

This probe, however, pattern is indistinguishable from the pattern that you see for Suspect 1, this is an inclusion and this means that the evidence could have come or is consistent with coming from Suspect No.1.

Q. Doctor, if you were to actually look at an x-ray, an autorad, for the purposes of determining whether there's exclusions or inclusions between unknown and known standards or known and unknown samples, what would you actually do, what would be the first thing that you would actually do?

A. I'd hold -- I'd look at the autorad, generally put it against a white background or something that makes it easy to see the bands and I'd simply look at -- make a visual assessment of the patterns. First look at the number of bands that you can detect from top to bottom.

Q. In each lane?

A. In each lane, second, look at the positions of the bands. Along with that you'd be looking at all the controls, et cetera to make sure everything worked.

Q. Perhaps, first of all, when you're looking at the bands, you say you look at the individual lanes, do you do it, all the lanes at once or do you look at lane to lane or how is it actually done in practice, practically how could you do it?

A. Well, you have the entire x-ray film and all the information in front of you, so a quick look

does cover all the information that is on that entire x-ray film. And then you would focus in on each lane individually going across the gel and making your visual assessment of each lane.

Q. Now, if, for example, the pattern in one lane doesn't match the pattern in another lane, the case you have there, Suspect No. 2, Lane D and Lane B, the evidence, you're saying that visually that does not match up.

A. Correct.

Q. If that is the case what conclusion do you draw from that?

A. If this is -- if the migration of these bands is indeed an accurate reflection of their size, the conclusion is that these -- Sample B could not have come from the same individual that the blood was drawn from, Suspect No. 2.

Q. Is that an absolute exclusion?

A. Yes.

Q. Now, with respect to Lane B and Lane C, what conclusions would you draw in that particular regard?

A. The evidence analyzed in Lane B could have come from Suspect Number 1, DNA analyzed in Lane C.

Q. And you made that conclusion based on a visual comparision?

A. That's the first level of analyzis.

Q. Is that an accepted -- generally accepted method in the scientific community as a first level of analysis, a visual comparison?

A. Yes.

Q. Is it a reasonable reliable method?

A. In my opinion it's the most reliable method.

Q. And what, if anything, is done other than a visual comparison of the lanes?

A. Other than a visual comparison of the lanes, you determine the sizes of these fragments. Visually you can say that this fragment migrated the same distance as this fragment in adjacent lanes. The next step you'd use is you determine the size of this fragment, you determine the size of this fragment and they should be in close agreement.

Q. How do you do that?

A. The way you do it is you rely on the reference lanes that flank the evidence that you've analyzed. We know the size of these fragments. So we compare, if we know the size of this fragment, it's the same size as this fragment, just for the sake of argument, we'll say that's 5,000 base pairs this fragment. We know now if you put a ruler across here that the top fragment from Suspect 1 and in the evidence is a little bigger than this reference fragment. So it's 5,000 and a little bit. The next marker up is 6,000, well, you can say it's somewhere around 5,200. If you were going to make that sort of assessment, again, visually looking at these markers. You don't make that assessment visually, what we do is we have a computer. And the computer will take this image, computerize the imagine and the computer itself has a program

which will scan the flanking markers, scan these lanes and tell you precisely relative to the flanking markers the size of this fragment.

Q. What you're saying, they'll actually give you sizes for each of the bands that are shown?

A. Yes, the computer will analyze, he will take this information and do a count, the known sizes of this, how far they did migrate, the computer will, the operators ask how many bands he sees in a lane. In this case I'd be the operator and I'd tell -- I'd punch in the computer, I see two bands. The computer would then identify the two bands, asking if they identified the correct bands, in which case, I'd say, yes, this band and this band. And then it would estimate their sizes relative to the flanking size standards.

Q. Now, doctor, as a hypothetical, assume for a moment that particular autorad had no visual matchings, no visual bands that visually compared, would you go to the computer?

A. Yes.

Q. If everything was an exclusion?

A. There would be no need to but we would.

Q. Now, would you repeat this particular process for each probe that's applied?

A. Yes, it's part of the analysis, which is why you do it for an exclusion as well as an inclusion, you repeat the process from beginning to end.

Q. Now, doctor, in the particular circumstances here, you say, the computer, is the computer something that's used in forensic labs to back up the visual comparison?

A. Yes, the computer programs of this sort, they've -- they were -- have been developed for this type of work in other fields, they've been adapted and refined for forensics, but, yes, generally accepted.

Q. And do you have any opinion as to its reasonable reliability?

A. It's very reliable.

Q. Now, doctor, would you expect to find in computer, would you call that quantification, is that what it's called computer quantification?

A. We just call it sizing, it's an objective way to determine the size.

Q. All right. Would you expect, you say, a visual match, would you expect to get the exact same number of base pairs, for example, between the top band in Lane D and the top band in Lane C?

A. No, even for patterns that are visually distinguishable, the computer may say, this is 5,208 base pairs, and the next lane which looks identical in the migration pattern, it may say, it's 5,108, it may have a difference of a hundred base pairs.

Q. Would you explain why that is and what, if anything, is done to compensate or allow for that?

A. The reason for that is that the base pair unit is the smallest unit that you can break the DNA down into. And this technique, the RFLP procedure using agarose gel is incapable of exact resolution to the base pair level. It would be like trying to

measure my height to a thousandth of an inch using a ruler, you're using the wrong tool to get that type of resolution.

Q. And what is done to compensate or to allow for that fact, if you're not getting exact base pair measurements from band to band, what, if anything, is done to allow for that or to compensate for that?

A. Well, you establish tolerances. You know in this particular case that it's from an evidence sample and a suspect. But we know from experiments where we run the same DNA sample from one individual over and over and over again, like if I ran my DNA four times across, I'd get the exact same visual pattern, the computer would probably give me four different sizing estimates. And we know from running experiments over and over again how different those sizing estimates will be.

Q. And does each individual lab arrive at a conclusion in terms of their tolerance levels?

A. Yes, those tolerance levels are dependent on your protocol and they have to be established empirically in each lab.

Q. And these tolerance levels is there a name, another name that's used for that?

A. If you're applying to doing forensic matches, seeing how far apart could these sizes be and still substantiate my visual call, it's called a match window or a match criteria.

Q. Would you expect the -- is that expressed, how is that expressed in base pairs and percentages?

A. It's generally expressed in the percentage of a size, you can't express it in base pairs because a ten base pair wobble up at the top of the gel for a fragment of ten thousand base pairs. A ten base pair window is a very small wobble to the system, whereas for fragments of a hundred base pairs, ten base pairs is a big difference, it's ten percent of the size. So you generally express it as a percent.

Q. Do you know what the R.C.M.P. match window is?

A. They're match is 5.2 percent.

Q. And 5.2, would you just show the Court, please, where would that 5.2 be applied, is it all one direction or --

A. No, it's 2.6 percent up or down, that's the type of window you apply.

Q. So if you have a visual match and you back it with a computer, the band in one lane and the band in the other lane must be within 5.2 percent of each other?

A. Correct.

Q. Now, would you expect to find different percentages between different labs?

A. Yes, somewhat different, depending on how they derive that number and depending on their overall system, that number could increase or decrease.

Q. Does that invalid the system in place in each lab, the fact that the different labs might have different match windows?

A. No, conceptually you're doing the same thing, you're defining how much wobble there is in size estimates and the formal expectation there's no -- that you will not always come up with the same match window for different labs, different protocols.

Q. Is the use of match windows generally accepted in the scientific community?

A. Yes.

Q. Do you have an opinion as to its reasonable reliability?

A. I think it's reliable.

Q. Doctor, you were referring to comparisons from lane to lane within the same gel, the same membrane, is that correct?

A. Yes.

Q. Could you tell the Court, please, whether or not such a comparison could be made between, for example, Lane B, in this particular gel or membrane and say, for example, Lane D in another gel or membrane, separate from that -- can such a -- you say, there's a visual comparison, then the computer imaging or sizing is a gel to gel comparison, can that be made in forensics?

A. It can be made, it's somewhat more difficult. When you analyze samples on different gels and conduct experiments on different membranes, the markers, they'll always appear like this because you do the procedure the same, you follow the same procedure for each analysis. But they won't

migrate precisely the same way. So you don't have the benefit of, say, overlapping, overlaying the two results and making a visual call. You really have to rely on the size estimate. So I have to rely on the computer telling me that on my one autorad or x-ray film, it's 5,208 and then I have to rely on the computer giving me an answer that's either close to that or not close to that, depending on whether it's an inclusion or an exclusion. You have to rely on those numbers to make the call when you're dealing with samples that were analyzed effectively separately. It's much the same as if a sample were analyzed in the FBI lab and a sample were analyzed in the R.C.M.P. lab, you would be able to compare those results using the same system eventhough they were analyzed in different cities, in fact different countries if you have sizing data.

Q. Sizing data, what do you mean by that?

A. We know the benefit of making a visual comparison because they weren't analyzed together, so you have to rely on that sizing data, you have to rely on comparing the numbers, comparing the sizes that the computer told you.

Q. Is there any attempt to make some form of visual comparison between gel to gel?

A. Other than, if gel one, you can make the visual comparison of saying, well, the top band is a little higher than this 5,000 base pair marker and then you go to the second gel, and say, well,

the top band is -- it's around this 8,000 base pair marker. So that's clearly an exclusion. You can sit down with the two in your hands and draw that conclusion fairly quickly. For the inclusion, you'd do the same thing, you'd look at and go, well, that's a little bit higher than 5,000 and then you'd go to your second gel, and you go, well, so is this, it's a little higher, too and say, well, in my mind that could be an inclusion. But I'm going to have to rely on the sizing data to back that up.

Q. Which, in your opinion, doctor, is the better form of comparison, gel to gel or lane to lane, within the same gel?

A. If possible you always want to analyze samples together.

Q. Is it always possible to do so in forensic cases?

A. No, a lot of times in a forensic case, there's a large number of exhibits and they don't all enter the lab system at the same time. You will begin your analysis, three weeks later there may be two new suspects that have to be analyzed or three new pieces of evidence. But you've already begun with part of your evidence samples your test.

Q. Once you start, for example, once you start the DNA typing test, putting your things in the gel and running your gel, is it possible when you get other items to put in the same gel?

A. No.

Q. Doctor, these interpretations, can an interpretation of an x-ray, an autorad be done by other than the actual person who conducted the test?

A. Yes.

Q. And could it be done, for example, a year from now after a test is done?

A. As long as people keep the x-ray films these interpretations can be made by people, anyone who's familiar with reading the x-ray films.

Q. Yesterday there was some terms mentioned, one was the monomorphic marker, I believe was one term.

A. Yes.

Q. Now, my understanding from where we are at this point in time, you look at the -- each polymorphic probe to see where the bands, whether there is an inclusion or exclusion, is that correct?

A. Yes.

Q. Then where does the monomorphic, that probe come in and where does the sex typing probe that you mentioned yesterday fit into this interpretation?

A. Okay, one thing I've been doing or I've been trying to do all along here when I talk about inclusions and exclusions, particularly exclusions is state that if everything worked properly and if these bands, the position of the bands is an accurate reflection of their size, then I would call this an inclusion. Now, that qualifier simply states did that, did the

electrophoresis work properly? Is the position of this band an accurate reflection of its size. What can happen and with especially with forensic samples is samples may run too fast or they may run too slow. And on occasion you can have the pattern not reflect the true size of the fragment. If I were, for the sake of argument, say, that something went wrong with the electrophoresis and the DNA in Sample C ran properly, this is exactly where this fragment should have migrated and it migrated according to its correct size. However, there was a problem and if DNA in Lane B ran a little bit too slow, so the fragment is in this position but it actually should be in this position. It ran a little too slow for reasons maybe it was contaminated with salts or dye or whatever. But in actual fact if everything did work it should be done here, this fragment should be done. That's called a band shift and if that were the case, this sample could not have come from this person. You always qualify your interpretation that this is an inclusion if the position of this band is an accurate reflection of its size.

Q. How do you determine that?

A. That's where the monomorphic probes comes in. If I see this result I tentatively call this an inclusion. And then I strip this membrane and I probe it with a probe that should be the same result in all individuals. So I should get a band, say at this position in the victim and

in the same position and in Lane B, C and D. You get a constant band going all the way across if it's a human sample. Now, if everything worked fine and these are accurate if the bands -- if the electrophoresis worked and it worked properly and the bands I see on here are an accurate reflection of their size, the bands from the monomorphic will be in a constant position and it will be in the correct position, we know the size of the monomorphic band. And the computer will tell you, how accurate is your electrophoresis? If there were a band shift here, you'd see the constant band shift and you'd see it shift. In this case the example I've used, you'd see it shift downward and that would flag to you -- or conclude to you that oh, oh, we had a band shift and something is wrong with this lane here.

Q. And the sex typing, how does that fit into your interpretation of an autorad, an x-ray, you mentioned yesterday there's a probe to actually determine sex, is that correct?

A. Yes. None of these variable probes or the first monomorph probe tell you anything about the gender of the DNA donor. That information has to be gained by actually analyzing sequences that are specific for males, present on the Y chromosome and not present on the females. And that's a simple test that you do at the end of the procedure. Again, all males will have a constant band from the Y chromosome. So if

Sample A, if this victim was a female, you'd see nothing in this lane. If Samples B, C and D were from males at position 3,650 or around that area, you'd see an intense band at the same position in all the samples that came from a male.

Q. Doctor, when you're in forensics, when a scientist is interpreting an autorad or analyzing an autorad or each autorad as you've described, what are the various calls or conclusions can be drawn in a forensic case by a scientist with respect to a DNA typing test?

A. As it's shown here, there's exclusions, there's inclusions and there's inconclusive results.

Q. All right, now, would you, please, just so we're very clear, when would you call an inclusion in a forensic case?

A. In a forensic case I'd call an inclusion first if my visual assessment is much like shown here, B and C, they're visually in the indistinguishable, the migration patterns. If I back that with a monomorphic probe that shows there was nothing wrong with the electrophoresis and that the results are accurate and if the computer sizing falls within my empirical observations, how close these sizings should be for a visual match.

Q. Again without being redundant, can such a determination be checked by another scientist inside or from outside the lab?

A. Yes, if he has access to your x-ray films and to your sizing data, that's all they'd need to draw the same conclusions.

Q. Now, is this conclusion as an inclusion, is that type of a decision made for each probe or after all the probes are made, decided or looked at?

A. I think that would depend on the investigator, certainly as you do these experiments you're not blind to the results that you've obtained. like you're analyzing, you have four suspects and on the first probing none of the suspects match the evidence. You don't have any inclusions then, there really is no need to continue excluding those suspects. With inclusions, generally when you formally make your final decision, et cetera, you take into consideration all the probings at the end. You look at the overall picture, the four probings, the monomorphic data, sex typing and then you formulate your final conclusions. Generally you do all the sizing at that point as well.

Q. Just as a hypothetical, as an example, what you have there, for example, Lane B, the evidence and Lane C, the suspect, assume for a moment, doctor, that's the first probe that's done in the forensic case, you would, from what I understand, you would call that an inclusion if you backed it by the computer and if the monomorph showed that there was no band shifting, is that correct?

A. Yes.

Q. If you went to a second probe and if, for an example, Lane B and Lane C did not match in the sense that C, the bands in C were different in a different locations than the bands in B, and again, there was no band shifting, would you

then continue on probing to a third probe?

A. Yes, that would be an exclusion at that point. Myself I probably would do a third probe. In most instances that would exclude again, there's no real need for it, you have excluded the person.

Q. If there is on one probe no match, being the fact that it's an absolute exclusion, that would be the overall call that would be made by the scientist?

A. Yes, the exclusion always overrules the inclusion.

Q. So we've talked about inclusions and we've also talked about exclusion, is there anything else you would like to add on either of those topics?

A. There's the area in between, inconclusive.

Q. Inconclusive, fine, doctor, would you please, could you tell us about, under what conditions would the results be considered by a scientist in a forensic case to be inconclusive and what does inconclusive mean?

A. Inconclusive means I can't determine whether it's an exclusion or an inclusion, there's insufficient data to draw those conclusions.

Q. Okay, would you explain, please, the types of things that would cause in a forensic case a scientist to call a particular result inconclusive?

A. The most common reason is, if your sample is limited, say, if the evidence sample is limited and limited to the point where I can barely,

barely, barely see any fragment on the x-ray film at this position, again at this position and it's pushing my level of detection with my eyes which again are more sensitive than a computer, and visually it's hard to make a call, the computer can't make the call, there simply is too little material to say inclusion or exclusion. Insufficient sample is probably the most common reason to come up with an inconclusive result.

Q. What, for example, doctor, test failure, if there was something went wrong somewhere, could you explain if that would have any impact on your call of an inconclusion or inconclusive?

A. Yes, if the controls, the controls indicated that there were a problem somewhere along in the procedure that I couldn't make an accurate call. Say, for instance, I did see a pattern or I did see a pattern that's indicative of a band shift. Say, this band migrated here and this band migrated there and I could document the band shift. At that point, scientifically, I feel you're justified in saying, that is a match, it's just that the sample ran incorrectly and I've shown that it ran incorrectly. Being conservative, generally through the forensic community they would call that inconclusive, eventhough there's evidence that it is an inclusion. You call it inconclusive because the whole system didn't perform optimally.

Q. When you -- is there a difference between having no results or results that you can't actually call, is there a difference between that?

A. Yes, no results is either the sample was heavily degraded or there was just too limited in quantity to get a result, that would be a case of no result. And as I mentioned before, there's the gray area between getting a readable result and not obtaining a result at all.

Q. These types of conclusions or results that you say a scientist could call in a forensic case, either an inclusion, exclusion or inconclusive, could you tell the Court whether or not these are standardized conclusions drawn by forensic scientists from lab to lab?

A. That general train of thought, there's subtle variations from lab to lab and from investigator to investigator but generally all the labs I'm aware of have pretty much the same criteria for calling matches both visually and computer assisted. They use that technique to call inclusions and exclusions and they all have a gray area in between that they would call a result inconclusive, eventhough themselves as an investigator and scientist would be convinced that it's consistent with coming from an individual, something in the procedure, given that evidence from something in the procedure not working optimally, generally there's a bail out clause for inconclusive just to be conservative.

Q. Perhaps, if we could use an example, you had mentioned earlier this morning, the case of -- the first thing you do when you're actually looking at an x-ray and correct me if I'm wrong, is that you look visually to see whether or not they exclude or they include or if they match or not. Assume for a moment, doctor, you had a situation where you looked and visually these bands, say, for examples in Bands B and C match, are indistinguishable from one another to the eye, and assume for a moment, doctor, that you went to your computer and your computer sized those bands and gave you base pair size for the band in each lane, B and C. And assume for a moment, doctor, that the sizing put any of those bands outside the match window, what would happen in a particular case like that?

A. In the case where the computer places visual matches outside of your matched criteria, as a scientist and personally I always trust my eyes, I would be convinced that it's still a match. However since it does violate your match criteria, it's not an exclusion, it's clearly a visual match but you would again opt conservatively to say that that is outside of my match criteria and I'll call that inconclusive because I don't have a computer back up on that. But your eye has more resolving ability that the computer does, your eye is the most sensitive instrument.

Q. Is that -- the use of the eye, is that something that in your opinion is generally accepted in the scientific community?

A. Yes.

Q. And reasonably reliable?

A. Depending on your eyes, yes.

Q. Under -- doctor, in your opinion, what are the risks of a false positive, that is declaring a pattern of bands in separate lanes or gels across multiple probes to be identical, when in fact they're not?

A. Okay, if the procedure is done correctly and interpreted properly, there's no chance of that happening.

Q. In your opinion, doctor, what are the risks of a false negative, that is declaring a pattern of bands across different lanes or different gels to be distinguishable, when in fact they are identical?

A. Again, if the test is done properly and interpreted properly, the chance of that happening, in my opinion, it won't happen, it's more likely to happen than a false positive.

Q. What do you mean it's more -- what would that more likely do with respect to any particular accused?

A. It would exclude him.

Q. It's more likely to -- the testing would more likely exclude him than it would include him?

A. Again, that's a false exclusion, if you have all the proper controls in hand and you falsely exclude, in my opinion, you've interpreted the test incorrectly. If I can give you an example,

if you have very small amounts of DNA, as a general rule the larger the fragment, the easier it is to detect. If I had a very small amount of DNA in Lane B, such that I could just detect the top band but I can't detect the bottom band. If I compared that to Lane C and made the call, well, I only have a one band pattern here and I got a two band pattern here and called that an exclusion. I've incorrectly interpreted the results and I've falsely excluded.

Q. Which would be nor to the benefit of the suspect, is that correct?

A. Yes.

Q. Doctor, in your opinion, for forensic -- what is your opinion for forensic purposes as to the general acceptability in the scientific community of the analysis interpretation of autorads as you have described?

A. I think in the scientific community this type of visual, computer assisted analysis and the logic behind calling inclusions, exclusions and inconclusive results, I think that would be viewed as, I think it is viewed as a very rigorous assessment of the data.

Q. When you say rigorous, what do you mean by that?

A. It's, if anything, excessive analysis of the data.

Q. In whose favour?

A. I think you're being conservative, trying -- no one's favour, you're trying to interpret the results correctly and you have a number of ways to do it, each of which assesses the same thing in a very redundant manner, all designed to show

results correctly. If I can say, a lot of researchers, a lot of them don't even use markers on their gel, a lot of researchers, the visual assessment, most research in a lab saying the visual assessment would be the only means to score it, it's a very reliable way of doing it. Forensically, you have several other approaches that you tag on top of that one, to take out the operator's subjectivity of the analysis.

Q. Doctor, do you know if there is any impact, what, if any, environmental conditions or do you know of any environmental impact studies that have been done to determine the effect on the accuracy of an RFLP call technique?

A. One of the things historically people do when you come up with a new test forensically, is you try to mimic what can happen to a forensic sample in the environment. So you take -- if you wanted to see what environmental factors would have on blood, you'd leave blood on various materials in various environments. You'd leave them out in the sunlight, high humidity, you'd mix them with various goods, say, household cleaners, Coca Cola, we put them on various fabrics, various surfaces and you do the test and try to see, do these factors have any effect? It's very hard to mimic everything that can happen in the wild. But studies have been done to try to assimulate.

Q. Can you think of any studies, who have actually conducted such studies, and if you could give the

Court, please, some examples of findings that they have made with respect to different kinds of environment factors or surfaces and things of that nature?

A. Probably every forensic lab has done environmental studies of some sort. Some have done more extensive studies than others, and some have done longer studies than others.

Q. Can you look at the results of other labs, could one lab look at the results of another lab's environmental studies?

A. Yes.

Q. Could you give us some examples of some of the things that you're aware of in the scientific community that DNA has been subjected to determine the effects on its accuracy and its typing test?

A. I'm aware of experiments where they've taken a number of fluids, like as I mentioned before, household cleaners, both acid and alkali, things you find around the house, soft drinks, lemon juice, tea, coffee, mix those with blood, mix those with semen, put those same materials on various types of surfaces with various fabrics, both synthetic and natural fabrics, again exposing biological fluids to environments, such as direct sunlight, high humidity in a greenhouse, high temperature, things like that, leaving DNA samples or biological fluids in various environments for various lengths of time, time course studies.

Q. And what are the conclusions that are drawn by these studies?

A. There are things that will destroy DNA. The most noted example I'm aware of, every lab that has done this experiment has met with the same result, is if you put blood or semen in soil, soil contains a lot of bacteria, the DNA is quickly degrading. When you run the test you get no result. That's an example of environmental influence which you can predict is going to destroy the DNA and at the same time destroy your ability to analyze the DNA and get a result.

Q. How would that impact, for example, and perhaps making a false call, including someone?

A. You have no result, it's a very easy thing to analyze. If all these samples were left in the soil for a week, all we have is markers on the gel and I would have to make a call, it's inclusive, I can't tell whether any of those samples came from any of those individuals. I have no results to analyze.

Q. Doctor, I am going to show you a couple of documents, and ask whether or not, you are aware of these in the scientific community. I'll show you this first document here.

A. Yes, I'm aware of that study.

Q. And is this one of the environmental studies you've talked about?

A. Yes, amongst others, this is one of the studies.

Q. And this is entitled, Evaluation of DNA Isolated from Human Bloodstains Exposed to Ultraviolet Light, Heat, Humidity, and Soil Contamination?

A. Yes.

Q. And this particular study was in the Journal of Forensic Sciences, and it's dated --

A. I believe it's 1990.

Q. Accepted for publication in 1988 but I don't seem to have the date that it was actually published, my lord. You believe it's 1990, doctor?

A. 1989.

MR. WALSH: If I could have this entered at the hearing.

THE COURT: VD-47.

Q. Doctor, I'll show you another document --

THE COURT: That last one was a paper on what, about the evaluation of DNA under certain circumstances.

Q. Doctor, I have another document here, would you look at that for me, please and tell me whether or not, if this represents one of the types of studies on DNA and its affect?

A. Yes, this is somewhat of a different study, where they've -- rather than taking samples from a lab and trying to mimic factors in the environment, they actually take forensic case samples that you do see in the forensic world, and analyze the effects of them being in these environments for long periods of time, the effects

on the patterns that they've obtained. And the title of it is, «THE EFFECTS OF ENVIRONMENT AND SUBSTRATA ON DNA», the use of casework samples from New York City. And it again is published in the Journal for Forensic Sciences 1989.

Q. When you use the term, substrata, doctor, would you explain, please, to the Court what that term means?

A. That would be the materials that you're dealing with, what the fluid or the substance if found on.

Q. For example?

A. Wood, cloth, on the ground, on a wall.

Q. That is another study of the type that you have been discussing previously?

A. They're summarizing they're findings, yes.

MR. WALSH: I would ask that that be entered as an item.

THE COURT: VD-48.

Q. Now, doctor, I am going to -- is there anything else that you would -- before we move on to another area, is there anything else that you would like to add with respect -- that you can think of, that you'd like to add or you think would be of benefit to the Court to know about the interpretation of the x-ray, the autorad?

A. Not at this point, no.

Q. Fine. If we could have the lights, please. Doctor, I am going to now move into a different area, I am going to move into the area of

population genetics. I am going to go into an area -- I want to know, doctor, if I can, elicit from you, the significance of the inclusions that you've talked about, the matches. If a match is made, if a call is made that something is included, what significance does that have, perhaps, we could start off by clarifying something, doctor, earlier yesterday you had mentioned that one of the acceptable theories in science is that no two individuals' DNA is the same except for identical twins?

A. Correct.

Q. How does that fit with respect to the question of inclusions in these particular tests?

A. Overall individuals, with the exception of identical twins, overall the DNA is going to be different, that's not in dispute anywhere that I'm aware of. That's one of those facts of life. But remember, we're not looking at all three billion base pairs, we're looking at selected regions of the DNA molecule.

Q. Does the technology at this point allow you to look at all three billion base pairs?

A. It's a current goal of research to analyze all of the DNA but right now it's not technically possible and the data just doesn't exist to do that.

Q. And the areas that you look at are these highly polymorphic areas?

A. Correct, there are areas that we know there's a good chance people will be different at those regions.

Q. And could you explain then, doctor, what significance then or how -- what is the significance of an inclusion at one, for example, at one particular polymorphic area as a result of one probe?

A. If you had an inclusion between two samples, a question and known, that means that the unknown sample could have come from the same individual as your blood standard, could have come. It doesn't mean it did come from there, it's consistent with it coming from that individual.

Q. And what do you do, for example, as a scientist, what would you/to do actually try and determine the probability associated with whether it did come from the same individual?

A. To determine the significance of that word, could, obviously if ninety nine percent of the people have that particular pattern, the fact that it could have come from that individual means very little because ninety nine percent of the population also have that pattern. That's a very weak inclusion, it's consistent with coming from him but it's also consistent with coming from every one else in the room. If you're dealing with regions that are highly polymorphic, you know apriori that there are a number of different patterns in the population, say, a hundred different forms and only a portion of the population is going to have the form that matches your DNA sample, and you use population

genetics to define exactly what that proportion is. Do one in a hundred people have that pattern?

Q. That one probe?

A. Correct, you ask those types of questions.

Q. All right, now, say, for example, just hypothethically, doctor, say, for example, that at one probing you know a priori a particular pattern is one in a hundred, one in a hundred people of a particular race have this particular type of polymorphic pattern, now, you go to the-- and there's a match. And you go to the second probing and again, hypothethically, and you know that the match, the pattern shown to match is again a priori, you know that it is one in a hundred people have this in a particular race. You go to a third probing and there's another -- there's again an inclusion, a match, and you a priori, for the sake of simplicity that the frequency is one in a hundred. What do scientists do to assess the probability or to put some kind of weight to the significance of all three inclusions?

A. The tests are designed to be independent. You're looking at genetically distinct loci. So the patterns that you see at one locus are not influenced by the patterns that you see at another locus, that's a starting premise.

Q. What mathematical --

A. What you do after that, the probability of somebody matching at all three independent events

is just fundamental probability calculations, you multiply the significance of the individual probabilities.

Q. Meaning that you multiply one probe by the second probe, by the third probe?

A. Yes, the frequencies that you associate with those patterns at each probing. So one in a hundred times one in a hundred, so now you're -- the frequencey of somebody sharing or having a match at not only the first locus but the second locus would be one in a hundred times one in a hundred which is one in ten thousand.

Q. And then you would go to the next?

A. If the next probe was again a match and it was one in a hundred, you apply the product rule again, and it would be one in a hundred times one in a hundred times, one in a hundred which is one in a million.

Q. And if you went to a fourth probe, and there was an inclusion and again, the frequency was one in a hundred, you would continue that multiplication?

A. Yes, you keep adding zeros accordingly.

Q. In science, what is that actual multiplication called?

A. The product rule.

Q. Is that, the product rule and the use in forensic, particularly in forensic use, is that-- in your opinion, could you give me your opinion as to its reasonable reliability?

A. If applied correctly, it's reliable and accepted method of determining probabilities.

Q. Is it used outside forensics?

A. It's a statistical method that's used throughout science and probably throughout business, et cetera, it's just a fundamental formulation.

Q. Do you have an opinion as to its -- I take it you have an opinion as to its general acceptability in the scientific community?

A. If applied properly, I think it's generally accepted.

Q. Before we go into the actual theory on how you go about this, how would you -- in a forensic case, doctor, how would you actually express, for example, what we've just hypothetically formulated, say, three probings and you've said there's one in a million. How would you actually express that to a court in a forensic case or to a police department or something, how would you actually express that if you have a match at all three probes and each probe frequency was one in a hundred?

A. The wording that I've used in the past, it's always with respect to a reference population. Obviously you have to determine the frequency of individual matches at a particular probe with respect to some population. If you say, the Caucasian population of Canada, for instance, that's the population that you derive these numbers from. You'd express the significance of the match across three as this matches across

three probes and the probability of finding somebody else who fortitiously has that matching pattern across three probes in the Caucasian population is one in a million.

Q. That's the probability of someone else having that particular pattern across three probes would be one in a million in our hypothetical?

A. Yes, that's how I've expressed it.

Q. That was a little insight as to where we're going, doctor, I would like you now to tell us, please, what a lab must do, a forensic lab must do first before it can make any probability, before it can determine how much that each probe pattern, whether it would be one in a hundred, et cetera? What must a forensic lab do first before it can even begin to make such probability estimates?

A. You have to undertake the task of determining how rare or how common these various patterns are in the population.

Q. How do you do that, what was the first thing you do?

A. You sample a population, you obtain DNA samples from a large number of individuals from the population and you'd conduct these tests on those individuals and you run through the same computer analysis to define the sizes of the various fragments. And then if you've analyzed, I don't know, a thousand individuals, you can ask the question, how often do I see an individual that has a fragment of the size that matches the fragment I detected in this particular case.

Q. When you're talking about a fragment, you're referring to what would be a band pattern or a band, an individual band?

A. Yes.

Q. Is there a term that's used in science for such a sample population?

A. The phrase that's used to describe that type of sampling and those types of experiments is you're building a data base, it's called a population data base.

Q. What are the considerations that go into the selection of a sample population to determine fragment frequency? Is there another term for the fragment, is there another word that's used in science to determine, to use the term fragment?

A. Allele.

Q. And what is the term or what goes into the consideration, what considerations go into the selection of a sample population to determine allele frequencies for this highly polymorphic areas?

A. The first consideration is its end use. If I'm going to be using this data base to make productions on a people who live in a certain geographical area of the world, I'll want to take into consideration what types of people live in that area. For instance, if I wanted to build a data base that would be applicable to Canada, it would be inappropriate for me to go out into the public and sample one thousand DNA samples from Hispanics, say, people of Mexican

origin, because it wouldn't reflect the population of Canada, my reference populaton.

Q. What other consideration would you take in?

A. Well, you take into consideration the various racial groups existing in the area that you want to assess.

Q. All right, for Canada, what would you have to consider in that regard?

A. You consider which groups and what proportions of which groups are represented in the Canadian population.

Q. And what other considerations would you have to take in?

A. The actual system that you're working with, how many different forms that system will detect. Obviously, if you go back to a very simple example, if a probe can only detect, say, three different types of variation, form A, form B and form C, I don't have to analyze millions of people to estimate how often form A and form B and form C occur in a population. I need only probably analyze forty or fifty individuals to get very accurate frequencies.

Q. What about the rare or the highly polymorphic areas that you're looking at with these probes?

A. Yes, if you're dealing with a test that will distinguish say one hundred different forms in a population, obviously analyzing one hundred people you're going to miss a lot of those forms and you're not going to get an accurate indication of how many -- what proportion of the

population has each of these one hundred forms. You have to analyze a larger sample population in those types of instances.

Q. So size is a consideration in your sample population?

A. Yes, you have to fit your population base size to the test that you're applying it to.

Q. What about -- just so I understand, doctor, you've indicated that race is a consideration in developing a data base, is that correct?

A. Yes.

Q. Size is a consideration?

A. Yes.

Q. What about, assume for a moment, you've selected the races that you want to sample, what, if any consideration do you have to give to the actual individual within the race, how do you actually go out and get those individuals?

A. Scientifically, you want to have a random sampling of the population or as random as you can make it. You certainly wouldn't want to have an unrandom sampling, say, pick every one who attended this family reunion. Chances are you are dealing with individuals or many of them who are highly related, closely related. So you are not making a random sampling of Canadians. You're making a random sampling of people with this particular last name or who are related to people with that last name.

Q. And in -- for scientists, how do they actually go about that, for forensic purposes?

A. For forensic purposes, you put the onus on somebody else to pick the people. What we have done and what we -- I mean, the R.C.M.P., what other labs have done, you obtain the samples from sources where acquiring a sample had nothing to do with the forensic end use. For example, if you wanted to sample a hundred people from this area, perhaps a random way to do it would be to go to the blood donor clinic on a Thursday and say, give me samples from the last hundred people that gave blood. Giving blood has nothing to do with what your patterns are going to be. And a hundred blood donors coming through the clinic is probably a fairly random sampling of the area. You know they live in the area, they gave blood in the area.

Q. That's something I wanted to ask you, doctor, what about geographic representation now, if you wanted to look at Canada, do you have to go to each particular area within each province, within each town, within each city, within each county, what concern for these types of purposes does geographic representation have?

A. Geographically you'd like to at some point in doing these studies assess if there are any differences geographically. I think it would be scientifically incorrect to start with the assumption that if I analyzed a hundred people in this particular town, that they'd look like a hundred people in Victoria, British Columbia. I think that would be a scientifically poor assumption to begin with. But I think when you've

done these studies and you realized that I've sampled from, say, five areas in North America, from all over North America and I get the same answers when I go from place to place, it's reasonable to conclude that if I go to a place that I have already analyzed I'm probably going to get the same answer again. You need not cover every square mile in North America to draw those conclusions. It would be a blind assumption and an incorrect assumption to analyze in one area and then extrapolate to the rest of the country or the rest of the world.

Q. What data bases do the R.C.M.P. presently have and what role did you play in the compilation of those data bases, if any?

A. I haven't seen the latest up-to-date versions of every group that they've tested. I can speak on the data bases that I've been involved in with the R.C.M.P. and the ones that I'm aware have been built since my leaving the R.C.M.P. Primary emphasis and again, it reflects on the end use of the data base. The primary emphasis was placed on building a Caucasian data base.

Q. Why is that, doctor?

A. Because ninety percent of the Canadian population falls under that racial group.

Q. And can you fit that in -- ninety percent of how many people?

A. Twenty five million, approximately twenty five million is the population of Canada.

Q. Divided male, female, a certain percentage?

A. It's not something that people do head counting on but the population is generally fifty percent male, fifty percent female, birth rates reflect that.

Q. And what other considerations, you say you've selected a Caucasian data base?

A. That was the first, the first goal would be to select people from the Caucasian population and ask the question how often do these particular patterns occur in the Caucasian population?

Q. And you say ninety percent in Canada are Caucasian?

A. Yes, the last census statistics included those types of questions, your racial origin.

Q. What about New Brunswick, how does that compare, you say, ninety percent of Canada is Caucasian, how does that reflect in New Brunswick?

A. New Brunswick is a little higher.

Q. More than ninety percent are Caucasian?

A. Yes, I believe ninety five, ninety six percent.

Q. Caucasian, what do we mean by the term Caucasian, for these purposes what do you mean by the term Caucasian, do you have a simple way of actually explaining that?

A. In Canada, just looking at the census stats Caucasians pretty much means somebody of British or United Kingdom origin or of French origin. There's a small percentage -- that's the vast majority of Caucasians, both in Canada and in New Brunswick are of either origin -- their

ancestory comes from the British Isles or from France, so they're French or English, white. There's also a small percentage of both North European, Scandinavian, South European, Eastern European.

Q. In terms of New Brunswick you indicated that the percentage -- you've indicated that Canada was about ninety percent Caucasian, you've indicated that New Brunswick was a little higher than ninety percent Caucasian, the British and French how does that compare in Canada as a whole in New Brunswick, how representative is New Brunswick of your description of Canada?

A. In Canada as a whole if you look at that ninety percent that's Caucasian and then you look at the proportions within that ninety percent that are of British origin, United Kingdom origin and French origin, the proportion of British origin is higher than the French, as it is in New Brunswick, the proportions are fairly similar.

Q. And you've indicated the population of Canada and you say, roughly, male, female about half each, what about New Brunswick?

A. In 1986 census stats, the most recent census statistics available it's around 750,000, I believe, the population of New Brunswick.

Q. And divided male/female?

A. Again, I'd be surprised if they were a bias -- a significant bias between fifty and fifty, fifty/fifty male female.

Q. Is Caucasian synonymous with the term white, white skin?

A. As were applying these things to the Canadian population, you wouldn't be far off if you said white and you wouldn't be far off if you generalized and said, white either British or French, you'd be talking about the majority of people that would fall into Caucasian in Canada if you simplified it that way.

Q. The gentleman sitting between the two police officers in the box over here with the white shirt, how would you characterize him?

A. He would fall into Caucasian. I couldn't make a statement as to whether he's of British Isle or French origin.

Q. Would the name help or is that of any benefit to you at all?

A. Some people use names to pick out somebody's ethnic background, it's not a very good approach, we have to do that in the clinical lab sometimes and you'd be surprised how many Chinese people have very anglo names. So it's not a very scientific method of determining somebody's ancestory.

Q. But if you were told that that man's last name was Legere, would that help you in any fashion in classifying within the Canadian population?

A. I'd say if you had to make a gambling bet, you'd say probably French.

Q. Continue, doctor, the compilation of the data base, could you continue, please? What role you played in the compiling of the R.C.M.P. data base and what you know of the R.C.M.P. data base at the present time?

A. Initially we sought to sample Caucasian individuals from Canada. We went about that through the Red Cross in Ottawa and we obtained blood samples from the Red Cross and ran these precise tests on all those blood samples. Initially and the part that I conducted personally there was some five to six hundred blood samples that we analyzed, that we obtained.

Q. From what area?

A. They're obtained through the Red Cross in Ottawa, a portion of those samples I believe somewhere around ninety or a hundred of those samples were people who were actually residents of the Ottawa area and gave blood at the clinics in Ottawa. So they would represent people who lived in Ottawa. The majority of the samples, however, came from a military base, Kingston. And those people were being trained at Kingston and they were from all over Canada.

Q. Are you aware, doctor, I'm not going to ask you to list them but are you aware of any other scientist that is going to testify this week or next week with respect to the details of that particular data base?

A. Yes, we have several collaborations with people analyzing this type of data and I'm aware, it's

been brought to my attention that since I left the R.C.M.P. that they have actual breakdowns of the military population in Kingston and where these people are from et cetera across Canada, their representation across Canada. And those studies have been done. Dr. George Carmody at the University of Ottawa is conducting all of those studies on the breakdown geographically of where the Caucasian samples that I analyzed originated from.

Q. And the-- apart from the Ottawa and the Kingston area, are you aware whether you were involved or not, are you aware of the compiling of any other aspects of the data base, the Caucasian data base?

A. Well, while I was in Ottawa, we built a -- or we compiled a second data base and I was involved in that data base and that data base involved several hundred individuals, I can't remember the exact number, I believe it was three or four hundred individuals, several hundred individuals, and they were obtained from the Vancouver region of Canada. So this would be residents of the Vancouver region. I believe they were people -- blood samples of people who came to medical clinics for routine medical checkups. That's the information I'm aware of.

Q. What instructions are given to actually obtain these blood samples, what are you actually asking people to give you?

A. You're asking them to give blood samples from people who fit the ethnic group that we're looking at. If we ask for black samples, people will give us samples that came from people in their opinion that were black. If we ask for Caucasian or white, they will take a little bit of blood from -- left over from people who they perceived as being white. You ask that they avoid -- a family comes in with seven brothers and you ask that they avoid giving you samples from all seven brothers, pick one and give us that. You don't want to have people who are related, because you are in effect analyzing the same family DNA over and over again. You don't want to bias it that way, you don't want to be analyzing one particular family. You want them unrelated and you want them to fit the ethnic group. You don't want a person represented twice in the data base as well. So you try to collect blood samples that were -- you try to get blood samples that were all collected around the same period of time. So you can avoid the possible complication of analyzing somebody twice. Say, if you got one lot of blood samples collected in January and another lot collected six months later, somebody might have given blood during both of those time periods and you've got them represented twice in your data base. You want the person represented just once in your data base.

Q. Doctor, just, I wanted to back up a bit, you indicated that you would guess from the name, Legere, it was French, would that have any relation to the actual language the person spoke at this point in time?

A. Not necessarily, no.

Q. What are you referring to?

A. The last name is -- it's not a very scientific method of determining somebody's ethnicity and not a very reliable method. In general, that name would be more common amongst people of French ancestory than it would be of people from the British Isles. That is a scientific statement that you could make that if you polled those two groups of ancestory that name would be more common in one than the other. But I don't think it would have anything to do with the language that the person spoke. Obviously if he's of French ancestory and again, you were betting, you were playing the probability game, speaking French might be more likely than speaking English.

THE COURT: Why are you dwelling on the name, surely that wouldn't have very much significance.

MR. WALSH: No, I wanted to -- no, that's something that I really wanted to clarify, my lord. I didn't want to leave anything to speculation. I just wanted to clarify this. I expect the other, like, for example, Dr. Carmody and things of that nature, it will all tie I would hope in relation to why the data base is compiled in the fashion that it is. I simply wish to point out the various statements that the doctor is making --

just the statement that you're making that name is not -- can be of some help but it's not indicative of anything in particular of any particular thing. I wanted to -- just not leave to actual speculation. I don't want people speculating, when in fact I can ask people what significance it may have or may not have. And if it turns out to be irrelevant, so be it.

Q. Doctor, you've indicated and that's from the Vancouver area?

A. Yes.

Q. Have you had occasion, doctor, to look at data bases, Caucasian data bases compiled in other areas?

A. In Canada?

Q. Yes.

A. There's a Caucasian data base that's put together in Toronto.

Q. For who or by who?

A. For and by the Centre for Forensic Sciences.

Q. Fine. And how many individuals are in that data base?

A. There's several different data bases. They have a Caucasian data base and they also have a what they call a criminal data base, it's a data base put together just from criminal samples in the lab without regard to their race. It turns out it is mostly Caucasian. Both of those data bases, I'm familiar with those.

Q. Any others?

A. There's a Caucasian data base from Montreal.

THE COURT: Just a matter of curiosity, what possible use would a criminal data base be?

WITNESS: It was actually put together initially for the acquired samples that were of known Caucasian origin. So in a forensic lab that's handling literally thousands of blood samples a year, the way they started up a system was to find out the variability in the general populations. They went to the blood samples they already had in their freezers, samples from old cases, cases that have gone through the court system. They had a blood standard from doing conventional serology, and took several hundred of those and built a data base of basically convicted criminals.

THE COURT: It wouldn't deviate very much from another data base would it, than a Caucasian --

WITNESS: Well, it would if all of the criminals blood samples that you looked at were, say, from Espanics. As it turns out when you go through those files and you look through it, the majority of the samples were from Caucasians and no, it did not deviate.

Q. Doctor, how do they compare, the Caucasian data base within Canada that you've looked at, how do they compare in terms of the frequencies that are being calculated?

A. The data that I've looked and so the data base from Vancouver, the data base from Ottawa, Kingston, the data base from Montreal, looking at them, they're more similar than different,

they're extremely similar in their frequencies. In fact no one data base is more similar to the other or different, you can't predict which data base came from which region.

Q. What conclusions can you draw from that, doctor?

A. Looking at all that data, geographically or regionally, there's no difference, no significant differences in their frequencies of the things that we are measuring. That is if I had a data base -- if I had a particular pattern and I want to apply these statistical formulas to it, it really wouldn't matter whether I used the data base from Vancouver or the data base from Ottawa or the data base from Montreal, I am going to be able to determine whether the pattern is rare or common and I am going to get pretty much the same statistical measure of whether it's rare or not.

Q. Suitable for use for forensic purposes?

A. Yes.

Q. What about an individual from New Brunswick, if you wanted to compare to an individual from New Brunswick, what, if any, opinion, do you have with respect to the suitability of using the data base from Vancouver or Kingston or Ottawa or Montreal, the ones that you've actually looked at?

A. Again, knowing that the population of New Brunswick doesn't deviate significantly from the populations in Canada in general and knowing that for instance, data bases of predominantly English

people, say, the Vancouver data base and predominantly French people in the Montreal data base are very similar, there's no basis to believe that New Brunswick would be different from any of those other data bases. So you could apply a data base from Vancouver to a case in New Brunswick.

Q. Does the Kingston data base help you in that determination?

A. It's a nice place to start, you're dealing with a mosaic of people from all over Canada. After that you've effectively dissected groups that you can distinguish, say, the French and the English.

Q. Doctor, the methodology for selecting a data base for the purposes for forensics of the RFLP purposes, in your opinion, do you have an opinion as to its reasonable reliability?

A. It's quite reliable, these types of questions that you ask by literally polling people and doing their DNA analysis are standard practice in genetics. In fact in order to publish a new polymorphisms, et cetera, it's required that you determine the frequencies of the various forms in a reference population. It's something that's done throughout science.

Q. In obtaining the reference populations for Caucasians as you've described, could you give me an opinion as to its general acceptability in the scientific community?

A. I believe it's acceptable.

Q. And as to its reasonable reliability?

A. I believe it's very reliable.

Q. Just as an additional matter, doctor, do you know of any other data bases that you were -- for the R.C.M.P. that you were involved in actually compiling or you are aware of that presently exist?

A. There are data bases for various populations of native Indians.

Q. Why is that done?

A. Again, if you have a crime occur in an area of Canada where the population of individuals who could have committed the crime doesn't reflect the population of Canada. Say, you had a crime occur in the far north where for thousands of square miles, it's predominantly native Indian, it really wouldn't be appropriate to go to another racial group to determine the frequencies of a native Indian that could have committed that crime.

Q. Are you aware of studies that determine that between races frequencies for these particular purposes are different?

A. Yes, among the first studies that were ever done with these types of probes and with other types of probes are to use the conventional racial groups, blacks, whites, orientals and assess the frequencies in each of those populations for that precise purpose to determine if there are any differences between the races and it does occur.

MR. WALSH: My lord, it's eleven o'clock, whatever you prefer, I intend to, my next category I wish to go into, I've covered I believe the data base --

Q. Doctor, is there anything else, you would like to add with respect to the data base itself, the compiling of the data base?

A. I think I would add that these types of data bases aren't restricted to Canada. There's data bases that have been compiled in a great number of the United States, and certainly geographically from coast to coast, there's data bases from various countries,et cetera, as well as Europe. Caucasian data bases have been made globally wherever Caucasians are prominent and the forensic labs are using DNA analysis. This type of approach isn't restricted to Canada. The data exists for various other regions in Europe.

Q. And about that data, in your opinion, doctor, what, if any comparisons can be made and what conclusions have you drawn from looking at data below the border and in Europe?

A. The frequencies that you derive from the data bases don't change because of political boundaries again, geography has very little to do with the frequencies that you find in the Caucasian population.

Q. Is there anything else, doctor, that you'd like to add on that area?

A. Not at this time.

MR. WALSH: My lord, at this time I intend to commence the actual method of frequency calculation. I am going to ask the doctor to give us an overview of how a scientist would actually go about such a process using a data base and it might be a logical place to have a break, if you wish.

THE COURT: We'll take fifteen minutes here.

COURT RECESSES FOR 15 MINUTES AT 11:08 A.M.

COURT RESUMES AT 11:25 A.M.

THE COURT: All right, Mr. Walsh, you want to continue.

MR. WALSH: Thank you, my lord.

DR. JOHN WALSH, still under oath, continued to testify:

DIRECT EXAMINATION CONTINUED BY MR. WALSH:

Q. Doctor, we've talked about data bases, the compiling of data bases, once you have a data base, what, if anything, is done to determine the frequency of an individual allele, that is if I might, that is a band, an allele, what would you do to actual determine the frequency that you would expect to find a particular allele or band to appear on a certain location at a polymorphic area?

A. The first thing you do is actually create the data base information, that means you take if your sample is five hundred blood samples, you do exactly the procedure that you use to analyze the forensic case. You extract the DNA from those five hundred blood samples, run, cut them with the same enzyme, run them on the gels

A. Yes, in North America it's called the binning method.

Q. That's B-I-N-N-I-N-G?

A. Yes.

Q. And who developed this particular method?

A. It's actually a spin off of some work that was done in the academic community, in the research community, it had nothing to do with forensics. People working with these types of probes several years ago came with a method of grouping fragment sizes and characterizing them in groups, it's called binning. The FBI and the R.C.M.P. took that philosophy and adapted to this type of data.

Q. Did you have anything to do yourself with respect to that?

A. Yes, I was involved in the initial formulation of the concept of binning as it applies to this system and some of the decisions we made about how we were going to organize the data and analyze the data.

Q. And what, if any, publications resulted as a result of adopting or using this binning method for forensic purposes?

A. There's been several presentations and several publications of this method and of the data derived using the method.

Q. Are you an author of any of these publications?

A. Yes.

Q. Has this binning method been disseminated throughout the scientific community?

A. Yes, since it's -- since the idea first came into focus, I believe it was sometime in 1988 at a meeting in Belgium we started--myself and Bruce Bedoley from the FBI started putting together a system in our minds and how we'd apply it to the system. Since that time it's been presented to numerous working groups and international conferences, the idea and the application of this method.

Q. And Bruce Bedoley, for the record, is who?

A. Dr. Bedoley is a scientist, a research scientist at the FBI academy.

Q. Doctor, I am going to show you this particular document here and I am going to ask you if you could recognize it?

A. Yes, I do.

Q. What is it?

A. This is a pre-publication draft of an article to be published in the American Journal of Human Genetics sometime later this summer.

Q. And is that, apart from the actual publication, has that article been disseminated throughout the scientific community?

A. Through the scientific community and the legal community, this article has been mailed all over the place.

Q. Have you ever seen this article appearing in any other cases, in case reports?

A. Virtually any case that's gone through the United States court system since this article was written will have some version of this paper introduced into evidence.

Q. And is this binning method set out in this particular article?

A. Yes, the purpose of that article is to present the method to the scientific community.

MR. WALSH: My lord, I am going to ask that it be entered, the name for it is quite long, «FIXED BIN ANALYSIS FOR STATISTICAL EVALUATION OF CONTINUOUS DISTRIBUTIONS OF ALLELIC DATA FROM VNTR LOCI FOR USE IN FORENSIC COMPARISON».

THE COURT: VD-49.

MR. FURLOTTE: What's the date on that one?

MR. WALSH: I think it's January 3rd, 1991, it's the final draft if I'm not mistaken, January 3rd, 1991.

Q. And that's to be published this year?

A. Later this summer, I believe.

Q. Doctor, could you perhaps, so we can conceptualize it, would you describe what the binning is, what it does and what you're attempting to do?

A. Okay, you remember when I was talking about sizing before, for the sake of argument consider that two of these samples are both DNA from one individual, say, myself. And you come up with identical patterns because the DNA has a sole source, myself. The computer will tell you the size of these fragments and although their migration patterns look identical and distinguishable, it would be unlikely that the computer would say that they're the exact base pair size. You could get again 5,208 here, you'd get 5,108 there, it would be a hundred base pairs off.

Q. That relates to what you were saying, testifying about this morning, a match window, the reason for the match window is that you won't have exact measurements.

A. The reason for the match window, when you look at a population as a whole though if you know this type of imprecision exists in this system that you can't define to the base pair in the DNA samples derived from the same individual, it would be scientifically incorrect to look at my five hundred people or my thousand events that I scored in the population and say, how often have I seen a band of 5,208.

Q. Base pairs?

A. Base pairs, because you'd be asking an exact question, how often have I seen this one event. To the exclusion of all the other numbers, like, 5,000, 109, 110, they're the same size band but you can't resolve it to the base pair.

Q. So what do you do as a result of that?

A. Binning is simply, divide the length of the gel up into sectors, physical sectors and what you do is you look at your thousand events and you say, how often have I seen an event from this size to this size. So you cover a range of sizes that will compensate for the various values that you're going to obtain for examples that are indeed from the same individual and the same, exact same fragment length. So what you're doing is you're adding up all the events between points that flank the region of interest.

Q. Okay, how do you do in these particular sections -- do they have a name to them?

A. That would be called a bin, you take all the events and you throw them into a physical category, a bin.

Q. Okay and how do you determine the boundaries for each bin?

A. Their fixed -- their fixed numerical values from top to bottom, I can't remember the exact values but it would go 12,000, from 12,000 base pairs to 11,500, from 11,449 to 11,000 even, and it would continue down in a gradient. Physically, they're fairly uniform. Size -- the number of base pair size that changes as you go down.

Q. Okay, just to reiterate so I understand it correctly, what you're doing is you divide up the gel into these bins?

A. Arbitrarily, yes.

Q. Okay, and just hypothetically, say, for example, could you -- you have a bin from zero to a thousand base pairs.

A. Correct.

Q. And any individual bands that you see when you do your sample data base that fit, that have a base pair of either five or a hundred and five or two hundred or four hundred base pairs or nine hundred base pairs would all go into the one bin?

A. Correct, like if this particular band here was five hundred base pairs in size and this one was nine hundred and ninety nine base pairs in size,

eventhough I can clearly distinguish them from each other, they would fall within the same category because they're within those boundaries of zero to a thousand.

Q. Now, when you're actually doing this binning, placing them in these fixed bins, are there any considerations to be taken -- anything that you consider?

A. If you want the boundaries to be large enough that this imprecision is unlikely to move a fragment from one bin to another, that is, if on average my sizing capability is within, say, five percent each time, I wouldn't want to use a bin size of one percent. Because depending on your measurement and precision, you'd be moving things from one -- you'd be moving the fragment from one category to another when you want it to reproducibly fall into the same category. So you want the bins to be larger than your measurement and precision. So that was one of the design considerations.

Q. What other design considerations?

A. Well, the whole system is designed to be conservative, so that was the other design consideration.

Q. Conservative, what do you mean by that?

A. The example that I always use is, if you have two fragments that are very close in size, simply add another band just below here, two fragments that are very close in size. And one fragment is very rare in the population and one

other fragment is very common in the population. Now, when you go to your casework sample and you get a band that's somewhere in this area due to measurement and precision you don't want to fall into the situation where you're taking something that is very common in actuality and confusing it with something that's very rare, just because it lies next to something that's a rare event. What you do with binning is, is you take both the rare and the common events and you add them together. So what you've done is you made both of those more common, artifically more common that they actually are, than your actual observed events.

Q. So if you have a common band and a rare band that's close together, by putting them both in the same bin the rare band becomes more common in frequency?

A. It becomes much more common and the common band, well, it becomes a little more common, adding a couple of rarer bands to a common band doesn't change. But what it does is it really compensates for overemphasizing these rarer events and putting too much stress on a rarer events that are very close that could be mixed up with very common events.

Q. Just so we understand, would that make the numbers that you later generate higher or lower, would the probability be higher or lower than in actuality?

A. You would be predicting events to be more common

than they actually are, artifically biased to make things more common than they are.

Q. Is there any other concerns that you have or considerations that you assess when you are actually using this fixed bin trying to determine your individual frequencies? How about, for example, the number of fragments that would go into a bin, what, if any, consideration do you give to that?

A. The number of -- well, if they fall within the boundaries, you can really, if a bin goes from zero to a thousand, they're obviously from one to nine hundred and ninety nine, nine hundred and ninety nine different fragment lengths that could theoretically fit in that bin.

Q. What, for example, you've divided a bin into that category, zero to nine hundred and ninety nine and say, for example, you went out and you took your sample population, seven or eight hundred people, Caucasians, in this -- my hypothethical, and you did your RFLP test on their samples, and it turns out that in the category zero to nine hundred and ninety nine base pairs you only find two bands that actually fit into that particular bin. I would assume that would make a very, very rare occurrence or a rare occurrence, would it not?

A. It would be a rare event, you'd be looking --

Q. What would you do with that? Would you leave just the two in there or would you do anything different?

A. Your observation is that it's an extreme rare event, in fact things that you see once or twice. Statistically you can't put very much faith in them. You don't really know if something you see one in a thousand events, if you did it ten thousand times, you don't know whether it would occur ten, twenty, you just don't know. Statistically single events aren't statistically significant or to put two events in a sample size like that. So what we do there is remove the bin boundary and essentially pool that one event with the next bin, the adjacent bin.

Q. Which could --

A. It gives you the next size class from one thousand and one to two thousand I observe twenty five events. Well, that's statistically significant. Now, I'd add that one lower event to that bin, I'd merge the bins, collapse the bins, make them larger, more conservative and add an event to that more common event, I'd have twenty six.

Q. Is there any -- in your binning method that you've described in the paper and what you're describing now, is there any -- have you agreed on any number of bands that must fall into a bin before the bin stays the way it is or before you collapse a bin into another bin?

A. A bin must have five or more observations, that's the rule that we've formulated for this. So if I observed in my sample population four events, if I look at a thousand events and I

observed it four times. In the next bin I observed twenty five events. I would simply collapse those bins, add them together and add the four to the twenty five and now, I treat that full size block as twenty nine events out of a thousand.

Q. Which would make it more common?

A. Precisely, you're taking an observation of four in a thousand and you're artifically making it twenty nine in a thousand, you're making it more common to be conservative.

Q. And what is our purpose, to be conservative?

A. And to again, increase the emphasis on things that are rare and that you don't have confidence in that number being precise.

Q. Because of your sample size?

A. And the rarity of the observed event.

Q. What happens, doctor, if, for example, you're dividing up the -- perhaps, my lord, for the record as you indicated earlier and we didn't do yet, this particular chart that we've been referring to, the doctor has been referring to since the break, what number is that, VD-40, VD-45 is the chart for the record that the doctor has been referring to since the break. Doctor, I am going to ask you, if you were doing your binning and you were dividing up the gel and you have your bin, what, if, for example, in your bin zero to nine hundred and ninety nine, it's just a figure we've been using, what happens, if, for example, it was to fall right on the bin

boundary, like instead of falling at fifty between zero and nine hundred and ninety nine, it actually fell on nine hundred and ninety nine, or right where you go into the next bin, what would you do in a case like that?

A. Well, fragment always falls into a bin, it's a very common question, what if it falls right on a boundary, well, it can't fall right on the boundary, it will fall in one bin or the other. because they are precise matters. It will either be zero to nine hundred and ninety nine or it will be a thousand to two thousand. You don't have a base pair in half, sort of thing.
If it's right on the boundary, you're dealing again with a little bit of measurement and precision, so if you actually knew the size of that fragment, one measurement it may be in the lower bin, the other measurement it may be in the top bin and that will happen if you analyzed ten times in a row, something very close to a bin boundary, it will flip back and forth from -- between those bins.

Q. So in the binning method, what would you do in a case like that, if you found one that was very close to a bin boundary in that regard?

A. If it was very close to a boundary and those two bins had equivalent frequencies, it really doesn't matter which one you put it in.

Q. What happens if you have one bin with very rare frequency and the other bin is a much more common frequency?

A. Again, you're dealing with a situation if it fell into the rare one, you very well could be giving it a rare frequency, when in fact the next measurement may put it in the more common bin. So in those cases, if your measurement and precision studies tell you that there's a good probability that the next measurement would have put it in that other bin, you put it in the other bin, you take the more conservative approach, and you adopt the more conservative figure to use -- to describe that fragment length, the frequency of that fragment length.

Q. Now, this is a method, doctor, to reiterate, this binning method is for the purpose of determining what individual band -- the individual band, you see what their frequency is in the sample population, in the population is that correct?

A. Yes, it's for the sole purpose of when you look at a profile like this, I want to be able to know how often this band would occur --

Q. The top band?

A. -- in the population. And then the same for this band, I'd like to know how often that occurs in the population.

Q. Okay, now, you do that for each probe?

A. Each probe.

Q. So you have a collection of bins, you take your sample population, you run your RFLP test and put, say, for example, the probe on chromosome -- that you identified earlier as being from

Chromosome 1, the highly polymorphic probe for Chromosome 1, you run that against your sample population, you look at all the bands that that displays and you start putting bands in the bins that you've designed, is that correct?

A. Yes, and at the end of that analysis I'll have classified all the bands that I saw in my population sample size into distinct bin cateogries.

Q. And then when you've finished that, you're able to determine, I take it, using mathematics to determine the percentage or the frequency of each particular band as displayed by that probe?

A. Yes, what you end up with is a table and if my computer tells me that this 5,200, I can go to a table that will say, I can go to a table that will say, well, that falls in this particular bin, that it's boundaries flank that and I've observed this many events.

Q. And you get a frequency from that?

A. Correct.

Q. And then you would do the next with another probe, on your sample population and fill another collection of bins separately?

A. Yes, you would repeat the same procedure on those five hundred individuals, score one thousand events and place them in their appropriate bins.

Q. Again, to find out the individual frequency for each band as displayed by that probe?

A. Yes.

Q. Now, doctor, that -- I take it, then that's -- the binning method is a method for determining individual band frequency, the individual band itself?

A. Yes.

Q. Okay, now, what, if anything, do scientists do to actually determine the frequency, that -- if your binning shows the frequency of an individual band, for example, this one on VD-45, what do you do as scientists to determine the frequency that you would find this band and this band in this particular location together.

A. That's a different question, you've already defined that this band is say, found in one in fifty individuals, this band is found in one in one hundred individuals.

Q. Using binning?

A. Using binning. The next question is, how many what's the frequency of finding both of these bands in the same individual in a population. How many in a population will have not only the top band but the bottom band. And that's the next question that you ask.

Q. Okay, and what do scientists do to actually determine that question?

A. That's done using a simple mathematical relationship which dates back to Gregor Mendos(phonetic), the founder of genetics, his initial observations more than a hundred years ago, and then formalized about eighty some years ago. It's a very simple formula.

Q. It's a mathematic equation?

A. Yes.

Q. And does it have a name that scientists use all the time?

A. It's commonly known as the Hardy-Weinberg formula.

Q. And what does the Hardy-Weinberg formula mean?

A. It means if you wanted to know the frequency of individuals in a population that have this band and this band, you simply take the frequency of this band and multiply it by the frequency of this band and multiply that by two.

Q. Now, again, --

A. So I can use the numbers that I did before, this is one in fifty, this is one in a hundred but the number of people using that formula that you'd predict would have both bands, would be one in fifty, one in a hundred times two, which is one in ten thousand.

Q. So what you're in essence saying then, is that the frequency of this band pattern appearing with that probe is that particular percentage or that particular number?

A. Correct.

Q. Again, I just deviate just for a minute, I don't want to muddy the waters, earlier in your testimony you referred to the fact that the two band pattern is the mother and the father, but you indicated that there is -- and that's the heterozygous, a term you used earlier.

A. Yes.

Q. Now, you did mention earlier in your testimony that sometimes you could have in the lane a homozygous, which would be from what I understand your testimony to be is that you'd have a band from the mother and a band from the father but they'd be in the same length, therefore, on the same location, one on top of the other and it would appear as one band.

A. Correct.

Q. So how do you actually, if you had a one band instead of a one band pattern as we were referring in VD-45, what would the calculation be according to Hardy-Weinberg or the Hardy-Weinberg equation if you had a one band pattern?

A. You'd square the frequency of it, it would be that frequency times itself. So the frequency of that band is one in a hundred, it would be one in a hundred times one in a hundred.

Q. And that forms part of the Hardy-Weinberg equation as well?

A. If the equation is P squared, plus Q squared plus 2PQ equals one, with P and Q being the frequencies of different bands.

Q. So, doctor, do you have a simplistic way, I know you do, do you have a simplistic way of actually expressing Hardy-Weinberg?

A. I have a way of explaining what it's designed and intended to do is if I know this fragment occurs in X number of individuals in the population, this fragment occurs in Y proportion of individuals in the population, I can apply

this formula and determine Z proportion of individuals that will have both of these. That's a simple formula that's used throughout genetics.

Q. Is the use of the Hardy-Weinberg equation, do you have an opinion as its acceptability in the scientific community?

A. If applied properly, like all these techniques if applied properly, it's accepted and reliable.

Q. What does the term genotype scoring refer to or mean?

A. Genotype scoring is essentially what we've done here. We're taking a visual -- an x-ray, which actually is what is called a phenotype, it's an outward, the outward appearance of something, it's due to a genetic difference which would be the genotype. In genotyping, you look at the bands and you make your judgments and you just -- it's based on what you know about the system. You'll say that this is -- this represents one allele either maternal or paternal and this represents the other of them, that's genotype scoring, you've scored this as a heterozygous.

Q. Now, doctor, once we've actually determined the individual frequences of the alleles or the bands by your binning method and after we've actually determined the frequencies of individual band patterns using the Hardy-Weinberg equation, what is the next step that the scientist will do in arriving at an overall frequency?

A. Well, again if this was a Chromosome 1 probe and we strip the membrane or repeated it with a Chromosome 2 probe, and obtain a match again and went through all these simple mathematical calculations and determined its frequency, the probability of matching at both the Chromosome 1 and the Chromosome 2 probe is simply the product of those two frequencies that I derive.

Q. That's what you've discussed before the break I believe.

A. Correct.

Q. The product rule.

A. The product rule.

Q. So that would be, to reiterate to make sure I'm clear, that would -- what you're saying is that if you know the individual band frequency of one probe to be one in a hundred as my example earlier this morning was, and if we do it again and you'd see another set of bands that match and you know that with that probe using the Hardy-Weinberg equation and the binning method, that you'd have a particular frequency that comes out to one in a hundred, the pattern of those bands being one in a hundred, you would multiply them together using the product rule?

A. One in one hundred times one in one hundred, which would give you one in ten thousand a likelihood of finding somebody that matches at both the Chromosome 1 and the Chromosome 2, that's the frequency in a population that you could predict.

Q. That's the final -- the product rule is the final the-- how should I put, the total derived from the product rule is the figure that's given by the scientist as the probability?

A. If I have analyzed four of these regions that would be the number that I would affix to the overall profile, probe 1, probe 2, probe 3 and probe 4.

Q. And again, is this particular type of procedure of multiplying one band pattern by another band pattern by another band pattern, do you have an opinion as to its acceptability in the scientific community?

A. Again, if applied properly it's scientifically accepted.

Q. And as to its reasonable reliability?

A. If applied properly very reliable.

Q. If I may just make sure we don't have left anyone with, particularly the judge or the Court with any confusion, without being too redundant or leading, I just want to clarify, doctor, correct me if I'm wrong, you're determining each band, the way you determine each band pattern, an individual band is using the binning method, correct?

A. To determine the frequency of a given band, you use the binning method, yes.

Q. But if I want to determine the frequency of a band pattern as in this particular case, two bands that you would see in a lane, if I want to know what the frequency of seeing that in that location?

A. You utilize the numbers that you obtain from the binning method and you subject those frequencies you use them -- you apply them to the Hardy-Weinberg formula and that will give you the frequency and you will see both of them.

Q. Of that particular pattern?

A. Correct.

Q. And if that pattern was one in a hundred, if you'd determined that to be one in a hundred, and at another probing, you determined another pattern to be one in a hundred?

A. Another independent locus, then you -- if the tests indeed are independent, you simply multiply those probabilities, one in a hundred times one in a hundred.

Q. And that's the -- the end product is the figure that is given by the scientist?

A. To all of the loci analyzed, yes.

Q. Does the product rule in forensics is it actually applied or used only for DNA typing, was it developed just for that or adapted just for that or do you know of any other forensic field that it's used in?

A. Apart from binning, the manipulations or the strategy, there is nothing particular to DNA typing. Throughout genetics people have determined frequencies of genes and frequencies of combination of genes, genotypes and done statistics that way. In forensics, conventional serology you generally analyze a number of independent blood grouping systems and derive

frequencies, say, for the A B O systems, if somebody is an A type, you derive the frequency for that. If you go to another enzyme system, say, S^D and you've determined what type, what polymorphism at that locus, it's a protein polymorphism but nevertheless it's a genetic system and you determine its frequency, you multiply them together, those are independent tests.

Q. So that's done forensically, and as you say for serology?

A. It's been used for years.

Q. Doctor, I am going to show you a paper, you can have a seat, I'll ask you if you could please describe this particular paper and what, if any, relevance it has to the discussion that we've been -- your testimony up to this point in time?

A. This is a text that I prepared after attending a meeting in -- the end of 1989 in Madison, Wisconsin.

Q. Is there a common name for that meeting?

A. Yes, It's the International Symposium on Human Identification and in particular, the meeting subtitle is Data Acquisition and Statistical Analysis for DNA Laboratories.

Q. I understand it has another name, the Promega Paper?

A. Promega, the company sponsoring the symposium and played a big role in organizing all the contributors and actually publishing the proceedings is a company that's involved in molecular biology, and they sponsored the meeting we call the Promega meeting.

Q. Would you describe what the -- what that -- could you give me an overview of that paper, please, could you give the Court an overview of what your intentions were behind writing that paper and what it describes?

A. The intentions of the paper were to describe the system in use at the R.C.M.P. at that time to the rest of the scientific community and the legal community. It was a way to take the system from beginning to end, describe it both conceptionally and practically how you'd do it. and get that information out in a very quick way over a short period of time, rather than waiting a year and a half for it to come out in a journal. These proceedings were published quickly. So it's a nice way to get the information to interested parties in a short period of time.

Q. Doctor, in this particular paper, in relation to the testimony you've had this morning, this binning, et cetera, is there any reference in there to that particular method and how the R.C.M.P. were applying it at that time?

A. Yes, the binning procedure is described in this, yes.

Q. If I could have that document for a second, doctor, please.

MR. WALSH: My lord, if I may with the Court's permission, I would like to have this document entered at the hearing.

THE COURT: VD-50.

Just before you leave binning --

MR. WALSH: I wasn't going to leave it, my lord.

THE COURT: You weren't going to leave it?

MR. WALSH: No.

THE COURT: This may emerge in your further questioning, I think you indicated, doctor, that you and another have devised this binning method, I mean, did it originate with you?

WITNESS: The concept actually came from another lab, a non-forensic lab, that was where I first saw the concept. But the concept of grouping similar events, I'm sure you could go back through different disciplines and find it's original source, it certainly wasn't in forensics.

THE COURT: But is this rather universally used by the FBI, in Europe and so on?

WITNESS: In North America it's used and versions of it in Europe are used. Again, the Europeans develop their systems prior and independent of the labs in North America, so there are differences. But conceptually all of the labs using these types of loci group fragments into some sort of bins. The boundaries change and things like that but conceptually they do the same thing.

THE COURT: But when you deliver a paper to an international symposium on it, are you merely telling them what they're all doing or are you showing them that you're using a procedure that is technically superior to theirs to what may be employed elsewhere?

WITNESS: At that point both the FBI and the R.C.M.P. labs were using binning methods and our methods were devised mutually, so they'd be compatible with each other, we use the same bin boundaries. We can compare data back and forth, we can compare data bases. At that meeting a lot of the labs that were developing and trying to pick a way to analyze their data looked at what we were presenting and they subsequently adopted that method. So they could be compatible with the federal labs in North America, like State labs in the United States, for example, they would look at our presentation and say, well, there's no reason for them to adopt the system used in Britain, it would be much more logical to adopt the sytem used throughout North America.

Q. Perhaps, at this point, we could clarify something, we've been talking about the use of single locus probes as you've described that yesterday, am I right, doctor?

A. Yes.

Q. Can the binning method be used with the multi locus probe that you described yesterday?

A. Not that I'm aware of. In that particular system where you generate a complex pattern of thirty to fifty bands, you actually don't even size the bands, what you are looking at are the positions of the bands in that complex pattern and it really is a visual assessment.

Q. You get your numbers right in what you're looking at?

A. Correct, if the fifty bands line up visually you're left with something like an actual latent fingerprint, it's a very complex pattern and they match visually.

Q. So it's not necessary to go out and try to find out the number of actual, the frequency of each individual band that you saw in that print?

A. No.

Q. But because you only have in the single locus probing, correct me if I'm wrong, one band per lane or two bands per lane, it's necessary to go out and do this particular type of procedure?

A. Yes.

Q. And in England there is still multilocus probing going on there?

A. I believe so.

Q. Perhaps if you would give his lordship that last document. I have a duplicate here of the document, I am going to ask the doctor just to refer to. My lord, if you would turn to page 149 at the back and again, it's for the purpose of -- the numbering is at the bottom of each page, my lord.

Doctor, for the purpose of kind of hopefully cementing what we've discussed to date, I am going to ask you to look at Table 3, 4 and 5 of that paper, Promega paper, I'll call it the Promega people. Could you please just give

us an overview, give his lordship an overview of what those tables represent and how they connected with what you've been -- the evidence you've been giving to date?

A. Table 3 defines the bin boundaries that in 1989 were employed by the FBI and by the R.C.M.P. labs. And I guess the points to notice are other than the boundary that includes very small fragments, the top boundary and the bin that includes very large fragments, I've noted here Bin 31, all the other bins have the same boundaries and there are some minor technial reasons why. We collapsed Bins 1 through 5 used at the FBI and just called it a single bin, everything from zero to a thousand seventy seven. And they had five bins encompassing that boundary. So there's some minor technical reasons, but virtually all the other bins have the exact same boundaries. So we have a system that is compatible. If I know the frequency of a fragment that falls in Bin 11, for example, at the R.C.M.P., that same bin is characterized in the FBI's data base and I can ask them, well, what's your frequency in Bin 11.

Q. Continue, doctor, tables 3, 4 and 5, if you could just -- I just want you to more or less summarize what we've done to date?

A. Table 4 summarizes all of the probes, all of the variable probes that were in used at the R.C.M.P. lab and the FBI lab for that matter, again in 1989. The locus, D1S7, the locus on D2, on

Chromosome 2, 4, 16 and 17, those were the five probes or loci that we were looking at that particular time. This table just lists some of the characteristics, it tells you which chromosome they're on, it tells you the number of individuals at that time that I had analyzed to derive the frequencies. It tells you the number of bins that we observed events in. For example on D17S79, out of analyzing 468 individuals, so that would be 936 fragments, you have two in each individual, only 11 of the possible 27 bins we observed events in. Other probes that have much more size varabilities, say, the Chromosome 1, D1S7, all of the bins had some observed events. So some probes are more variable than others, that's all that tells you.

Q. And in Table 5?

A. Table 5 is the actual data, the frequencies.

Q. The data derived from what?

A. From analyzing those individuals.

Q. From the binning?

A. From the binning, and this is the raw data, this is data that hasn't been corrected for rare events. So in this data there'll be, for example, for D2S44, the second column with numbers, for Bin 24, I get a frequency of .001, that's based on a single observation looking at 1130 bands, I saw it once.

Q. You hadn't collapsed that bin in accordance with what you discussed before?

A. No, what I wanted to present at this meeting was the raw data. So people could actually look at how many events I observed in each of these bins in these number of people. And actually at that time we hadn't addressed exactly how we were going to collapse the bins to correct for these very rare events.

Q. Doctor, if you could perhaps give his lordship some indication who would actually be at that type of -- that meeting there, that Promega meeting, just people who you actually would be presenting this data to?

A. Scientists from virtually all over the world who are doing DNA typing for forensics. There is also a number of scientists from the academic community who had an interest in how this technology was being applied. There were a number of prosecutors from various regions of the world and a number of defence lawyers who were either doing DNA cases or had been doing DNA cases, and people actually presenting work fell into those categories as well. There was defence lawyers, prosecutors gave talks, scientists both academic and forensic.

Q. And that particular paper that we're looking at now, has that been published, you indicated, I believe, it has been published?

A. Yes, the proceedings of that meeting were published.

Q. And that would be -- I take it, then this would be one chapter of those proceedings, so to speak?

A. Yes.

Q. We have dealt with Tables 3, 4 and 5, have we not?

A. Yes.

Q. Again, I just wanted to do it for the purposes of an overview as to what bins look like. Doctor, you mentioned that that was the raw data, is there such a thing as rebinning, okay, I have bins, is there such a thing as actually rebinnings, doing it over again, something of that particular nature?

A. Yes, anytime you're starting data changes or your raw data changes there's a need to go back to the computer and tell the computer to resort that data and do its bins. This is all done by computers.

Q. You mean, if I have more samples, for example?

A. If I added more samples to my data base, if I increased it, say, from five hundred to six hundred. Well, I'd have to go to the computer and say, take into account the last hundred people I had and put those into bins and see how the frequencies change or don't change.

Q. And what, for example, doctor, you've mentioned in this Tables 3 or 4, you were referring to certain particular probes that were being used at that time, having any probes -- I believe yesterday you mentioned there was the addition of D10?

A. D10 has twenty eight, yes, that's a locus that has been added to the system. It wasn't being used at that time, so naturally it's not included in that publication.

Q. So you would have the bin for that particular probe as well?

A. You'd have to go through the task of building the data base, sizing the fragments, putting it into bins and generating those tables.

Q. And the use of the match window, how is that applied to the binning?

A. It's not.

Q. Doctor, very briefly, doctor, you had indicated that and I expect this will be coming from another source but you had indicated that if applied correctly, when you were talking about the determination of individual band frequencies, when we were talking about determination of band patterns, the frequencies of two bands using the Hardy-Weinberg equation and we were talking about the use of the product rule and each time you would preface your remark by saying, if applied correctly. Now, again, doctor, very briefly at this point, I would like you just to tell me, what you mean by, if applied correctly, what factors are taken into consideration by population geneticists in determining whether or not individual band frequencies, band pattern frequencies and the overall patterns derived from the product rule were accurate or rare or they demonstrate a significant event?

A. The biggest concern, the biggest concern, you can break it down into a number of different areas and they're all given, there's a lot of jargon associated with what they call these

various factors, but the biggest factor and the critical factor in all of this, is your data base population, your population sample homozygous, is the population comprised of people who are randomly interbreeding? What you want to avoid is a situation where you have sectors of your data base that are distinct, and don't freely interbreed.

If I could give an example, if you took--if you took black individuals, white individuals and treated them as one population. If the frequency of a given band was very rare in the blacks, very common in the whites and you treated that as one population, you'd derive frequencies that don't apply to either of those racial groups. So that would be an improper application of both the Hardy-Weinberg formula and the product rule. That's call sub populations and I believe we talked about that yesterday.

Q. Is there things that population geneticists do to actually determine whether or not there is subgrouping and the effect its having on the frequency calculations, is there general things that are being done, that have been done and are being done by population geneticists?

A. There's empirical things that you can do, yes.

Q. Empirically, meaning you actually look at data?

A. Correct?

Q. From other areas?

A. Yes.

Q. And what other things are done?

A. There's statistical tests and again, these are based on empirical observations. What you actually do is, if you've analyzed five hundred people, you can actually look at those five hundred individuals and say, how -- and now, we're not talking about frequencies of individual bands, how often have I observed individuals in that five hundred person population sample, how often have I observed individuals that have both of those bands that were in the question sample. And you'll come up with an observation, a certain number of individuals in your population sample may have that exact pattern, that exact two band pattern. Now, you've already derived a prediction using Hardy-Weinberg equation, right. You can now compare your observed events to your predicted events and there's statistical tests that you can run when you have all of your observed events. So you've taken all the combinations that you've seen in that population sample, and then you've derived the frequencies and you've come up with numbers of how often you'd predict.

Now, if I'm doing -- I'll give you an absurd example here, if I go to my population sample and I ask how many individuals in those five hundreds I've tested have this pattern? And I say, a hundred people from data base happen to have that pattern, a real common pattern. And I go back to my statistical test, and my statistical test said out of my five hundred I

only saw one with that pattern. We've got a problem, something has been misapplied, there's a problem with your data base. You're coming up with predictions that say, this occurs one in five hundred, when in fact your observed events is one in five. You've got a hundred fold bias against the accused in this particular case.

Q. Do you know of anyone with the R.C.M.P. laboratory that is actually doing statistically with respect to their data bases?

A. Again all of the data bases when it's compiled, the computer is capable of querying those data bases and compiling how many people have each observed two or one band pattern and again, the computers can generate the predicted values as well. We have experts in statistics in population genetics that then take that data and do the appropriate statistical test to say, the differences that we see between observed and predicted frequencies are those statistically significant? If my observed frequency is say, one in a hundred and my predicted is one in ninety five. Are those statistically different?

Q. And do you know anybody in particular who is actually doing this work that would be relevant to this particular matter here, this case?

A. Again, I mentioned the gentleman earlier this morning, it's Dr. George Carmody is doing a lot of that work for the R.C.M.P. He's a faculty member at the University of Ottawa. And there's statisticians in the United States as well that

are handling the FBI's data as well, I believe, as some of the R.C.M.P. data.

Q. Now, these are statistical works but I take it that population geneticists look at data from other parts of, not only Canada but of other parts of North America and other parts of the world as well, do they?

A. Yes.

Q. To look at the frequencies that are being generated for other racial groups?

A. Yes.

Q. So they would look, for example, doctor, you would look at Caucasians in Canada and different Caucasian groups within the country if I wanted to empirically look at their frequency data, is that correct?

A. Different investigators doing this?

Q. No, if, for example, when you talk about empirically, I just want to clarify what empirically means, empircally if I wanted to look at-- empirically would mean, looking at, for example, you described Vancouver, Kingston?

A. An empirical observation is just a direct observation, there's no statistics involved. If I had a bucket with a hundred marbles in it and one of them is white, if I dump them out on the floor and count the one white one, that's an empirical observation, one in a hundred there is white.

Q. Thank you, that's what I wanted to clarify.

Q. The paper that was previously marked on this hearing was the last number?

THE COURT: VD-50.

Q. V-50, I would refer your lordship to page 29 of that paper, it states in that paper, doctor, that, a conservative statistically approach was developed to compensate for the possibilities of sampling error and differences in racial subgroups, limited sample population size and limitations in agarose submarine gel electrophoresis and Southern blotting technology. When they say, a conservative statistical approach, what are they referring to?

A. The binning method and all the manipulations that you do with those frequencies afterwards.

Q. Would you tell me, please, what they meant by a conservative statistical approach to compensate and they've mentioned a number of things, sampling error, what do they mean by that?

A. A sampling error, if you've sampled -- if your sample is not a truly random selection from the population, say, you did bias it more towards a particular family, perhaps analyzed an individual twice instead of just once or analyzed two brothers in your data base, that would be a sampling error.

Q. Okay. And do you agree with that statement, obviously you're an author of that particular -- do you agree with that particular statement that it's a conservative statistical approach that was developed to compensate for the possibilities of sampling error?

A. Yes, again, if you had extreme sampling error, like you analyzed the same person many times over and that was erroneously put in your data base, these types of manipulations really wouldn't compensate for that type of thing. But minor sampling error, yes, minor measurement imprecision, minor frequency differences within a subgroups, all of these things are compensated by using an overly conservative binning method and an overly conversative statistical approach.

Q. And is the size of the R.C.M.P. data base, is that an appropriate size for the work that's being done?

A. It's viewed as a large data base by people, both in the field and out of the field of forensics.

Q. And what do they mean by limitations in agarose submarine gel electrophoresis and Southern blotting technology?

A. That again is our ability to analyze DNA or inability to analyze DNA and come up with the exact base pair size of these fragments. So that's the limitation of agarose gel electrophoresis, Southern blotting, when I analyze the same DNA ten times I'll probably get ten different size estimates.

Q. A limitation of the technology itself?

A. It's a technical limitation.

Q. Doctor, could I have your opinion, please, as to the scientific acceptability of the Caucasian data base employed by the R.C.M.P. and the

method of pattern frequency calculations made by the R.C.M.P. from that data base for forensic purposes?

A. In my opinion it's acceptable for forensic applications to ask these types of questions, how common or how rare are these patterns in the population.

Q. And scientifically acceptable in the scientific community?

A. To answer those questions, yes. To answer other questions you wouldn't view it as acceptable, if you wanted to know exactly how many people you had to look at to find that pattern, is it one million, is it one million one hundred and one. If you wanted to know the exact number of individuals, the exact frequency it wouldn't be relied on as an accurate or a reliable method. If you wanted to know whether it was one in a hundred or one in a million --

Q. If you wanted to know whether or not it's a rare or common occurrence?

A. The system is designed to provide information as to whether something is common or rare and how common or how rare, not precisely the exact frequency in a given population that something will occur.

Q. Is that recognized and understood in the scientific community?

A. For that use, I don't think too many people would dispute its acceptability and reliability, no.

Q. Doctor, do you have an opinion as to what, if any, bias would be found in the probability figures generated in forensic cases by the R.C.M.P. lab?

A. At every step in this procedure there's an element of bending over backwards to overestimate the frequency of an event.

Q. In whose favour would that be?

A. That would be in the favour of the -- in the favour of whoever is being linked to the evidence match whoever was included in that match. And when you walk through the entire procedure and you come up with your end result, what you've in fact done is compiled a lot of bias or a lot of conservativeness and at the end of this, the system is designed that you're probably citing a number that is not accurate and it's not accurate in the sense that you really have overestimated the frequency of that overall profile. You've been overly conservative at every stage and the end result is --

Q. Meaning that if -- if a lab was to quote a figure of one in a million, where would -- you say that figure is a high or low number?

A. In my opinion the way the system is designed and the way the system is applied, if I had to know the exact frequency of that profile in the population, I would say it would be rare, the actual frequency.

Q. Higher than one in a million, in the sample I've given you?

A. The denominator would be higher, it would be a rarer event and actually that's a lower number.

Q. Is there anything, doctor, I am going to leave that particular area, is there anything that you feel that you would like to clarify or add to it that perhaps I'm not covering.

A. Not at this point.

Q. Doctor, perhaps we could go into another field, I'm interested, doctor, in informing the Court as to what efforts and we've covered it generally but what efforts, what scientifically acceptable methods are there for having a particular system, such as, the R.C.M.P. RFLP typing system and data base held out to general scientific scrutiny, what is acceptable? What kind of methods are used to actually say, here is what I have, I want to show you, tell me, I want to hear your criticisms, I want to hear your comments, what ways in the scientific community is that done?

A. Again, like any piece of science or any opinion you have to present your opinion or your data to people who are in a position to judge it, judge its merits both pro and con. That's generally done by peer review. You present your ideas or your work at a meeting attended by people who are knowledgeable in the area. You attempt to publish your findings or your ideas in journals that are read, widely read by people who are interested in this area. Again, they can form their own criticisms and write rebuttals, they can in turn take your data and do with it what they please after you've published it and write a paper countering your ideas, actually take your data

and publish it in another form, if they want to.

Q. Apart from peer review, doctor, are there any other scientifically aceptable methods of disseminating information about a system?

A. Like anything else you can mail it to all interested parties or anyone who requests it.

Q. What about these symposiums and abstracts and organizations and meetings and conferences that you've described, that are described in your C.V., what, if anything, does that do in relation to this?

A. Again, those are public forms for exchanging ideas and public in the sense that the scientific community attends those and anyone who wants to know the current status of a science really doesn't go to a journal, because a journal takes a number of months, sometimes years to publish material. You go to a meeting, you find out what happened yesterday in an area of interest.

Q. Could you tell me, doctor, what, if any things you did or you participated in to hold out the R.C.M.P. DNA forensic system to general scientific scrutiny, could you give us examples of what you actually did to do that?

A. Well, myself and other people at the R.C.M.P. and and the FBI, since we are dealing with comparable systems, the FBI and the R.C.M.P. we travelled extensively during the development of this system attending scientific meetings both in Canada, the United States and Europe, describing these systems, meeting with other scientists, an

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enormous exchange of ideas at these meetings. There were meetings, such as, the meeting in Madison, Wisconsin, the Promega Meeting, where we actually, not only gave the talk, but prepared a manuscript to go with the talk. That was published in a rapid manner. That's a method of getting all of your ideas and your raw data to interested people.

Q. And these abstracts and posters, would they be related to actually dissemination of information related to this system, the R.C.M.P. system?

A. Yes, you take all of your population tables, et cetera, mount them on a board such as that and during the course of an afternoon several hundred people will come by, if they are interested they will sit and chat with you and ask you questions, exchange ideas with you.

Q. Have you -- you have indicated that you don't mind, earlier, yesterday you mentioned that you had talked to defence lawyers and experts who had been called by the defence, do you have any inhibitions about doing that, talking about the system, discussing it?

A. If it's my data, I have absolutely no problem talking to people about it. There's a scientific courtesy, courtesy amongst scientists that you don't take someone else's data without their permission and disseminate it or publish it yourself, et cetera.

Q. Use it for purposes other than for what it was given?

A. Yes, matters like that, if I obtained scientific data through a third party, it wouldn't be correct for me to present it at a meeting or write a paper on it myself, not without contacting the actual author and exchanging some views with him. It's just not scientific courtesy.

Q. Doctor, I'm trying to give the Court information in relation to how the R.C.M.P. system, how much information has been disseminated about that, I don't want to ask an unfair question but I am going to show you your C.V. which was the item, probably the second item that we've introduced yesterday, VD-25. I have a duplicate of VD-25 here and under the heading of Publications: Peer Reviewed Journal Articles, now yesterday I asked you questions about whether they were related to DNA and whether they were related to human DNA, the subject matter. Could I ask you now, doctor, if you would look and tell me how much or what percentage of those articles would be related in some way to the R.C.M.P. system or the technique used in the R.C.M.P. system?

A. The precise system described in those protocols, not just RFLP technology?

Q. Not only in the protocols but the RFLP technology as applied by the R.C.M.P. or adapted by the R.C.M.P.?

A. The RFLP technology itself as applied by molecular biologists, in general the majority of these thirty articles would employ that type of

technique to generate data. The specifics of the exact procedure used forensically at the R.C.M.P., a number of the papers from that time frame when I worked for the R.C.M.P. deal specifically with that method.

Q. For example, the Hae III paper that we've introduced into evidence, the ethidium bromide paper, things of that nature?

A. Yes, just scanning it, I'd say, maybe five or six of these papers deal specifically with that method, that's about the accurate number, five or six.

Q. And your abstracts, your publications, your book chapters, your symposium proceedings?

A. Again, of short reports, letters and peer reviewed journals, two of the four deal directly with RFLP issues, forensically, book chapters, four of the five deal with that specific area, RFLP as applied forensically. And abstracts, published abstracts there's again three or four of these are forensic abstracts. There's many more abstracts that weren't published, meetings attended that they don't publish the abstracts. Of the ones that are published, there's a few here that apply to that, specifically to that.

Q. These workshops and symposiums and meetings that you attend, did that involve discussions of the R.C.M.P. system, forensic system?

A. Yes, the workshops and the meetings that are entitled Forensic DNA are something similar to that, those all involved both formal and informal discussions of the methods and the theories and the applications.

Q. And the people involved, you had mentioned scientists in the field and actually doing forensic work and you indicated they were people from outside the forensic field that would be interested and attend these symposiums, workshops and meetings?

A. Yes, it's been the habit of forensic labs adapting DNA technology to have reference people. That's generally people outside of forensics who are involved in molecular biology. And generally the first thing you do when you're setting up a lab is you look locally towards people who are very familiar with these techniques and you collaborate with them, you exchange ideas with them on a regular basis, they help you out getting things going. A lot of those people attend those meetings.

Q. In relation to non-scientists, in these meetings and symposiums and workshops, et cetera, would you expect to see or have you seen non-scientists at those meetings?

A. Again, people dealing specifically with the court applications of this technology, both prosecutors and defence lawyers, legislators, people deciding how laws are going to be formulated to deal with this technology, they attend these meetings.

Q. Is there anything more in this regard, doctor, that you wish to add or clarify for the Court?

A. Not at this point, no.

THE COURT: Mr. Justice Flannagan says about you that Dr. Waye also in his evidence stated that the media have written and spoken more on the results of DNA testing than any scientist in North America. And then he adds, he also goes on to add, without any general benefit to anyone.

Is that a fair statement?

WITNESS: Yes.

Q. What did you mean by that statement, doctor?

A. Rather than specific studies or when you ask a scientific question, you design an experiment to answer tht question and you conduct the experiment and you analyze the results and you come to a conclusion. That's the scientific method and that's the sort of things scientists do and publish. That would be -- and there's a limited number of publications pertaining to forensic DNA typing that are done in that manner. There's many, many more publications that are either media people interviewing people and either quoting or misquoting their views on it and there's many, many more commentaries from people who either have an interest for or against the technology. And a lot of times there are published in peer reviewed journals as fact when in fact they're rolling commentaries either for or against DNA typing. And there's been exaggerations both ways. DNA typing has been started up on a pedestral doing much more than it is ever capable of doing and it slid down as far as being incapable of doing nothing properly.

And all this is represented in the popular press.

THE COURT: Would you say the same thing about lawyers and judges in the judgments in DNA cases? You don't have to answer that.

WITNESS: No, some of the best accounts, some of the best descriptions I've ever had of the whole procedure have come from judge's ruling at the end of long hearings.

THE COURT: No, but they hardly amount to peer reviews?

WITNESS: No, but they're understandable and they have a way of getting away from all the complex scientific jargon and putting it into simple terms and they're actually a nice place to start.

THE COURT: Well, do you want to --

MR. WALSH: In fact, I believe I could finish his direct examination in about a minute, my lord.

THE COURT: Oh, okay, sure.

MR. WALSH: At least this part of it, I'm going to be asking he be stood aside.

Q. Doctor, have you any involvement with respect to the matter of The Queen vs. Allan Joseph Legere?

A. Direct testing involvement?

Q. No, have you had any occasion to review any tests in relation to this case?

A. I've reviewed the test results, yes.

Q. Prepared by whom?

A. Dr. John Bowen.

Q. Have you also reviewed the statistical and the probability figures generated by Dr. Bowen?

A. Yes.

Q. And are you prepared to testify in relation to those test results and the figures obtained?

A. Yes.

MR. WALSH: My lord, at this time I would request permission to stand Dr. Waye aside, subject of course to cross examination until after, until later next week, hopefully next week until after Dr. Bowen has testified.

THE COURT: Well, you have no objection, Mr. Furlotte, 1'll be asking you in a minute if you want to cross examine on this portion of the evidence now or do you want to leave it until all of Dr. Waye's evidence has been completed. But in so far as the standing aside itself goes, do you have a comment on that?

MR. FURLOTTE: I have no problems with standing him aside.

THE COURT: What do you want to do? Do you want to go on, we'll recess now for lunch, but do you want to cross examine him on this portion of it after lunch?

MR. FURLOTTE: I wish to cross examine him on this portion now.

THE COURT: You see no problem with that, Mr. Walsh?

MR. WALSH: No, in fact, I think it's probably a wise decision on Mr. Furlotte's part.

MR. FURLOTTE: Most of this will be gone from my mind next week, so I better do it now.

THE COURT: Well, you're luckier than 1 am, it hasn't gone a lot of it now even. We'll recess until two o'clock, two o'clock then.

COURT RECESSES FOR LUNCH AT 12:45 P.M.

COURT RESUMES AT 2:00 P.M.

ALL COUNSEL PRESENT

ACCUSED PRESENT

MR. WALSH: My lord, if I may make a suggestion before Mr. Furlotte commences his cross examination, we have a number of -- the intention was to number the charts that have already been displayed to correspond with the items that have been entered at the voir dire. As well, we have a number of charts on the easels that we haven't turned around, some of those charts -- all of the charts correspond with some of the items that have been entered on this voir dire. It may facilitate future reference without the necessity of turning on the slide projector. They duplicate a number of the things on the slide projector, particularly, in cross examination, it's an aid. If I may be permitted to turn them over and we could have them marked to correspond with the -- what's entered at the hearing.

THE COURT: Have you marked those up yet, I can't see them?

MR. WALSH: These haven't been marked yet, no.

THE COURT: Those are VD-30 and VD-40 and VD-45, left to right. I think that next one is VD-29 if I'm not mistaken, the DNA molecule, is it?

MR. WALSH: There's two DNA Molecules --

THE COURT: One with probe attached.

MR. WALSH: With a Probe which is over there and this one without.

THE COURT: That's VD-28, I think, that one and that's 29, am I right? Yes. VD-29 is that other one marked, DNA Molecule.

MR. WALSH: My lord, for the record, what we have displayed as charts that correspond with the items that have been entered at the voir dire as VD-26, 27, 28, 29, 30, 40 and 45.

THE COURT: Correct.

MR. WALSH: Thank you, my lord.

THE COURT: Are you -- you had finished?

MR. WALSH: I had finished and asked that Dr. Waye be stood aside.

THE COURT: I'm sorry, I was waiting for you to continue. Mr. Furlotte your turn here.

DR. JOHN WAYE, still under oath, continued to testify:

CROSS EXAMINATION BY MR. FURLOTTE:

Q. Well, Dr. Waye, there's probably a couple of dozen ways to jump into cross examination here and I'm trying to figure out which is the best one but I thought for maybe organization purposes I would jump into what I learned about case law - what I learned about DNA evidence reading the case law. That's where I began in my little understanding of it. Maybe I can just go through some of the things I read about it in case law and see where either myself or the judges have misunderstood the propositions being put forward by expert witnesses in this field.

Now, in the Andrews case the judge found that usually a process of verification, a second test would be appropriate but it usually is never used. For what purpose would that be?

A. To repeat a test?

Q. To repeat a test?

A. Any time you repeat a test and you get the same answer it verifies the first result.

Q. So you should get the same answer when you repeat a test?

A. If the test is done the same way both times you should get the same answer, yes.

Q. If it's done the same way both times. So if a test is done by the same individual, the same scientist, he should be doing it the same way both times?

A. Yes.

Q. And that would generate what we call reproducibility and if the same results are reproducible and then it would be reliable, is that generally accepted?

A. That's a true statement, yes.

Q. A true statement, and if it wasn't reproducible it wouldn't be reliable?

A. If you couldn't demonstrate that the technique applied properly gives the correct answer, you could come to that conclusion, yes.

Q. It would be more appropriate too if the second test could begin right from scratch, such as the breaking down of the DNA from the stained material?

A. If the question you wanted to ask initially is, can this technique if applied properly give the same answer twice, you repeat the experiment from beginning to end, if that's the question you wanted to ask.

Q. That's the question. Or if there's enough evidence that you could conduct two different gel tests, it would be appropriate to run two separate gels at the same time, maybe save some of the sample for -- to be performed by another scientist?

A. It's possible if you have unlimited samples surely you're going to save some of the material, you're only going to use a portion of your material, it certainly isn't necessary to do the test in duplicate or to repeat the test once after the other.

Q. You say, it's not necessary.

A. No, that's a separate issue.

Q. If you had enough material, say, two separate tests, would you just use the bare minimum in the first test or would you, say, if you had enough for two tests that you would run it all in the first test?

A. The amount of material that you run is within limits, there's an upper and a lower limit, you have a lower limit of detection, you have to run a certain amount of material to be able to do the test. And there's an upper limit as well, you can't load unlimited amounts of DNA on the gel, it's limited both by the amount of DNA that

can be analyzed in a well of a certain size and the volume of the solution. So there's just parameters that have nothing to do with reproducibility that would determine that.

Q. Could you tell me what those limits are?

A. They vary with the particular gel system you are using. Obviously if you had a gel that had wells or depressions that hold volumes of fluid equivalent to this glass, those are the parameters we're dealing with. If we are dealing with wells that are the size of a thimble, those are the parameters you're dealing with in that situation. relevant to these tests it's smaller than a thimble, you're dealing with small volumes, small amounts.

Q. Okay, the gels, the R.C.M.P. were using at the time of these tests, would it be in your protocol as to what the upper and lower limits were?

A. Yes, you use a standard gel apparatus is one type of well, or a cone to form those wells in the lab, that's used for casework. So those sizes are known, those volumes are known.

Q. Those volumes are known?

A. Yes.

Q. Just for a further explanation, the difference in the testing in forensics and in paternity testing, in genetic type disease testings, the difference is in basically the probe that's being used?

A. In both medical applications, paternity testing and forensics, some of the same probes are used for all of those applications.

Q. What some probes would be used for forensics and paternity testing?

A. Any of the probes that I've discussed today.

Q. What about testing for diseases, you wouldn't use the same probes that they use for forensics, would you?

A. If you were interested in a diseased gene that's located near one of these probes you could. One of the probes that was either discussed today or yesterday on Chromosome 16 happens to be very close to the diseased genes that I study, and yes, we do use that probe in diagnostics.

Q. If you are using a gene probe, do you know the specific sequence of the base pairs?

A. Sometimes you do, sometimes you don't, it depends on the disease. There are diseases where they found probes that are very close to the diseased gene but they haven't found the diseased gene yet.

Q. Now, there's mention in the Andrews case about voltage fluctuations, that if there was voltage fluctuations, problems like that, you wouldn't get any reading at all, not an improper reading, is that still held true?

A. A change of voltage, when you mean fluctuation it would go from thirty volts to forty volts or some other way.

Q. You would still get a reading though after, it wouldn't abort the whole test, would it?

A. If the power went off and for example, I loaded my lanes, turn on the gel, went home and immediately after I closed the door, there was

a power failure, well, the DNA will not have had time to migrate through the gel. And the next morning I'll find that my DNA hasn't migrated and we'll probably have to repeat that test.

Q. Do you have a timer on the system to tell you whether or not the voltage went off?

A. It depends on the lab you're in, some labs have auxiliary power to deal with those sorts of things, some labs don't, it depends on the facility you're in.

Q. What about the R.C.M.P.?

A. I can't recall. I worked there, there's been a major renovation to the lab since I left, I can't recall whether we had auxiliary power there or not.

Q. Could voltage fluctuations account for band shifting?

A. No.

Q. Wouldn't voltage fluctuations cause your lanes to run faster or slower?

A. It would cause all of the lanes to run faster or slower.

Q. Yes, but when you measure band shifting and you measure it in relation to the monomorphic probe.

A. Correct.

Q. Twenty seven hundred and thirty one base pairs.

A. And it would cause it to run slower or faster as well.

Q. It would cause them all to run faster or slower?

A. They'd actually run the correct speed, they'd run the speed which the current dictated.

Q. So when the judge found that -- in the Andrews' case that and I'll quote from page 849, it says: «-- if there were any voltage fluctuations or problem with the solutions ordinarily no result is received as opposed to an erroneous result.» So the judge, I suppose, didn't quite understand the evidence given by the expert witness or the expert witness gave the judge false information?

A. I think he probably took one example and over-generalized a little bit, the word, fluctuation, I think --

Q. It could have been the expert witness that did that?

A. I'd have to read the whole transcript, sir.

Q. Also in the Andrews case, the judge found that several courts have questioned whether a leading proponent of a particular technique could fairly and impartially testify concerning admissions of the technique. That you people possess a built-in bias towards your own system and you can't fairly give opinions. Do you confirm that or would you think that you may be a little bit bias or not bias at all?

A. Scientists -- I don't think that personal bias or financial bias or anything like that enters into the picture. In that particular case used, that was a case done by a company that charges a fee for their service and I believe defence point was that they make money doing this, this is their livelihood, their company's future depends on this stuff being accepted and these are the people who are saying it is acceptable.

Q. You helped developed the system as set up by the R.C.M.P.?

A. Yes.

Q. You worked hard at it?

A. Yes.

Q. And you, I suspect, well paid for it?

A. I was paid.

Q. You were paid, well, we'll leave that, we'll leave that one open. So if there were legitimate criticisms against the system that you set up you might be a little bit hesitant into admitting it, would you not?

A. That's the point of having working meetings, et cetera, the protocol that I initially set up with other people evolved and it evolved through constructive criticism, that's part of science.

Q. But eventhough you would like to keep an open mind as much as you could, unknowingly you may have subconscious, your biases may be in your subconscious, not deliberately closing your mind to all criticims but at least trying to explain them?

A. That's the nature of science though, you can't close your eyes to criticism, you have to deal with them.

Q. No, but you're only human also?

A. Correct.

Q. It would be also in the nature of psychology to defend your position?

A. Yes, you defend your position if you think your position is right and you feel you can back that position, substantiate that position, certainly you back it.

Q. Okay, in your questioning as to the reliability of the system that you've set up, technique, would it be true to say that a very low rate of errors strongly indicates a high degree of reliability?

A. A very low rate --

Q. Operator error, very low rate --

A. The reliability of a system is really a different matter from operator error. The system can be very reliable, that means if it's done properly it will work every time, that to me is reliability. Now, if you put that reliable method in the hands of somebody who is incapable of performing the task, that does not make the technique unreliable, it makes its use in that--

Q. It makes the test unreliable?

A. It makes that particular test unreliable, of course. You've got somebody who is prone to making errors. That's different from the test itself being unreliable, the test procedure.

Q. What about the room for error in a test?

A. In the test itself, not the use of the test?

Q. In the test itself, you would like to keep that at a minimum, would you not?

A. Certainly.

Q. So therefore if you had a very low rate of potential error in the test run, then you would have a high degree of reliability?

A. Yes.

Q. And vice versa, if you had a high degree of room for error, then you would have a very low degree of reliability?

A. Yes, if you demonstrate that if the test is done properly, it will not give the right answer a percentage of the time, that is a reflection of reliability.

Q. Okay, there was evidence given in the Andrews case, too, that the judge stated that the testimony, at page 850, states:
«The testimony reveals that as the data base expands, the probability numbers do not change statistically--» a sample of two to five hundred samples would prove to be adequate. Would you agree with that?

A. Yes, in that context what he's saying, in my recollection of that case. What he's basically saying is if I analyze, I'll take the middle road there, three hundred and fifty people of a particular racial group. If I analyze six hundred people those frequencies aren't going to change significantly.

Q. Okay, I understood from your direct testimony that, whether you were -- your degree of reliability depended on the number of people analyzing the data base, and I asked you, when I was cross examining you yesterday.

A. What was the question you asked me.

Q. That if you had a higher number in your data base, whether you were analyzing five thousand people or five hundred people and the more people you analyzed then the higher degree of accuracy you would have, when I say whether it was one in fifty, you know, for the statistical difference, you said, it depended on the number of your data base?

A. It depended on a lot of things and I think I pointed that out at length yesterday, that it would depend on the number of different forms that you could have -- that you were trying to measure. Obviously if you're looking at two possibilities, say, flipping a coin, it's head or tails, you don't have to flip a coin five hundred times to flip a coin five hundred times to figure out the probability of heads and tails is fifty/fifty. If you did it three times though that would be an insufficient number of times to judge it, because you get two heads once, a tail the other time or the other possibility, and you'd be saying the odds of a tail is two thirds. So in that case, you'd have to analyze more and your number would become more precise and accurate as you analyzed more. You probably do hundreds.

Q. The judge also found that the test was highly technical and incapable of observation and requires the jury to either accept or reject the scientists' conclusions that it can be done if it was done properly and the results reliable. Do you feel that you can properly explain your technique, your system and reliability to a judge or a jury, without them having any prior knowledge?

A. I think it's like a judge or a jury explaining the law to myself. I think if proper time is given to it and you think through the problem of explaining to somebody from a different field, I think it's not a monumental task to convey what you do and how you do it.

Q. Do you believe it would be a legitimate concern for defence lawyers that juries are going to rely strictly on conclusion and won't be able to comprehend the facts upon which you base that conclusion?

A. Which is why when we have a jury, I think we go to -- I think, unprecedented lengths to explain exactly how the procedure is done. I know in other fields of forensic science, say, drug analysis, I'm not aware of juries actually knowing how these machines operate. I'm not sure a chemist could explain to me how they operate, they're very, very complex compared to this type of technology. But we do go through the process with them, we try to.

Q. But you know how much education it took you for you to understand this technique or process, and the theoretical aspects behind it, do you really think you could teach a jury within two days what it's all about.

A. I could teach them how to do it in two days.

Q. You could teach them how to do it in two days?

A. If they wanted to stay up late, a week if they worked a normal day.

Q. And they'd have no problem understanding it?

A. If they listened to me and they followed what I was doing they'd generate wonderful results, I've done it, not to jurors but people who have absolutely no experience in the field.

Q. So I probably wasted about four months going through this case law, is that what you're saying?

A. You could have come to the lab and done a hands-on.

Q. I know in the Bourguigon case, you did a preliminary hearing in March of 1990?

A. Yes.

Q. And you did the voir dire in January of 1991?

A. Yes.

Q. Nine to ten months later, I suspect Mr. Barnes in that case wasted his time also.

A. You'd have to speak to Mr. Barnes.

THE COURT: Who is he?

MR. FURLOTTE: He was the defence lawyer.

Q. Now, polymorphisms are described as junk DNA by some scientists, is that correct?

A. I don't think you'd find that definition written anywhere, it's a very poor definition of the word polymorphism.

Q. Okay, in the Wesley case at page 649, the judge said, polymorphisms was «junk DNA» by reason of the fact that their function is not clearly understood. So maybe it's a poor definition. Are the functions of polymorphisms understood?

A. The biology of a polymorphism is understood. The effects of a polymorphism is understood. You have to define what is polymorphic. DNA is not the only thing that's polymorphic. Proteins that DNA make are also polymorphic. The simple blood group antigens that determine your blood type that is a polymorphism. Polymorphism just means a detectable difference.

Q. Well, let's say, the sites that we are dealing with in the probes that you've used for forensic purposes, are those polymorphic sites understandable or do you know the purpose of them?

A. The precise function of those sites in the geno, no, I don't, I don't know what they do.

Q. So because you don't understand them, that doesn't mean, they don't have a purpose?

A. They're part of the chromosomes, which is part of the geno and which definitely does have a purpose and to casually write off pieces of DNA as garbage because you haven't defined a purpose for it is probably not good use of the English language or scientific logic.

Q. It would be reasonable to assume that they do have a purpose but we are just ignorant of it, is that correct?

A. They could have a purpose, it may be an abstract purpose, often times these pieces of DNA that apparently have no present function throughout evolution they may have had a function.

Q. Or a function that you are simply not aware of, maybe particular diseases that we are not aware of yet?

A. Correct.

Q. Diseases which could be common in a lot of people but really haven't shown enough effects for us to recognize them?

A. Well, you can answer those questions with a lot of these pieces of DNA, does it make a protein that could be involved in a disease, those sorts

of things could be answered just by looking at the sequence.

Q. You also mentioned on direct evidence that when the honing device, when the probe goes in as a honing device it hooks on to a fragment, that fragment could represent all of a honing device's sequence or a part of it, is that correct?

A. Yes, if you're trying to detect a ten thousand base pair, ten thousand base pair, just for an example, ten thousand base pair piece of DNA. You could use a hundred base pair probe that represents a part of that ten thousand base pairs to detect the larger fragment. The probe need not be the length or the exact sequence of the target.

Q. Your one hundred base probe, say, of -- I don't know how many bases they have, but say, one of your probes has a hundred bases, that probe has a specific sequence of base pairs, does it not?

A. Correct.

Q. That probe could also hook on to a fragment which does not have the same sequence of the base pairs in your probe, is that correct?

A. It doesn't have to have the exact linear order of the bases from one to a hundred, it doesn't have to be the exact order. It has to very closely resemble it, if you're using high stringency conditions.

Q. Do you know what percentage of exact base pairs it would need before it would hook on?

A. Again, it would depend on the base composition of the probe and the target and the length of the probe. It depends on a lot of variables, there are theoretical and empirical ways to determine termperatures and conditions for a probe to bind to a target.

Q. Have you ever done any studies on this?

A. I don't have to do those studies, those studies were done years and years ago.

Q. So would be the minimum percentage of base pairs that a fragment would need before a probe would latch on to it?

A. Again, it would depend on how you're using the probe.

Q. Explain that, please.

A. The most pertinent example here is that I can take the same probe, use it under one set of conditions and generate two bands. Alec Jeffrey who coined and discovered this multilocus fingerprinting technique, you can use an alternate set of conditions using the same probe and generate a forty or fifty band pattern. The same probe, the same piece of DNA, the same procedure, some technical differences.

Q. So when a probe in VD-45, which Lane B and Lane C appears to be identical, okay, now, if one of your probes hooked on to your top fragment in B lane and your top fragment in C lane, even if you could determine that those fragments were exactly the same length, you don't know whether or not they have the same base sequence, do you?

A. I know that they have a high degree in homology with the probe.

Q. You know what?

A. I know they have a high degree of homology or sequence identity with the probe.

Q. Right. What degree would be necessary for the probe to hook on to one of these fragments?

A. Again, it would depend on how you used the probe.

Q. The way you use the probe at the R.C.M.P., would it differ for different probes or would it be pretty well the same?

A. It would differ for different probes, depending on their base composition.

Q. On the probes that the R.C.M.P. use, which probe would hook on to a base pair with the least amount of base pair sequences there?

A. With the least amount of homology or likeness?

Q. Yes.

A. I can't answer that question.

Q. Why not?

A. I don't have enough information about the probe and the target.

Q. You told me the studies were done long ago before you even got into the forensics about this?

A. The studies are done, if you know this about the probe and you know this about the target, these are the conditions you do to reach this point.

Q. And what do you know about your probes in order to be able to use that knowledge or expertise as to answer my question?

A. I don't have enough, I don't have all the available -- the point is you don't need all the information. What you can do is just simply empirically define the conditions that these probes will identify the homologous locus and then use those conditions for the experiments. And again those are standard conditions that generally don't vary, whether you're talking the Beta globin gene probe, the alpha globin gene probes, probes for around Huntington's disease or these probes, the same sorts of conditions that have been used for years. So you really don't have to know everything about your probe and everything about your target to use that probe.

Q. Maybe the bottom line then would be, although a probe would latch on to the fragments of this length, you haven't got a clue whether half the base pairs are the same or all of the same, is that correct?

A I know most of them are.

Q. Good, now, we're getting somewhere. What do you mean by most, how much, how much is most?

A. Under these conditions if you wanted to nail me for a number, drag a number out of me, it would be a high percentage, closer to a hundred than it is to seventy.

Q. So somewhere between a hundred and seventy percent, maybe eighty five?

A. Maybe ninety five, maybe ninety nine, maybe a hundred.

Q. You mentioned before that your conservative method is always in favour of the accused or suspect?

A. That's the way the system is designed.

Q. Now, I know you're saying maybe ninety, maybe ninety five, maybe a hundred, now, let's go back the other way and be conservative, something in favour of the accused here, could it be maybe eighty five?

A. Not and get the type of detection we see.

Q. You're guessing, aren't you?

A. No, I know from, again from experience. If I were -- somebody synthetized a probe, which had seventy or eighty percent homology to the target sequence found in different individuals and I used these types of conditions, I wouldn't get a very sensitive detection system.

Q. You wouldn't get a very sensitive what?

A. And we have a very sensitve detection system.

Q. And how would that show up on an autorad?

A. It would be harder to detect the bands.

Q. It would be very light bands, in other words?

A. They'd be light bands, yes, they'd be harder to detect.

Q. The bottom line is, very light bands on an autorad might show that the bands are actually binding to fragments which are far from the base sequence of which is attached?

A. That would be a poor interpretation of light bands, poor and --

Q. But it's a possible one?

A. If you want to talk in things that are possible or impossible, you're -- that's you're --

Q. We're talking about giving an accused or the suspect the benefit of the doubts here and we're being conservative in his favour?

A. Speaking as a scientist, if you have to talk in absolutes that's not a good interpretation. If I have to speak in absolutes I'm --

Q. You've admitted that your system is -- we're not dealing with absolutes here, the procedure for DNA recognitions, for identification, we are far from dealing with absolutes?

A. The probe is binding to its target. If you want an absolute statement from me, that's it.

Q. Now, again, in Wesley, the Judge according to his understanding of the evidence, he stated at page 650:

«If the known and unknown biological specimens are from the same person, one can expect to find the probe on fragments of identical length and, consequently, in identical positions on the two patterns.»

That would be a misstatement also, of his understanding, would it not, according to your testimony on direct examination?

A. You'd have to define or have to know what he meant by identical, how he was assessing whether things were the same or different.

Q. Maybe what I'm getting at, Dr. Waye, is maybe expert witnesses coming to court and not doing

are not doing as great a job as they thing they are in teaching us what DNA analysis is all about, is that a possibility?

A. That's a very big possibility, there's no school for scientists to teach lawyers, judges and laymen, what they do. We're not trained to teach in that sort of environment.

Q. And we haven't been trained to understand?

A. Well, if you haven't had any biology courses so, yes, you're not -- generally who we're teaching are people who have a foundation of knowledge that it's quite easy to build upon.

Q. It might be that you can't take a person off the street and teach them in two days?

A. I could teach them how to do it.

Q. You could teach them how to do it, oh, how to run the test?

A. Correct and hopefully I'll teach them to understand what they're doing as well. But there's certainly going to be people that you can't teach or you can't --

Q. You're telling me if I was going to be a technician and come to your lab and does this test, it would only take you two days to teach me and I'd be an expert.

A. I didn't say that.

MR. WALSH: He never said that, my lord.

Q. Well, he can say he never said it?

A. I just said that I didn't say that.

Q. You didn't say that?

A. Correct.

Q. When you said that you could take somebody off the street and teach them in two days, what was it that you said, what was it you could teach them in two days?

A. I could teach them to do the technique, they could physically do the technique themselves. They could draw blood from themselves or whatever fluid they wanted, extract the DNA and determine their own profile.

Q. And run the whole test, and you could teach them how to run that whole test in two days?

A. If they wanted to stay up late, it's possible. The time frame is the only variable thing.

Q. And again, I would assume they would be doing the test right if you taught them, they could do it -- they would be doing it properly?

A. If they did it properly, my teaching them to do it properly has nothing to do with them doing it properly.

Q. So after that the R.C.M.P. might hire this person as an individual technician to run these tests?

A. I don't think that's really fair to the R.C.M.P., that they'd hire somebody who had done it once.

Q. I'm not saying they did that, but you're saying it's possible that they could if they wanted to?

A. I'm sure they could hire anyone, they could hire somebody -- somebody incapable to do the test, the hiring practices are the R.C.M.P.'s, I don't think that would be basis for hiring somebody that the statement, yes, I did this once and got the right answer, hire me. I don't think that would hold any weight with R.C.M.P. or anyone else.

Q. I'm surprised that in the early cases of DNA analysis, experts come to court and experts for proponents of DNA analysis and they said that there's no way you could get a false positive, did I understand your direct testimony to say the same thing that you can't get false positives?

A. I said if the test is conducted properly and interpreted properly, you won't get a false positive.

Q. If it's conducted properly and interpreted, you can't get false positives. So contamination or degradation could not create false positives, that's what you're saying?

A. Again, that would be part of your interpretation.

Q. That would be part -- oh --

A. If you interpret those things properly, you account for them, you're not going to falsely include a sample that shouldn't be.

Q. Okay, so at least we're down to that, if you don't interpret contamination and degradation properly you could end up with a false positive?

A. You'd be much more likely to get a false negative but if somebody just followed blindly rules of matching that, they weren't scientifically valid, and I gave an example earlier on about limited amounts of DNA and you can only detect the top band, not the bottom band.

Q. Okay, that's something through all my reading I could never under the logic of, you can false negatives but you can't get false positives, could you explain why?

A. I gave you the example of the false negative this morning and again, that was something that was, excuse me, incorrectly interpreted. If I can twist that example around and again this will be a false positive, I must underline after that, if incorrectly interpreted, would be the same sort of example. If your blood standard had a two band, just one band, let's forget about this and the sample from the scene of the crime if there were a lot of material had two bands. Now, if all worked out well and you had unlimited amounts of DNA, that's the pattern you're going to get, two bands, one band, that's an exclusion right.

A. Right.

Q. If you had very small amounts of DNA, such that you can detect this band here, follow me.

Q. Yes.

Q. Now, you've got a match and you interpret it as such, through all of your probings incorrectly, you'll get a false positive. You've done the test wrong, you've interpreted it wrong and you've got the wrong answer.

Q. You'd get a false negative?

A. You'll get a false positive there.

Q. False positive.

A. The same as if I'm given a bloodstain from the police officer and a tube of blood, I take the blood stain and use it, and analyze the tube of blood in the adjacent lane, I'm going to get a match because I've analyzed the same sample twice.

That's operator error and that's a false positive. I'm not going to come up with an absolute statement, you can't get a false positive because then I have to account for every one in the world being perfect and analyzing things perfectly.

Q. Could you get a false -- what about when your bands are, say, on the borderline of your window and you're allowed a plus or minus 2.6 percent for each band, right, so if these bands were staggered, this band was actually down here and it was less than 5.2 percent in between, you would call that a match, a positive, right?

A. I wouldn't.

Q. You wouldn't?

A. It's not a visual match.

Q. Are you saying you cannot visually match something less than five percent or something around five percent?

A. There are instances where you can have bands that are visually identical and be five percent off.

Q. Right, if they're --

A. There are instances also where you can have bands that are visually identical in mobilities and be six percent off.

Q. But there are also instances where you can have bands which are visually different and be within five percent?

A. Correct.

Q. Now, these bands which are visually different and within the five percent and I'm going to say,

right at five percent.

A. Correct.

Q. Could there be a degree of degradation or contamination that would actually, that band should actually be outside the 5.2 percent rather than at five percent?

A. So the visual patterns should look even worse than they actually do, should be further apart from a match than they actually are.

Q. Yes, so the actual would be further than what the visual tells you and what your sizings tell you?

A. Could that happen, you're asking me?

Q. Yes, could there be enough degradation or contamination of one of the bands to actually ought to be if there was no contamination, degradation, it ought to be more than 5.2 percent than the band you're matching it with but because of contamination and degradation, it's five percent within the band you're matching it with?

A. Well, you're talking about band shifting and yes, it does happen, it can happen.

Q. No, I don't think I'm talking about band shifting

A. Yes, you are.

Q. I'm talking about your measurement imprecision, not --

A. That's not measurement imprecision.

Q. Not measurement inaccuracy.

A. That's band shifting, you're saying, you're saying there's something in the sample that causes the fragments to migrate somewhat independent of their actual size, that's band shifting.

Q. That's band shifting and you interpret that as what, measurement imprecision?

A. It has nothing to do with measurement imprecision, it's band shifting.

Q. It's band shifting.

A. Something has happened to that sample not to that fragment only but to that sample, to the DNA in that sample that causes the fragments -- that causes their mobility to be determined, not only by their size.

Q. How do you describe your matching window, your 5.2 matching window, do you measure that as a system imprecision or system inaccuracy or do you apply any terminology to it?

A. It's a number derived through measurement imprecision.

Q. It's a number derived through measurement imprecision?

A. Yes, if you analyze bands that you know their size and you know their the same size in all individuals, a monomorphic band, and you analyze many, many individuals and the bands always migrate to the same spot, and when you determine the size of those bands you can come up with several different values. You can determine how close they are to each other or to the average, you can determine how close they are to the actual, to reality. In a good system those values would be very close because reality should reflect the measurements.

Q. Could it have anything to do with actual fragment length?

A. I thought I just explained that, perhaps I didn't.

Q. I'm a little dense.

A. I'll explain it again. It's determined by actually measuring how fragments of known size migrate. So it is very related to size. You can say, that the values I'm getting are in fact accurate, they reflect reality.

Q. Maybe where I'm losing you, I thought that only related to band shifting and what you could do with monomorphic probes when you knew the actual size? But when you're dealing with polymorphisms, you don't know the actual size?

A. Right, which is why even when you have a situation as to, we have up there, where the fragments match a good scientist will always allow for the possibility that that could be a match, that also could be a band shift that shifted a mismatch into a match, which why you run the monomorph afterwards, to exclude that possibility.

Q. So are you saying the monomorphic probe and the degree of band shifting you ought to be able to use that to show that the two bands are identical in length?

A. To show that they ran as they should have.

Q. Now, if you use the monomorphic probe and you adjust them with the monomorphic probe, and they still show that sizes are not the same length?

A. You don't adjust with the monomorphic -- it will just answer the question, did they run properly or didn't they, did it run accurately

or didn't it?

Q. I thought I understood in reading some of the case law that some of the laboratories were attempting to use the monomorphic probes to bring bands which were further from their match window, outside their match window to bring them back into their match window, adjust them that way?

A. And force a match, justify a match.

Q. Yes. Has that been done in some cases that you know of?

A. I believe it has been done, yes, not in the R.C.M.P. system.

Q. No, so what I'm saying is, what they've done, they've used the monomorphic probe and the band shifting which is determined by a monomorphic probe, the degree of band shifting is determined by monomorphic probes?

A. Monomorphic probes can be used to --

Q. And they would use that degree of band shifting to bring their bands closer together so that they could declare a match? It might be legitimate, I don't know, but I'm saying they do that?

A. This is one particular lab, a private company, I believe you're talking about if I understand where you're going and I've never worked for the lab and my understanding of it exactly how they do things is again through transcripts, and they do run monomorphs and they do try to justify non-visual matches and correct, at least they did at

one point. Beyond that we probably have about the same understanding or first hand knowledge of their protocol.

Q. In VD-45 where it shows Lane B and C, it shows that they -- visually they are matched and they're the same -- should be the same length, is that correct?

A. Visually they match and --

Q. You would like to interpret them as being the same length?

A. Correct.

Q. But as a scientist you know that eventhough they look to be the same length, they very well may not be?

A. The only way definitively if you want to know exactly how long each of those fragments are is to clone them and sequence them and determine their sequence.

Q. That's the only way you can be sure?

A. If that was the question you wanted to ask. That's not the question we want to ask. Just as you said before, how can you be sure that the composition of the fragment is the same. Well, we know that they're similar because we know how hybridization works. But again, you'd have to sequence them, it's a different question, sir.

Q. The question I was getting at is that if these two bands are five percent of their value separating them.

A. Hm-hmm.

Q. Which puts you within the match window, so let's take that band over here just for instance and

maybe put it right underneath here with five percent difference. What I am asking is, could -- so if we had this one over here and we can visually see a space or maybe you can't see a space at that difference but you already say you could in some of them.

A. We'll call it a noticeable shift.

Q. A noticeable shift, okay, for your purpose we'll call it a noticeable shift, so if you had this band it was actually over here but for explanation purposes, we put it right underneath and I say anyway we can see a noticeable shift and that there is a space in between and that space, for argument's sake, we'll say is a five percent difference and it's in within the R.C.M.P.'s 5.2 matching window. What I'm asking is, could contamination of either, we'll take the unknown sample, if contamination or degradation of the unknown sample, if it was not contaminated and not degraded, could it be either closer to that band or farther away from that band?

A. If everything ran perfect could it be closer or farther away?

Q. Yes.

A. If you're throwing in whatever you want from the environment, sure, that possibility is open in either.

Q. That possibility is open.

A. If I could go to the end of this perhaps, what you just described would be called inconclusive and wouldn't --

Q. Inconclusive.

A. It would neither implicate nor exclude your client.

Q. So it's possible that an unknown sample because of its state of degradation or state of contamination, it may be within the R.C.M.P. matching window when actually it should be an inconclusive. If you knew how to compensate for the degradation or contamination?

A. Whether it's in or out it would be inconclusive.

Q. Whether it's in or -- as long as there's any degree of degradation or contaminatin, it's inconclusive, is that what you're saying?

A. Well, we can't analyze the source of why these things happen or if in fact they do happen. But you made this match inconclusive by talking about noticeable shifts or however you wanted to phrase it before, it's not a match, you look at them and they're not a match.

Q. So as long as there's a noticeable shift, it's not a match?

A. You looked at it it's not a visible match. Now, I can/the monomorph afterwards and show that the monomorph shift and that's when the companies, say, well, everything is consistent with this being a match but it shifted, that's a perfectly valid scientific conclusion. The conservative thing to do and it will save a lot of battles in the end is to say, we're not going to call anything on this, neither way.

run

Q. Okay, if I understand you, that if when you do your sizings you have a five percent difference, and you can't notice the visible match, you would call it a match but if you could notice a visual match and when you take your sizing and it only says there's a three percent difference you would say it's inconclusive?

A. Again, it would depend on the sample, if there's a -- what you call a noticeable shift and what I'd call a noticeable shift may differ.

Q. What do you call a noticeable shift?

A. You would have to show me some examples.

Q. No, I want you to tell me an example, you're the expert.

A. It's like saying, what do you call a beautiful scenery? I don't paint so.

Q. So it's purely subjective?

A. The visual assessment, yes, if you're blind you can't do it, depending on your eyesight there'd be degrees of whether you can do it, depending on your experience, that is a subjective analysis, the initial visual assessment, the subjective analysis that anyone with vision can do. If you look at things I'd be surprised if anyone said that they see a visible shift there. And I think most people who looked at that would say the same thing. Now, if you moved that down one one thousandth of an inch, I'd look at it and I'd say, um, there's no physical shift there. You might get out some precise micrometer or whatever to

measure how far that down -- I detect a one thousandth of an inch shift there. A defence lawyer might call that a shift.

Q. It's easier to argue then that there's no visible shifts if the specimens are -- the samples are run in different lanes but if you run them in the same lane it would be easier to --

A. Why in the world would you run them in the same lane?

Q. It's called mixing samples, you mix your samples add a mixing lane?

A. Take the two samples that you want to compare you know nothing about what the patterns are going to look like at the end, put them in one lane and then analyze them.

Q. No, no, not without you're -- running the separate lanes and have one mixing lane, to see if there's any visible shifts?

A. I think that's been something that's been tossed around by some people who aren't forensic scientists and they've since -- a lot of humilities, come to the conclusion that that really wasn't a viable way to be doing forensics. That's quite a matter of scientific record now.

Q. You would probably have many more inconclusive results, wouldn't you, if you used that mixing lane?

A. I think you'd be in a lot more trouble for using improper scientific practice for using that method, it's not a scientifically valid way to be looking at these things, not with forensic samples and I'm not aware of anyone who

takes the position that mixing experiments are proper for forensics.

Q. Did Sellmark use mixing samples in their first protocols?

A. I've never read Sellmark's protocols, they were kept closely guarded for awhile anyway. People testing paternity samples certainly have, again, that's a different application, you're dealing with samples of known history, i.e. blood samples.

Q. When you opened the lab in what year was it for actual testing, DNA for forensic purposes?

A. I believe the first exhibits for casework came in late in 1988, November or December, '88.

Q. In October and November of '89, were there -- was there any quality control programs in effect then?

A. In what year?

Q. In '89, October or November of '89, were there any quality control programs into effect?

A. Quality control programs were in effect prior to even accepting casework samples. Quality control is in effect, it goes hand in hand with good science, if you're doing good science, you're doing --

Q. What about quality assessments?

A. Quality assessment, could you define that?

Q. Were there any proficiency trials, line proficiency trials open?

A. Of who?

Q. Of your technicians?

A. My technicians weren't doing casework.

Q. Your technicians weren't doing casework in '89?

A. To my knowledge they were not doing casework at all to this day.

Q. Maybe I'm using the wrong term then. You've done some tests yourself for forensic purposes?

A. If I've testified in a case other than this one -- I've --

Q. You did those yourself?

A. I've conducted the test myself.

Q. Were any proficiency tests done on you in the R.C.M.P. lab?

A. The tests I did were amongst the initial ones and the person who would have does the proficiency testing I would have been testing myself.

Q. Did you do any proficiency testing on Dr. Bowen in '89?

A. I didn't, no, I didn't.

Q. Did anybody do any proficiency testing on Dr. Bowen in '89?

A. I can't recall, Dr. Bowen was trained and Dr. Bowen analyzed a number of samples. I did proficiency tests and certainly that was part of the procedure, I'd be outside of my knowledge if I talked to you about proficiency results or when he was tested or how many samples he was tested or who tested him.

Q. As I understand at this point in time what we're getting at where we're relying on a theory that

says no DNA of two individuals is the same except for identical twins, that's the theory that we are relying on, to support the identification, that's DNA analysis on suspects?

A. I don't think theory is a good word for that. I think even a defence lawyer would have a hard time finding anyone who would dispute that fact, fact would be a better word.

Q. Okay, that fact then or theory, whatever you want to call it, it's based on the premise that everybody's DNA sequence of base pairs is at least different except for identical twins?

A. Yes.

Q. And you're using that theory, so you say, to identify known and unknown samples of DNA?

A. To identify their source.

Q. Now, you don't -- you'll admit that you, through this identification you don't use the -- or attempt to establish what the DNA sequence is on these base pairs?

A. The precise sequence.

Q. The precise sequence?

A. No.

Q. Whenever you measure your DNA fragments or restricted length fragments you're measuring the length of them, in between them?

A. Yes.

Q. You're cutting -- and again, whenever you do declare a match, you are assuming that the sequence is the same?

A. No, I just -- I think you've read into the test a little too far. All I'm saying is that those fragment size are the same approximate size.

Q. So what value is the theory then or the fact that base pairs are the same, what value is it if you don't use it?

A. So you're suggesting that we sequence these regions.

Q. If you're going to use a theory, I would suggest that you'd have to sequence them, otherwise there's no need for a theory if you're going to detract from it at that rate? If you don't know the bases that you're analyzing to compare it with your known facts or theory, why even consider it a theory?

A. If I understand you correctly and maybe I'll exaggerate on the extent but I'm sure if I said, I'll sequence a little of this for you, you'd want me to sequence from probably the beginning of Chromosome 1 to the end of the Y chromosome, there's no reason not to sequence the whole genome, I suspect. Would that be the appropriate test? That's the most discriminating way to conduct this. I take DNA from the two samples and I sequence from the beginning of Chromosome 1 to the end of the X chromosome. And then we read that three billion base pairs and if they're the same, we've got identity, is that the test you're suggesting? That's the extreme form.

Q. What I'm suggesting is you're coming to court and you're proclaiming a theory based on DNA structure?

A. Yes.

Q. And you're conducting tests that are so removed from that theory that the theory is no longer applicable?

A. They're not removed from that theory though.

Q. They're not removed from that theory.
Okay, whenever you do declare a match and because you are assuming they are the same length --

A. I don't assume that, I thought I just said that.

Q. You don't assume they're the same length either.

A. The exact same length in the exact same composition, I just finished saying that, I say, their mobility is, I can't distinguish them, they're either the same size or they're very close.

Q. Right.

A. Which is why we put statistics on these things, they could be a little bit different, that's why we looked at different people and I don't look at that pattern and say, that those are identical and those came from the same individual. I say, that's identical and one in fifty people could have that.

Q. But in the end when you get down to your data base and you're, what you're relying on your data base for the frequency of it, it really doesn't matter if they're in the same base sequence or not, does it? It could be totally

different and it wouldn't make a bit of difference in the final --

A. Well, the probe wouldn't bind if it was totally different.

Q. The probe wouldn't bind to something totally different now but it will bind to something that's within eighty five percent or even less?

A. I don't know whether you've missed the point of the test is that you conservatively estimate how often these events occur in the population. You don't say, this is a scientific fact that the length and base sequence of this band is the same as the length and base sequence of this band. If we did that we'd be pointing fingers at people, we wouldn't associate statistics with it. I come up with a conservative statement like consistent, that the word that you'll hear and one in fifty, something like that, a lot of people could have fragments identical or similar or identical in sequence or similar. That's what you're measuring and that's why you'd put a conservative statistic to it, because other people could have the exact, they could have similar ones, that's all you're measuring and that's all you're trying to express not precise sequence of that region or any other regions on these chromsomes.

Q. Right, the point I'm trying to make is, in your system of figuring out these statistical probabilities, it really doesn't matter if these are of identical length nor does it matter if

they're of the same sequence?

A. No, it doesn't and when I scan my five hundred people, when I see fragments of that length a lot of those people it's not going to be precisely the same length or the exact same --

Q. Same sequence?

A. -- linear order along that length, but it's going to be close because the probe does bind under those conditions and it's going to be close because it's sized at that size.

Q. So the fact that no two people's DNA is identical it really has no relevance as to the system that you're using --

A. You're racing around --

Q. -- you know, the bottom line is so what?

A. You're -- if that's the easiest way for you to deal with it, then that's your point of view. I'm not sure I can change your mind on this one. I think what you're looking for is for me to start sequencing at the end one chromosome and stop at the other, or even selected regions. And that's part of a global initiative right now that's costing billions of dollars and it's worldwide project and it's been compared to going to the moon. It's the most titanic project that's ever taken place in biology. If you want to do that for every known and unknown sequence, the U.S. Congress would be-- they'd like that because they're paying the bill for that right now.

Q. But as the system or identification in DNA is set up in forensics at the R.C.M.P. lab, the

only benefit of sequencing would be to an accused person is he could prove that if the sequencing wasn't identical, then you would have to exclude him, otherwise it has no benefit to you, is that right?

A. See, I think what we're getting at here, is that you think, if I understand this correctly that this test is incapable of saying that this sample did come from this person.

Q. Definitely, not incapable.

A. And unless I've led you astray somewhere, I'm not sure I've ever said that this test will show that this sample came from this person.

Q. No, you didn't lead me astray. But with the figures that you would like to put to a jury or a judge sure leads to that, doesn't it?

A. Well, you're taking -- they're two different things again, if you want me to definitively say that this sample came from this person, you've got to take an approach like that. This test isn't designed to reach that end point. So we're really talking apples and oranges, and the logic behind the argument are as far apart as well.

Q. Okay, when we talk apples and oranges again, if I was going to use a diagram -- if I was going to take, let's just say, for instance, we're going to use these two bars in Lane C on VD-45, okay, and we're going to -- for arguments purposes, we're going to say, this is a known sample and this is the unknown sample.

A. They're in the same lane.

Q. They're in the same lane. In order to see how your matching window works --

A. How did they get in the same lane?

Q. How did they get in the same lane.

Well, you can move it over into this lane if you want -- for demonstration purposes --

A. I would like to analyze the two samples in different lanes.

Q. Okay, let's take this one right here, okay. These two would be in Lane A and Lane B, take your bottom fragments on VD-45. Let's say, for instance that there is only 5.2 percent difference in between these two fragments, okay.

A. Mm-hmm.

Q. You would call that a match?

A. No, we've covered that ground. I think you just defined what both of us agree would be a noticeable shift, I think it is. I don't want to speak for you but that's a noticeable shift to me.

Q. Why is it that you can only notice a noticeable shift visually but you can't notice a noticeable shift when you read the sizings?

A. We went through that-- again if --

Q. If one base pair -- in the sizings you have a base pair with say, a thousand base pairs, the known sample has a thousand base pairs.

A. Yes.

Q. In the evidentary sample, the known base pairs

ninety five hundred or yeah, nine hundred and fifty, okay.

A. So they're fifty base pairs apart.

Q. So we have a fifty base pair difference which would be within five percent?

A. Yes.

Q. Now, if you were going to put them on a graph or if you were going to put them under one another, you might be able to see the noticeable difference?

A. I'd have to do the experiment but you might.

Q. You might. So if you did that experiment and you were able to see a noticeable shift as daylight between them, you would call that inconclusive, is that what you're saying?

A. And they're five percent, for that particular probing I would call it inconclusive.

Q. For that particular probing you would call it inconclusive.

A. Which is why we do more than one probing.

Q. If they're five percent apart and you can't see daylight between them --

A. And they look identical and they're five percent apart.

Q. Yes.

A. You'd call it a match.

Q. You'd call it a match. See, I can't understand that.

A. What part don't you understand?

Q. You're attempting to measure the fragments from the distance they move from the starting --

A. Correct.

Q. Okay and --

A. And we've really admitted that our ability to measure them doesn't come to the base pair limit.

Q. All right, from the sizings you put on them, you've judged them from your marker lanes.

A. Yes.

Q. Of known values?

A. Yes.

Q. So you put a sizing on that fragment?

A. Yes.

Q. Or let's go back to the bottom fragment here in Lane A, so you put a sizing in that fragment, say, it's a hundred base pair for argument's sake?

A. Yes.

Q. Then again with your marker lanes, you measure the bottom one here, the bottom fragment in Lane B and for argument purposes you'd put a sizing on that at nine hundred and fifty base pair.

A. Yes.

Q. Now, what is more accurate the sizings you put on them or your visual observations?

A. In my opinion?

Q. Yes.

A. Your visual assessment.

Q. Your visual assessment.

A. The sizings will mirror that. The example that you showed me there, when I sized those and if they're in adjacent lanes as you've shown them and one's shifted down, like, I'm -- the computer is not going to tell me that this band

is a thousand and this is eleven hundred.

Q. The computer is not going to tell you that?

A. No.

Q. So how do you get your sizings?

A. With the computer, that unexpected the computer would not tell you that because these fragments do migrate according to their sizes. If it's visibly smaller the computer is going to tell you it's --

Q. I thought I understood you to say that when you're visually observing the autorad, you tell the computer how many bands you see in each lane and it automatically sizes them?

A. The computer scans each lane on the screen and it will say how many bands or something to that effect, I can't -- I haven't done this in a while, you punch in one, two or how many bands there are in there.

Q. The computer will tell you that before you tell it?

A. Will tell you how many bands there are?

Q. Yes.

A. The computer has already scanned it and it's drawn the peaks where the densities, so it hasn't lit up on the screen, I see two, it asks you, but it's already got that information compiled, the two most likely bands. And as soon as you say, two, it picks the two most likely bands. if you said, one, it would pick the darkest.

Q. And when you say, it would pick the two most likely it would pick the two darkest bands?

A. It will pick, it will read down, if, for instance, these two bands were faint and while I was developing the x-ray film I got my thumbprint on here, the computer may very well go to that thumbprint and say, here's my candidate for a band, which is why we don't let the computer make all the judgments.

Q. It's too objective.

A. It's only capable of doing what it's programmed to do and it's not programmed to weed out a technician's thumbprint.

Q. It's not programmed to take in your biases?

A. Well, that's -- I think if you want to call that bias, I would call that a good judgment call, if I saw my fingerprint on an x-ray and I had two bands that looked like a band, in my experience to pick the two that looked like a band and not the one that had my whirls and swirls, bias judgment.

Q. I'll go back to the question again, if you had picked that one as a band, the bottom one in A.

A. Yes.

Q. And you picked the bottom one in B as a band.

A. Yes.

Q. Why agree that there were bands and you cannot visually see any difference, okay, there is no visual significance difference between them.

A. You can't see a difference.

Q. You would call it a match visually, but when you tell the computer to pick out these bands, and the computer sizes these bands and he has

them statistically different.

A. You clarify this, if those bands were in the same position visually because you're pointing at bands that aren't in the same position visually and giving me a scenario that --

Q. Sir, use your imagination.

A. Well, if you moved over a lane, we could reflect what you're trying to explain, you're jumping around --

Q. You mean these two lanes.

A. Well, if you're giving me the scenario that I'm looking at two bands that look identical visually, that's probably the example we should go with, I would think. I'm getting confused we've --

Q. Well, maybe I should draw it out on paper.

A. Please.

Q. In which I can put the bands a little closer together.

A. Please.

THE COURT: Well, let's do that after a recess.

MR. FURLOTTE: It sounds good to me.

COURT RECESSES AT 3:30 P.M.

COURT RESUMES AT 3:50 P.M.

ALL COUNSEL PRESENT

ACCUSED PRESENT

DR. JOHN WAYE, still under oath, continued to testify:

CROSS EXAMINATION CONTINUED BY MR. FURLOTTE:

Q. Dr. Waye, I have drawn a very crude diagram here for explanation purposes, I have here one band in Lane A and I have one band in Lane B, and I have drawn them which would approximately 5.2 percent apart, if we shifted the band in Lane B down by 2.6 percent and shifted the band in Lane B up by 2.6 percent, we would be within what you call your matching window, is that correct?

A. If it's within 5.2 percent, yes.

Q. So if you shift one up 2.6 percent and the other one down 2.6 percent that would be within your matching window?

A. That's within that number, yes.

Q. So if the band in Lane A had, we'll say, one thousand base pairs, according to your sizing and the band in Lane B was, well, we'll say roughly nine hundred and fifty, I doubt if that comes out to 5.2 percent.

A. It's close.

Q. It's close enough, right?

A. It's close.

Q. Now, what I was trying to explain awhile ago on VD-45, the differences in these two bands, although they're in different lanes they would be within your matching window, and you would call that a match?

A. No, I wouldn't.

Q. Why because you can see a visual difference?

A. They're not visually, the pattern for this particular probe doesn't look like a match.

Q. So you would not call that a match?

A. I wouldn't.

Q. Inconclusive or exclusive?

A. I'd call it inconclusive this particular probing.

Q. Okay, now, say Lane A, we change Lane A on the gel to number 2, Lane 1 is your marker, right?

A. Yes.

Q. So Lane A would be for a sample of something either known or unknown, say, if we changed Lane A to Lane 2 and Lane B now became Lane 19 or 20, you'd be quite a distance apart and the visual match might not be so appropriate, is that a fair assessment?

A. It's harder to make -- to notice small differences from samples that are analyzed with a lot of lanes separating them.

Q. So it would be more difficult to have a visual match.

A. Obviously it's like -- a good analogy would be putting two people of the same height side by side or putting them across the room.

Q. Would you then rely on the computer sizings to give you the match?

A. To fall within.

Q. To fall within the 5.2 percent?

A. Yes.

Q. Could you also not use the computer sizings to show that there is a distinctive difference in the two bands?

A. Visually.

Q. No, no, not visually, let's rely on some objective criteria here for a change.

A. We use the computer, what did you want to know if the computer would do?

Q. If you used a computer to bring them within the band, the window measurement, you see that from the computer sizings that they are within 5.2 percent, so you would call it a match. Why can't you use the computer sizings when they are even within the 5.2 percent window, why can't you use the two percent or -- why can't you use the computer sizings to show that they are distintively different?

A. The computer in both instances has shown me that the sizes are different.

Q. Right.

A. That's not an unexpected result.

Q. And why not?

A. We've gone through that many times, if I analyze my DNA in adjacent lanes or Lanes 15 to 20 apart the expectation is that I probably won't get the same number.

Q. Right.

A. That is a distinctive difference.

Q. So as long as you -- and because you have analyzed yours or somebody else's repeatedly, time and time again and you come up with a -- a what -- a 5.2 variation, then that's how you declared your matching window, is that right?

A. It wasn't done analyzing a particular person's DNA. It was done analzying, it was drawn from

the data base, analyzing with probes that are monomorphic.

Q. For monomorphic, okay, probes which are monomorphic which are of known sizes?

A. Correct, size.

Q. Drawing that information from monomorphic probes which are known sizes, you and you repeat the test over and over again, and you could come up with variations in -- with the 5.2 percent between known fragments, known size fragments?

A. In fact can come up with larger differences.

Q. And you can come up with larger differences, but you what, settle for an average, of 5.2 percent?

A. No, we, the 5.2 percent is actually an extreme value and it's that type of value that is precisely the example that you've given when you have things separated by a large number of lanes or perhaps on a different gel. You don't have this ability to have them side by side and say, I can see daylight between those eventhough they're within that. You don't have that ability, so you have to rely on the computer solely. Now, we are dealing with things we know are the same size. We're not dealing with these unknowns.

Q. But my comparison here is, with this, say, particular probe,you're at 5.2 percent difference apart, because they're close together you can see they visually do not match, so you would say it's inconclusive. Now, just the fact that we've moved --

A. Given just this information, I'd look at this not even needing the sizing data, I wouldn't be able to make a call either way. With the sizing data it would be inconclusive.

Q. What I can't understand is the mere fact that you've moved these apart, say, twenty inches apart or whatever and now, they're not so visual that there's a difference?

A. Well, now, I'm incapable of making this type of discrimination, I have got them apart, so why would I do it.

Q. Why can't we make the discrimination just on the computer's sizings of base pair per fragment?

A. That's exactly what we just went through, if they're twenty lanes apart I use that sizing.

Q. Why can't we do it all the time, even when they're lane to lane?

A. If I did it all the time, if I followed your demand, I'd be taking things that I don't think are a match and calling them a match. I'd be -- to my mind as a scientist, I'd be misinterpreting and I'd be walking into exactly what you were bringing up before, if you misinterpreted you've created a false match or you walked that line that you could be creating a false match.

Q. I thought we didn't have false matches?

A. If you do it improperly, you just did it improperly, you want me to do it improperly.

Q. No, I want you to see your data and your testing for what it actually could be, I want to realize the limitations of your experiments, your expertise, I'm showing you how you can get another false match?

A. You're going to have to explain it a little better than that then. You haven't come close to it. What I am doing here is I'm taking all the visual information and I'm being conservative.

Q. What I'm saying is if these two, one thousand base pairs, nine hundred and fifty base pairs, if they're lane to lane and you can see a visual difference between them, eventhough the computer sizes tell you they're different, great but you also see it visually, you will say, inconclusive. But if you move the same length that nine hundred and fifty base pair over a distance where it's not so obvious, then you rely on the computer sizing to say, uh, I'm within 5.2 percent, so I'm going to call it a match. How can it be a match in one case and inconclusive in the other?

A. Because you've got two different tests, one I have the ability to use my eyes and make that discrimination, the other I don't, not to the same degree.

Q. Well, your inability of your eyes to make that discrimination can falsely convict an innocent man?

A. No, it can't.

Q. You better believe it can. Why can't it?

MR. WALSH: That's not -- objection, now, if, objection, at this point we'd like to -- it's going to be a long day today and tomorrow and the weeks after, but if Mr. Furlotte intends to testify, perhaps we could get a carpenter to build another box.

THE COURT: Let's have that -- we had better have this marked, so that anyone reading the transcript would know what you were talking about.

This would be VD-51.

Q. Let me put it another way, you're saying because these bands would be in a close lane, therefore, you would say it's inconclusive because you can visually see the difference, am I correct so far?

A. This is the way I would call it, yes.

Q. But if we move that away over here --

A. If I could still tell that difference, I'd make the same decision.

Q. If you could still see the difference, you would make the same decision?

A. Sure. If I could lie a ruler across there and convince myself that those things are different--

Q. You will admit that the farther you move it away from one another, the more difficult it is for you to visually see?

A. Depending at the differnce at this point, if there's physically a big difference at this point it will be easy to see at the other end, it's fairly close.

Q. Now, because of the limitations on your eyesight to visually see the difference, you will say that that is a match rather than inconclusive?

A. Correct.

Q. Would that not prejudice an accused person?

A. (Witness shakes head).

Q. Where in one instance, you are going to call it a match, the other instance, you're going to say it's inconclusive?

A. No, the second is justifiable, I'm throwing out the first to be conservative.

Q. Why not throw your eyes out to be conservative and rely on the computer sizings? You want to rule in benefit of the accused person, be conservative, why not give him the benefit?

A. If I take your example here and I rely specifically on the computer sizings, the first example you presented, I just ruled against your client. I may have the same result, we're going to have a match on both where we had an inconclusive with my conservative judgment and a match on the other, that rules against your client.

Q. Let's go on and see how much more conservative you are. This is the computer sizings, right, where the dark line is on each size, I will put one thousand base pairs in Lane A, I will put -- for argument's sake, nine hundred and fifty base pairs in Lane B. They are roughly 5.2 percent apart, agreed?

A. They're not far from that.

Q. They're not far from that.

A. I'd need a calculator to do that math.

Q. I don't think we have to be that precise, not for demonstration purposes. Now, where the fragment lengths in Lane A ended and we sized it at one thousand base pairs, according to your theory and the measurement of imprecision or inaccuracies, whatever you want to call it, we know where the base pairs landed in

Lane A and we've given it the size of one thousand base pairs, correct?

A. That's the estimate, yes.

Q. On your own experiments, you admit that that could be anywheres -- the actual size measurement could be plus or minus 2.6 percent?

A. For some fragment lengths, yes.

Q. For some fragment lengths. So actually you're assuming then to get into the matching window that you're assuming that that base pair is maybe down to actually nine hundred and seventy five base pairs, right, to get it down here?

A. No, I'm --

Q. To bring it halfway in between one thousand and nine fifty you're assuming it's nine hundred and seventy five?

A. I'm not sure you understand how that number is derived. The number is not derived from how far we see the bands move up or down. It's derived from things that look visually the same, how far does the computer tell us they're up or down. The computer has to find the center of that band. You've got a band that's this wide, there's a little wash in there or a little wobble in there finding the center. Visually the centers look the same. The computer can place them ten or fifty base pairs from your example there.

Q. What I understood from your explanation before was that to arrive at 5.2 percent window you measured continuously and went to your data base to see how your technique, your system

measured known base pair lengths, fragments, twenty seven hundred and thirty one base pairs?

A. Correct.

Q. Correct, and in measuring those known you had maybe sometimes been 2.6 percent short and sometimes 2.6 percent long?

A. Yes.

Q. Okay, and you've admitted even greater than that?

A. Yes, it can be.

Q. It can be. So --

A. We didn't see that situation.

Q. Maybe you didn't look, did you look for this situation?

A. Yes, I personally did all that data.

Q. You personally did all that data?

A. Yes.

Q. Do you have any valid -- the Crown has been introducing all these articles that you put for publications and maybe what you call validation or put out for peer review, do you have any data on the tests which you conducted for this matching window?

A. They're described.

Q. They're described, in what, which articles?

A. The Promega article, what we've been calling the Promega article.

Q. You've stated what your size window was, and how you come about it?

A. Not in terms that you might have recognized in reading the article if you've read it. But the data is in there, it's in a form that another

scientist could pick it up and understand exactly what I did and how we formulated that.

Q. What I'm going to ask, Dr. Waye, is with this base pair recognized as one thousand base pairs in Lane A, ninety and fifty base pairs in Lane B, because of the data that you work with to gain your matching window you are saying to yourself, well, Lane A could actually be nine hundred and seventy five base pairs because you're allowed plus or minus 2.6 percent. You're also saying Lane B which is nine hundred and fifty base pairs, if we add on 2.6 percent could also be nine hundred and seventy five base pairs. Therefore, we are going to declare a match?

A. No.

Q. That's not the way it works?

A. That's not what I've said, you've been saying this --

Q. I'm saying this, that this would --

A. No, you've been saying this over and over again and I've been disagreeing over and over again. What in fact we would be saying when we make these when we make these -- what you're doing here is you're walking through diagnostic band shifting. You see a band shift, you do the next experiment, you look at the monomorph, it either shifts or it doesn't shift, and you make your call. What we see, and how we based all this stuff is you'd look at two adjacent lanes typed with the monomorph, they

look visually the same. And then you ask the computer, how far does the computer take these things. In my eyes they're the same. What difference does the computer peg to that? They look the same, you'll get--as we've said over and over again, you can't -- you'll get different values for things that even look the same. What we're trying to measure is how far the computer will say things that are the same look in base pairs.

Q. So what you're saying, the monomorphic probe to measure your band shift corrects all this, you can correct this phenomenon with the measurement of band shifting with your monomorphic probe?

A. No, you can understand it. I think I was quite clear when I was talking about Lifecodes and their method about using correction with band shifts, that's something that I'm familar only in the abstract through court proceedings where that's been criticized, we don't do that.

Q. So I understand the FBI does not use the monomorphic probe?

A. That's my understanding as of the last time I was down there, yes.

Q. There is no way of explaining this phenomenon within their system of DNA analysis?

A. If they saw something like this.

Q. Yes.

A. And it was shifted down, they'd call it inconclusive, I think, I can't speak for their investigators.

Q. But when they're wide apart that you can't visually see that they're -- that they've shifted, they wouldn't be calling it a match?

A. It would be a visual match. If you can't detect a difference and everything looks like a match, it's a visual match, it doesn't matter whether they're close or far apart. Your ability to do so is a little easier to do in adjacent lanes.

Q. So if you really wanted to convict a person, you'd make the gels what, twenty feet long?

THE COURT: Well, I think you're making that a little dramatic when you talk about convicting and --

MR. FURLOTTE: Well, sometimes it takes exaggerations to explain the argument.

THE COURT: You mean to get a match is really what you're saying. Would you ask the question again, Mr. Furlotte?

Q. Let's say, for example that your monomorphic probe would not correct this phenomenon, okay, if you're testing on your data bank, if you checked your data bank and you found justification for your 5.2 percent window, rather than Lane A which we brought down to nine hundred and seventy five base pairs, okay, to meet Lane B which was brought up to nine hundred and seventy five base pairs, because we don't know the actual distance that it should have travelled. If we put the 2.6 percent, if we added -- if we shift it upwards in Lane A --

A. Shifted size or shifted band?

Q. Well, if we are looking at Lane A and we're seeing the band as a thousand base pairs, we don't know for certain it's a thousand base pairs but it's -- we are going to assume that it is within, actually within nine hundred and seventy five or one thousand twenty five.

A. Again, I'd need the calculator to --

Q. Yes, but roughly, we're going to take twenty five off and add twenty five on, okay. So since we don't know and you're giving it a 2.6 plus or minus --

A. I'm not giving, I'm recognizing.

Q. You're recognizing, okay, let's recognize that we're possible in error here by 2.6 percent?

A. No, I'm recognizing a feature of the system, a feature of the system and it's not designed to do this. The feature of the system is that it can't detect the size of these to the base pair, it's a feature of the system, it's something that's not in dispute, it's something that was recognized when agarose gel electrophoresis was chosen for the system.

Q. And the feature of the system proves that it could be out by 2.6 percent plus or minus.

A. When we measure things that are visually indistinguishable, at that size or that monomorph, we do find that is an outside value, yes, that's a fact.

Q. What I am going to suggest again is, what the R.C.M.P. and the FBI are doing in order to get matches when they're base pairs are at one

thousand and ninety fifty, they are assuming that they could be both be nine seventy five when they're far apart, you can't visually match them, what you are actually doing is assuming that they could both be nine hundred and seventy five base pairs, therefore, we will call it a match. If you were going to give the benefit of the doubt to an accused, isn't it just as easy and to be conservative to assume that, well, maybe Lane A at one thousand base pairs is actually one thousand twenty five base pairs and maybe again, to be conservative, for the benefit of the accused, Lane B which is nine hundred and fifty base pairs is actually nine hundred and twenty five base pairs, so now we are nine twenty five in Lane B, we are at one thousand twenty five in Lane A and we are ten percent apart if we're going to be conservative?

A. Okay, let me just explain in real terms what you just proposed. It's actually -- we've gone in an amazing circle here. Keeping the same five percent, if you want to allow that, pop this down and pop that down and double it, for something to actually fall within that window, they'd have to be the same size to the base pair. So now you've just changed match criteria which is conservative and based on empirical data that we can't measure to the base pair. And now you're demanding that I narrow my match window to effectively nothing. I have to come up with the exact same base pair

estimate for it to fall within. They're one base pair apart and you moved 2.6, 2.6, you're at 5.2 plus a little bit, we're outside.

Q. But we don't know that?

A. You just said, you created this scenario and I just told you what it meant. That scenario means that our new match criteria, your new match criteria is that these fragments have to size to the base pair bang on, one thousand, one thousand, nine seventy five, nine seventy five, whatever numbers you want. But in every instance, we have to be able to do that. I told you you can't do that.

Q. What I figured I was doing was using your match criteria and showing that if you put it in favour of the accused -- rather in favour of an acquittal, rather than in favour of a conviction, this is what you'd get. If we followed your match criteria, the exclusion rate on a test like this would be, I'd say, about a hundred percent.

Q. About a hundred percent.

A. Because you're using your criteria that doesn't fit the test.

Q. So what -- you are saying that as if -- if for some reason or other, you are wrong and I am right in using this match criteria, that you may have been convicting or you may possibly have convicted a lot of people of innocent people?

A. I've been very bad if you are wrong and I am right, you're not right.

Q. That could be, that's a matter of opinion, I guess.

A. It's a matter of fact.

Q. Just to make sure we're still in the same wave link, the length of the polymorphic fragment is measured from the length it travels through the gel, the length of its migration?

A. It's estimated by that distance.

Q. So what we're doing we're assuming we know the length of one of these sites by the length it travels here?

A. The length of the chain.

Q. In the Cashwell case, page 989, oh, I'm sorry, page 981, the judge was under the impression that the restriction enzyme will cut everyone's DNA in the same place resulting in DNA fragments which are substantially the same length. Now, I understood on direct examination that you said your Hae III will cut at the site it's supposed to or close to it, did I hear correctly?

A. You might have misinterpreted it. It will either cut or it won't cut if the site is there or isn't there. If it doesn't cut at one site because the site is not there, it certainly will cut close to it because there will be a site just down the road.

Q. So you're saying if it's -- out of frustration it will cut because it can't find the place it's supposed to cut?

A. No, it will go to the next available site.

Q. Would it have to have the same base sequence in between?

A. No.

Q. So there's no way of telling how far away it will cut?

A. Where the next site will be?

Q. Where the next site?

A. Well, we can find those things out in the lab, that's just routine gene mapping, if that's the question you want to ask.

Q. As I understood your Hae III cuts between which two base pairs and in what sequence?

A. GG CC after the first G, before the second -- or after the second G before the first C, in the middle.

Q. So I'm going to see if I understand correctly, if we were going to run down the, whatever you call it, the molecule and it come to the first restriction enzyme site, it will cut, is that what you're saying?

A. If there were a GG CC it would cut.

Q. Okay, it would cut. And if you continued down and it can't find another sequence to cut at, it will cut anywhere at all?

A. No, it will -- if that's the only site in the genome, that's the only one it will cut at.

Q. That's the only one it will cut at, what do you mean it will cut at base sites or close to them?

A. Because I know how often Hae III cuts human DNA.

And I know if there isn't a site in the middle of that molecule, if we extend that molecule and continue it on as it is in the cell, there will be a site soon. You will come across a site before you go very far. There's only four bases, they can only be in so many orders, and the simple sequence GG CC, for thousands and thousands of times in the DNA molecule.

Q. I'll ask the question again, will it always cut in between those two base pairs when it's in that sequence or will it sometimes cut where it's not supposed to cut.

A. If the enzyme is used properly it will cut at the site GG CC and it will cut in the middle.

Q. How could you use an enzyme improperly?

A. Improperly, use it under the wrong conditions.

Q. What are wrong conditions?

A. Every enzyme has its own optimal conditions.

Q. You only use the enzyme, what are they for yours?

A. For ours, it's sold with the right conditions, it's sold with a buffer that will provide the environment for optimal cutting.

Q. So there's no improper conditions, that could cause your Hae III to cut where it's not supposed to?

A. These are things that you purchase, the manufacturer has already defined the optimal conditions for their enzyme to work at and it's sold as a kit, they sell you the enzymes, they sell you what to add to your DNA to bring those conditions up to optimal. The added feature of

Hae III is that if you stray from those conditions, say, salt concentration a little bit, Hae III it doesn't matter, it's a very hearty enzyme that can be subjected to a wide variety of conditions and still work properly. That's why it was selected.

Q. So it always works properly?

A. In my experience, yes.

Q. So, again, to explain what you said in direct examination, if I remember correctly, that it will cut at the site it's supposed to or nearer to it, what's your explanation again when you meant nearer to it?

A. My explanation?

Q. Yes.

A. There's thousands of Hae III's site on the DNA molecule, they're spaced fairly regularly down the molecule, if there isn't a site at one location there's going to be a site very close to that, it's the nature of that enzyme. It's the nature of its recognition sequence.

Q. Okay, I guess I misunderstood the first time, I think I understand you now. So what you're saying is it could actually bypass a site that it's supposed to cut at and not work on that site and cut at the next one?

A. That's a possibility if you didn't add enough enzyme or you didn't incubate the enzyme long enough to reach all of the sites, if you used the enzyme improperly, both of those are examples of using the enzyme improperly. It wouldn't

cleave to all of the sites, it didn't have time to find them all. If I put the enzyme in the tube and instead of leaving it in the tube for three or four hours, I left it in there for five mintues, well, it's only started its task. It will find Hae III sites, it won't find them all, you haven't given it time to operate or alternatively, if you left it in for the proper time and you didn't put enough enzyme in, it still can't do its job, it doesn't have enough workers, not enough copies of the enzyme to go around and find all those sites. Again, both of those are improper use of the enzyme.

Q. What about maybe contaminated DNA or degraded DNA might the enzyme cut where it's not supposed to or would it make any difference?

A. Well, degraded DNA, the DNA by definition is already cut up.

Q. Degraded means it's already cut up?

A. Yes, you start off with very long pieces of DNA, for instance, you push it back and forth through a syringe, it's called shearing the DNA. The DNA molecule gets physically broken, instead of an enzyme cutting it will physically break it. If you have already previously interrupted a Hae III site, well, you've broken it at the Hae III site, there's nothing for the enzyme to recognize and it won't cut at that site, you didn't give it a site to recognize, you've already broken that site.

A. The tendency for the molecule to break --

Q. For the molecule to break and for the restriction enzyme to work --

A. While it's still in your body, no.

Q. What if that molecule was diseased somewhat?

A. A mutation?

Q. A what?

A. A mutation?

Q. On mutation.

A. If you've changed the sequence of the DNA and you happen to change a Hae III site from GGCC to say, GACC, you don't have a Hae III site, you don't have a cutting.

Q. Now, I was curious you mentioned in the denaturing, the molecules, that you do that simply by heating it up.

A. You can denature it by heating it.

Q. What about a --

A. That's not the way you do it in a Southern blot, you only heat the gel.

Q. How much heat is necessary to denature?

A. It depends on the sequence. If I clarify that a little bit, if this particular sequence, was composed exclusively of GG's and CC's, the bonding between the GC pair is stronger than the bonding between AT pair. So a molecule that's, say, seventy percent of the basis are GC and a molecule where it's the opposite, seventy percent of them are AT pairs, those will have different melting co-efficients. They melt at different temperatures, because one, the bonds are stronger than the other.

Q. And what melting temperature do you use in the lab, in your protocol to denature it?

A. We don't denature by heat.

Q. You don't denature it?

A. By heat, we don't heat the gel to denature them before we transfer.

Q. How do you denature?

A. Heating is one way you can denature them a DNA molecule, an easier way to do it is to treat it with alkali.

Q. That's you do it, at the R.C.M.P.?

A. That's the way everyone does it for Southern blotting.

Q. How much heat, minimum, let's say your weakest base pairs, how much heat would it take to denature it?

A. Oh, that's a -- the minimum if it was all AT's?

Q. Well, I don't know which ones are your weakest pairs, are your AT's the weakest pairs?

A. AT is the weakest and if you had a molecule that was combined solely of AT's, you wouldn't have a viable organism. If we did have this organism with just AT's or high percentage of AT's, there's tables I'd have to go to look at that information, it's much like chemistry tables, it's not information you'd memorize.

Q. Approximately?

A. Approximately, sixty five degrees.

Q. Around sixty five?

A. Ranges like that, in that sort of temperature range.

Q. Sixty five degrees?

A. Celius.

Q. How would that have affect, say, on specimens, such as semen, blood and forensic sites, say, criminal sites when you're picking up evidence, if it's subjected to a lot of heat before hand, may it denature it?

A. Some of the studies, environmental heating, have shown it has surprising little effect, the one study that comes to mind was done in Quantico, Virginia and in greenhouses, high humidity and high heat, I can't remember exactly how high it was, it was in the summertime and it was in Quantico and it gets hot there and especially in a greenhouse, I would imagine it would be very hot. It had very little effect on their ability to get reproducible results, doing their RFLP technique on samples that they -- of known origin, so you knew what the pattern should be.

Q. But if it denatured to any degree, it would -- it might also cut the whole thing and you'd have a degraded sample?

A. That's shearing.

Q. Shearing?

A. Shearing and denaturing are totally different acts.

Q. Denature just cuts the base pairs, shearing cuts them all --

A. Yes, when you start boiling DNA you will shear it to a certain extent as well, you will denature it and shear it, that's a very harsh treatment, or extreme treatment.

Q. What about samples that are subjected to a lot of smoke?

A. What type of smoke?

Q. Bloodstains if it was subjected to a lot of smoke, could that contaminate it?

A. I have no knowledge of that particular environmental replication, people putting bloodstains in smokey rooms or whatever.

Q. Nobody has tried it. Nobody has tried this environmental insult?

A. There's an infinite number of environmental insults that people haven't tried, it's a type of experiment that if I think I've done them all, somebody is going to come up with something I haven't tried. As a scientist, they would have no effect or it would destroy the DNA or something in between.

Q. Do you know of any experiments by scientists who have found that people smoking cigarettes changes their DNA?

A. Tobocco smoke is a carcinogen.

Q. That could change the structure of the DNA?

A. Sure, in the lungs.

Q. In the lungs, and maybe get in through their whole blood system?

A. And change their whole body outlook?

Q. Yes.

A. At one particular base or whatever, it could.

Q. So it's possible that --

A. These are generally clonal effects, you're not

going to create a mutation in the lung that is going to spread to your hair follicles, your semen, your skin, all these other tissues. These tissues aren't, no, they're not clonal.

Q. But it if went through your blood system, long enough?

A. A blood cell doesn't become a skin cell or a semen cell, these are all tissues of defined lineage, you don't make a change in one and then change the whole body's complexion.

Q. No, but your blood travels throughout your whole body?

A. Yes, it's different tissue, too.

Q. Would it be possible, say, that two heavy smokers, maybe it would change the structure of their DNA in their lungs which make them similar, more similar to one another, than had they never smoked?

A. If you looked at the possibility that at one particular base pair on these people's DNA if initially, of all the three billion base pairs differing between these two unrelated individuals, three million base pairs on average difference. If in the one individual at this position you had a G and the other individual you had a C, so there are different, for the sake of argument, say, one percent difference or three million base pairs difference, of those three million differences, that's one of them, okay, a G in one a C in the other. If through

some environmental factor, such as, smoking, a mutation occurred that mutated one of the fellows to a G, so they both had a G in that position, out of their three million base pairs now they may have two million nine hundred and ninety nine thousand and ninety nine, whatever, they'd be one base pair closer to each other. So in the extreme since, yes, you've created in their lungs a very insignificant push towards similarity.

Q. Is mutation the same as adaptation?

A. Adaptation and mutation, those are evolutionary terms, they're distinct.

Q. They're distinct?

A. Yes.

Q. Could -- during an individual's lifetime could his DNA structure change in order to adapt to the society he was brought up in or would that have to be stretched over generations?

A. This is pretty much why the giraffe had the long neck for reaching for leaves. It started with a short neck when it was young and the long neck came as he had to reach higher. It really doesn't work on that sort of time scale. What generally happens and this is my understanding of my theories of evolution, your simple understanding, is that you have changes take place, some changes have no effect on an organisms ability to copes, some changes some negative effects on the organisms ability to cope and some those random changes actually enhance an organisms ability to cope in its environment. Now, if there are

selected pressures that over time, the ones who have had the mutations that enable them to cope a little better, they'll do a little better than the ones who have had neutral mutations and a little better still than the ones who have had negative mutations. This happens over generations and generations and generations in many, many mutations. These are evolutionary events in that done on the level of one generation or one individual.

Q. But it's to change at least gradually, so it's got to do some change in each generation, it can't change like that after the fifth generation, it's got to be a gradual adaptation would you agree with that?

A. That evolution goes progressively and gradually?

Q. Yes.

A. I think that's the -- you almost defined evolution that way, you know, gradual and slow and progressive changes.

Q. Just as people smoking in their lifetime, you're going to see a little bit of mutation and you could even call that adaptation maybe, couldn't you?

A. Those mutations lead to tumors and if dying is adaptive --

Q. But the DNA structure might change in order to fight it?

A. To fight the smoker, I'm sure a lot of smokers would like to think that could happen, they smoke forever and perhaps cope with it a little better, it doesn't happen, it hasn't happened yet.

Q. What about people being subjected to specific types of pollution, like coming from pulp mills, could that have the same effect as cigarette some or a greater effect on their DNA structure?

A. Those are epidemiology studies and certainly, take extreme examples like people who live around Chernobyl (phonetic) they've been exposed to radiation, radiation breaks DNA, makes changes in DNA. Those people have a higher incidents of cancer. Those people aren't adapting by being able to fight off radiation better, they're dying.

Q. So it has changed their DNA structure?

A. It's radiation, radiation penetrates a cell and it does a lot of damage including to the DNA molecule.

Q. Did it make a lot of their DNA now more similar to one another than it had been before the Chernobyl accident?

A. Again on the same level, a base pair at a time people might become one base pair more similar one one base pair more different. There's a lot of base pair differences between individuals, each mutation you draw it one closer, you know, one base pair closer when you're dealing with three million differences is arguably still different, I would think. The same thing if you drew people a little more different, they're not very much more different if they now go to three million and one base pairs difference.

Q. Could anything like that cause your Hae III to cut where it shouldn't cut?

A. The Hae III is going to cut where there's a Hae III site.

Q. And no where else?

A. If I get a radiated in my -- if I'm a smoker and I get a cancer due to a base change, let's just say a base change at a Hae III site. Normally, I have a GGCC throughout my body, the mutation that I get in my lung cell draws that to GACC. In that particular lung cell and in all the cells that result from divisions of that lung cell Hae III will no longer cut at that site. So if I biopsy my lung and take semen or blood or hair follicles from myself, because those tissues are not derived from lung cells, they never will, they're terminally differentiated cells. And I analyze that particular region on those three billion nucleui, I could detect that difference. And if I were doing an identity test to say, did that lung tumor come from the same person as that skin or blood and I took the test at face value, I'd say, no, because they have a difference.

Q. Now, what I understand for the data base system is that whatever standard of measuring error you use, say, your match window, that is also used in the data base, so applied the same --

A. In compiling the data base or using the data base?

Q. In using the data base?

A. Yes.

Q. Your window has to be at least as large or your data base bin has to be as large as your matching window?

A. That's a fact.

Q. That's fact. Again, that's a conservative measure?

A. That's the--just the system, the system is designed that way.

Q. Now, back to your bands in your match window, you do admit that when you compare two bands and call it a match that technically and realistically they could be different sizes because of your matching window?

A. Because of the technology itself.

Q. Because of the technology itself. They could actually be different sizes but yet you say they are different sizes and you put them in the same bin?

A. Could you repeat that, I think I missed something there.

Q. In VD-45, the diagram here, the fragments in Lane B and C, the top, visually they appear to be a match?

A. Correct.

Q. Realistically, they could be different sizes?

A. In actual fact they could be different sizes.

Q. And you submit because eventhough they're different sizes, if you put them in the same bin, that that is being conservative, it's prejudicial to the accused?

A. If I put them in the same bin, that would be conservative. The binning procedure itself is conservative, the fact that you put them in the bin is a function of its size. If the size is within that bin, you put it in the bin. The binning procedure itself is conservative, putting fragments into a bin is just an exercise.

Q. As described the window has a measurement of error in the system, 5.2 percent, would that be a correct analysis, that is your meaurement error or your room for error?

A. That's an expression of measurement imprecision as defined by the monomorph.

Q. What I'm concerned with is to begin with you're admitting that you could be, say, 5.2 percent in error, wrong, about declaring a match?

A. If the task was to identify to the base pair what size that fragment is then you could use the word error.

Q. Error.

A. Error implies you made a mistake.

Q. Maybe they are not the same size fragments --

A. I've been admitting this for several hours now that system is not designed to pinpoint it to the base pair and that you fully expect samples of the same size to be -- their sizes to be estimated to get different values.

Q. Okay, now, if you're relying on your theory of DNA and you're assuming that they are the same sequence, by measuring them and being the same length --

A. No, I don't --

Q. Now, you admit --

A. That the first statement before you go to the second one is false, I hadn't said that, I thought I made it, again, fairly clear that, because I size something and look at it, it's visual, that no way jumps you to the second statement that they're the exact same size and same sequence. That's somewhere where we can start.

Q. And your rule is that there could be an error there of 5.2 percent?

A. It's not an error.

Q. It's not an error.

A. It's an expression of that phenomenon I just said, you don't expect nor are you capable with this technology of defining it to the base pair.

Q. To get back to my explanation on the paper, that I drew out for you, if we say and you size, the computer sizes it at one thousand base pairs, you don't know if that's the actual length of that?

A. No.

Q. It's just a calculated guess?

A. No, if I looked at the gel and I didn't have markers on it and I knew that ten thousand was at the top and one thousand was at the bottom and I guessed eight thousand because it was near the top, that would be a calculated guess, that wouldn't even be a calculated guess, you had very little data to base that upon. This is not a haphazard, hand waving guess.

Q. I am just wondering how you calculate this room for error into the data base system?

A. I have a real problem with the word, error, error is synomyous with mistake and you're trying to do something with this technology that it wasn't designed to do nor is it expected to do and when it doesn't do what you're mistakenly say, I think it should do, you're calling it an error.

Q. Well, when you run one test, on a polymorphic-- on a monomorphic probe which is supposed to have twenty seven hundred and thirty one base pairs, and it tells you, it's got twenty seven hundred base pairs and you run another test on the same DNA sample or the same monomorphic probe and it tells you, you got twenty six hundred and fifty base pairs and you don't call that making an error, what do you call it? If the system doesn't make an error, what does it do?

A. It's not an error. I start off knowing that it's twenty seven hundred thirty one bases because I did sequence --

Q. Because you counted the darn things, right?

A. From beginning to end.

Q. Yes.

A. Now, that's the first part. If I wanted to take, say, that band was done with that probe there, and I wanted to say, and that person is a twenty seven hundred thirty one, that's the test I'd have to do, I'd have to pull that band over that paper, it's a little more complex than that,

pull that band out, put it in a tube and count them, it's a graduate thesis doing it.

Q. What I understand you to be telling me is that your system just can't get it right?

A. It's not designed to do it.

Q. No, there is room for error?

A. It's not an error, it's not designed to do that.

Q. It's not designed to do that.

A. It's designed to provide the approximate size of the fragment, not the base pair exact size. I'm not sure I can be any more clear on that.

Q. When you compare your system to another DNA lab, one of the say, private companies, Lifecodes or the FBI even, there is still quite a variation in -- not between the R.C.M.P. and the FBI but the matching window between the R.C.M.P. and say, Lifecodes, there's quite a difference, isn't there?

A. I don't know presently what their match window is. I'm not privy to all their decisions or all their data, I've never even been to Lifecodes.

Q. The R.C.M.P. has the biggest match window of all forensic labs in North America?

A. I just said I don't know what their windows are, it's pretty hard to compare ours to something, I don't know. That's facts.

Q. Have you ever thought to inquire as to what their windows?

A. I have known at various points in history what they've been using as match criteria. If you want to present, I'm not aware of what they're

doing right now, nor did I have first hand knowledge of what they were doing 1989 or 1988. They are a different company, a different lab they do things differently.

Q. Have you ever cared less about comparing your procedures with other peoples, to make sure you obtain the highest efficiency?

A. We did the necessary experiments with our system to ensure that we're obtaining the highest degree of activity or of accuracy. I'm not sure it's practical or needed for myself to sit down and evaluate whether someone else's system is doing the job that it set out to do, I was concerned with our system actually.

Q. Do you know whether or not the FBI molecular groups, Budowle.

A. Budowle.

Q. Do you know whether or not he criticized the large R.C.M.P. window?

A. I haven't talked to Bruce in quite sometime, so I'm not aware of any criticism.

Q. I understand the -- I guess I won't call it a rate of error any more for your sake but the -- in determining your match window, you've run that on pristine samples?

A. These are blood samples from the data base, yes.

Q. From the data base, they're pristine samples, they're not --

A. You'll see shortly, in the next few days that it's run on casework as well, it's been run on a lot of casework samples.

Q. And do you know whether or not, do you know how the FBI run theirs, to get their data match window, whether those are pristine samples or contaminated or case samples?

A. Again, it's not firsthand knowledge and it's not current knowledge, so I'm not sure of the value of it, but I'll give you my understanding as it was --

Q. What I've understood, you're an expert witness coming here, you rely an awful lot on hearsay and other opinion evidence?

A. I'm just qualifying what I'm going to tell you, that -- had you wanted me to give you the current and accurate information, I'd give Bruce a call in advance and find out for you. What I understood -- what I understand from when they compiled their number, which they use, they took a series of evidence samples from sexual assaults and compared the female fraction, the vaginal part of the swab, DNA from vaginal cells, they compared that to the blood standard from the victim. So you've two samples you know came from the same person. One is a forensic sample because it comes from out of a vaginal swab, the other is a pristine blood sample. You compare the two, and you look and see how far apart the bands are.

Q. And as far as you know they come up a smaller matching window than the R.C.M.P.?

A. Comparable match window.

Q. Plus the FBI also uses ethidium bromide in running their gel from the start?

A. That's my understanding, they --

Q. Which your paper said --

A. That's my understanding right now, yes.

Q. -- your paper on the use of ethidium bromide says that it can drastically cause, you know, band shifting which is unreliable?

A. Are those words in the paper?

Q. Well, something to that effect.

A. Is the word, drastically in that paper? Could I read it?

THE COURT: Which paper was that? Was that the --

WITNESS: It was published in Applied and Theoretical Electrophoresis, it was entered yesterday.

MR. WALSH: It's Agarose Gel Electrophoresis of Linear Genomic DNA in the Presence of Ethidum Bromide.

THE COURT: 38, did someone say, you did that with Dr. Fourney?

WITNESS: Yes.

THE COURT: January, 1990.

WITNESS: That was when it was published.

THE COURT: VD-38.

MR. WALSH: I have an extra copy, my lord --

THE COURT: Well, you mean, for me to look at?

MR. WALSH: Yes.

THE COURT: All right, yes.

Q. Basically, we'll find something else later, but at the top of page 195 in the right hand column the fourth line, you state that, this could result in significant deviations in the electrophoric mobilities and calculated fragment by hybridization bands detected from samples containing different amounts of the same genomic DNA, an ultimately could present problems in the identification of RFLP pattern matches?

A. Yes.

Q. Would that be correct, and that's because of excessive band shifting?

A. When I used, when the comparisons were made and this again is in the R.C.M.P. system, using our system as it existed at that time and when we did the comparison with and without we showed that band shifting did have an effect.
I described the degree of the effect, not with words like, drastically is not a good scientific term, I would be astonished if you can find that word in here in the abstract, which is summary of the paper, mobility shifts were greater than six percent. That's a scientific statement of a quanity, six percent. The degree of ethidium bromide induced shifting is proportional to the differences in the amounts of DNA being compared, well, that's just an observation we made. All these observations are true, none of them were done on the FBI system. All they were done -- the experiments were done to show that, conducting experiments

the way we were in our lab at that time, adding ethidium bromide induced band shifts and this created -- this observation was retested in many, many labs in their own systems, et cetera, some of them found exactly what we found in their system, ethidium bromide really did have an effect. Others did the tests -- and this includes the FBI, I haven't seen the published results but they actually went to town with their system, did these types of experiments and show that it didn't have a great effect in their system, doing things the way they were doing it. They certainly didn't dispute the fact that ethidium bromide can cause band shifting. The degree of it in their system wasn't significant enough to invalidate their procedure. They did the proper experiments to both confirm our observations and check to see if it was having a significant effect on their results.

Q. So when you say at the bottom of the first column on page 195, you say, in particular this practice should be avoided for forensic identity testing since the amounts of DNA being analyzed may vary substantially, example, a comparison of a small amount of DNA from a bloodstain of unknown origin to a large amount of DNA from a known standard, that the shift could be significant. But even if the shift as the FBI has it, their matching window is, as I understand it, five percent rather than 5.2 percent, so the shift is still smaller than your shift but yet you are

actually condoning the size of their size window, are you not, when you criticize the use of ethidium bromide?

A. No, I'm not.

Q. You're not, then what's the harm in them using it if they still have a smaller match window than you?

A. I have no problem with the FBI using ethidium bromide. I have a problem with adding it to our system and that's why we did the experiments and that's why we published the findings. They did experiments that showed it didn't induce significant band shifting in their system. I have no problem with that. That has nothing to do with match windows.

Q. Again, in Castro, at page 994 and 995, the Judge rightly or wrongly found that a mixing experiment would have been benefical in order to accurately determine the molecular weight of these fragments. But you say that what is it again that you say about mixing experiments?

A. They're not appropriate for forensic tests. Again, we have to put time frames on when these things happen. Castro was done several years ago, although the ruling is fairly fresh in people's mind because it made a big impact in the press, the case itself goes back quite sometime and the actual Frye hearing was quite sometime. I was with the R.C.M.P. then, so it's at least a couple of years that that happened. So all the statements in there are with reference to what was known then and the testimony in that trial

which is old testimony. And he's basing his testimony, if I recall correctly on the defence expert testimony, Dr. Eric Lander, who in his testimony there and in his subsequent opinions expressed in scientific journals stated that matching -- or mixing experiments might be a good idea for forensic samples.

Q. And you disagree?

A. He disagrees with it now.

Q. He disagrees with it now?

A. I've watched video tapes designed to train defence experts where he backs off that position, I've watched it with my own eyes, very humbly, admitting he was wrong.

Q Do you know why?

A. Why, because the forensic company being criticized in Castro actually did some experiments and showed what I had published about mixing experiments, that they're not appropriate for forensics.

Q. The problem is that DNA is affected by contamination?

A. It can be.

Q. It can be, right?

A. That's not the appropriate experiment to show it.

Q. That's not the appropriate experiment to show it, but that's the reason the FBI uses or is not using the mixing experiment, because it is going to tell you nothing because the DNA could be contaminated, and you're going to get different bands showing.

A. It's not -- the experiment doesn't do what it's designed to do. If it's intended to show that samples in separate lanes that I say migrated to the same difference, I mix them together, I should get one band. It's not -- if you design that experiment with the intention of proving that' it's a flawed experiment, it's flawed logic when you apply it to forensics.

Q. Are your experiments designed to include close matches or are they designed more to exclude accused individuals?

A. Experiments are designed to answer the question, could these have come from the same individual or not? They're designed to answer questions.

Q. And at one time it was thought that mixing experiments would be the best approach to be able to exclude an individual?

A. It was thought by that judge on the opinion of one defence expert who -- these things were all worked out in the technical working group, and we all came to the same conclusion very quick with good logic, that that's an inappropriate experiment.

Q. Right, but don't forget that Dr. Landers based his opinion that it was beneficial for mixing experiments, because all the expert witnesses for the people at that time were coming to court and claiming that contaminated DNA and degraded DNA will not show a band, it's either all or nothing and that it did not affect the migration readings?

A. And have I said that?

Q. Is that the reason that Dr. Landers expressed that opinion?

A. I have no idea what Eric's logic behind preparing that experiment was, he clearly backed down from that logic, if that was his --

Q. Does the explanation I gave you sound logically?

A. I'm a scientist, I suppose if I were a lawyer and somebody were saying something not true, two non-truths would probably balance. Scientifically the people who said these things can't affect the way DNA migrates, they were wrong. Subsequently the opinion of Dr. Lander was wrong. So you have two people or two groups of people, if that was the testimony, I know -- I'm familiar with Dr. Lander's testimony in that manner because he wrote so many articles subsequent about the testimony. If in fact that was the testimony of prosecution or defence people before him, I mean, you get it bang on or you don't get an answer, then, they were both wrong.

Q. Okay, you admit that at first expert witnesses did not think that degradation or contamination of the sample would interfere with an accurate reading of band measurement?

A. This is court testimony, there must be some sort of case we're referring to.

Q. That's all I got to go by, I'm sorry --

A. But there must be some sort of particular case that I could read and actually see what they're

saying and I'll tell you what they mean or what they don't mean, I could try to.

THE COURT: Well, you're -- could you not show the witness the sections of Castro that you have in mind here, Mr. Furlotte?

MR. FURLOTTE: I don't know if I have those particular ones noted in my book here or not.

THE COURT: Well, you are talking about page 995, 991, is it, 994?

MR. FURLOTTE: 994 and 995.

THE COURT: 994 and 995.

Q. I think Dr. Waye is quite correct, we've moved away from that problem that was in Castro or the misconception that was found in Castro, about the value of mixing experiments, but I just wanted to bring out as to -- which is not in Castro, as to why there was a misconception, that mixing experiments could benefit, that misconception is based because --

A. As I said I --

Q. -- at that time the testing of forensic samples, we did not know that contamination could affect the migration of DNA fragments, is that right?

A. I think if you wanted to be absolute again, I'm sure there's some people who thought DNA migrates, it migrates true under all circumstances or it doesn't migrate at all. I have no doubts in my mind, myself, that there were scientists, forensic scientists, myself included at that time who didn't have that view. I wasn't giving testimony before the judge in Castro,

so if all the experts came up with the view that DNA actually runs like that cardboard schematic, that's neither representation of the views of all the scientists in forensics, nor is it accurate.

Q. Do you know which view now is generally accepted in the scientific community?

A. Well, the word band shift has come into our vocabularies, people --

Q. But in the early cases, there was no such thing as band shift according to the experts, is that right, they denied band shifting occurring, that could affect --

A. Globally, they, all the experts thought band shifts --

Q. Globally, and say, the first -- maybe even before, maybe all the ones before Castro.

A. As I said just a minute ago, there may very well have been scientists and lawyers that oversimplified the matter and thought that yes, DNA runs perfect and I can size it to the base pairs and had all of these misconceptions. There certainly were people, myself included at that time who knew that you can't take perfect migration as a given, and the word band shift was coined in the courtroom. I'm not sure of the instance that band shifting all of a sudden became common, that argument by defence certainly became very common. It still is common, we're doing it now.

Q. Would you say that band shifting can cause false positives?

A. No. If the test is interpreted properly and the possibility of band shift is recognized and you have tests to confirm or reject your hypothesis of band shifting, I think your biggest danger is taking a match and calling it inconclusive.

Q. Let me put a hypothetical to you, if you had a band from a known sample and you had a band from an unknown sample, and they differentiated by four percent and you checked your monomorphic probe and you found out there was only a band shift of two percent, you are now left with a two percent differential between these two bands do you call that an inclusion, an exclusive or inconclusive?

A. What do the bands look like?

Q. Does it matter?

A. It does, it certainly matters.

Q. Why?

A. You've given me sizing data again, we don't do this experiment blind with just sizing data, you use your eyes first.

Q. Why can't you use sizing data to the benefit of the individual if you want to be conservative?

A. I don't believe that's the way to be conservative nor do I think you've explained that to me today either through your schematic or otherwise.

Q. It appears to me that your interpretation and the way you want to interpret autorads, you interpret it favourably for inconclusion rather than

exclusion. And yet on the other hand, you're always saying, we are being conservative, we're always giving the benefit of the doubt to the individual. You can't have it both ways.

A. I'm not favouring one interpretation over the other. Maybe what you're misunderstanding what I mean by inconclusive. Inconclusive doesn't mean, I can't call a match but I still think he did it. It means I can't make a call.

Q. Or you don't want to call an exclusion?

A. I shouldn't be here, because I scientifically can't justify an exclusion. I can justify an exclusion, looking at it I convince myself it's an exclusion. That's in every test, most -- an analyst will say that's the result you want, the testing stops there, generally, you don't go to court and nobody argues the validity of the test.

Q. There's no problem for a heterozygote, who has two bands for them to be less than five percent apart in different size, is that correct, that's quite possible, it might only even be two percent, they're different but they're only a two percent difference?

A. I'm comparing samples from two -- in two lanes, both of them are two banded patterns and both of those bands are two percent off, is that what you just --

Q. Well, no, I'm not saying two lanes, I'm just saying in the one lane, you could show in the one lane, a person, heterozygote shows two bands, they're only about two percent apart and it's quite visual that they are separate and individual bands?

A. There's regions in the gel, two percent is pretty close but I'll give you that.

Q. You'll give me that.

A. If I -- I'd have to alter the way we do things but you know, two percent.

Q. So when you can show bands that are two percent apart --

A. These are their actual sizes.

Q. These are your actual -- well, no, I can only go by the sizings that you would put -- what the computer would put, because we don't know what the actual sizes are.

A. So I'm just trying to get your example straight in my mind, you got two bands, you can see daylight between them, they're in the same lane, the computer says they're two percent different.

Q. Right.

A. Got you.

Q. And if those two bands were in opposite lanes, you would probably say they are identical?

A. No.

Q. You would probably call them a match?

A. A visual match, yes, if they look like a visual match, I'd call them a visual match.

Q. You would not exclude or you would not exclude the individual eventhough -- if you put them in the same lane, you would say, it's an exclusion, they're definitely different sizes, so it can't come from the same individual, if they're in the same lane, in a mixing experiment where there was no contamination, we didn't have to worry

about it, we're dealing with pristine samples, they're definitely two different bands.

A. And you're only capable of doing one probing, because that's the extreme situation you're giving me here, you're giving me the extreme example of samples from two individuals that are different but the differences are so small that I can't see.

Q. Right.

A. That's quite realistic, we keep harping back to the fact that the bands may look the same, may actually be fifty base pairs difference and I will say, they're the same, then I tag a frequency to it, which details the significance of that and it's a conservative significance, recognizing the fact that I don't have that ability to do base pair discrimination, they could be different.

Q. What I'm getting at, Dr. Waye, is again showing how far removed you're getting away from the theory about DNA being, you know, totally different for everybody, how you're relying on that theory to show that, well, the fragments are either the same in sequence or the same in length, now, you know that they don't have to be the same length in order to call them a match, but you're just using the binning frequency in order to calculate the frequency of your different matches?

A. I'm using binning so myself as an investigator, when I put a frequency of these, I don't --

through this measurement imprecision, attribute a very rare event to in fact the common fragment length, I just happen to migrate a little bit off, I don't want to put undue bias on my call of a match and that's the sole purpose of that.

Q. When you're gathering the criteria or the empirical data to put into your bin, you're using an awful lot of assumptions, aren't you?

A. Such as?

Q. You're assuming they're the same length, you're assuming they're the same sequence.

A. Those assumptions aren't made.

Q. We know we have --

A. You've been making those assumptions all afternoon that visual matches are the same length and the same sequence and I've been denying it all afternoon. So I'm certainly not going to admit that that's the assumption you make when you put something into a bin, it's not true, it could be.

Q. It could be?

A. If they're from the same individual, that's why we use the word could for inclusions. And again, if we were doing what you seem to want us to do is actually analyze the precise length by counting them up, then we'd be coming in with statements like, it wouldn't be could, it would be is.

Q. They could also be from different individuals?

A. Either way it would be definitive, it came from or didn't, you wouldn't be using the word could.

Q. If you're going to look at each individual probe, is there any way that you can draw some kind of calculation as to, like you said, it could be

from different individuals, I'm trying to think percentage wise, would you say there's one percent chance, it could be from different individuals --

A. It depends --

Q. -- or would it go up to your matching window of 5.2 percent chance, could you go that far?

A. You've really lost me there. When I want to determine the likelihood of someone else fortuitiously having bands that migrate to the same region of the gel and match this other sample, I have to first know the size of those bands, that's why we size them in the first place, we can -- you have to put a size to it so you can go to your data base and say, how often have I seen something in that size or within that bin where that size falls. That's the real value of sizing.

Q. You've got to, at least from my point of view, I want to look at it from the other way around, you're looking as to how you can calculate conclusions, I want to see how you can calculate exclusions, which is reasonable, is it not? If it's possible that I can figure out, there's an exclusion here, then I should try to figure it out?

A. The probability --

Q. If I can argue against your --

A. The probability of an exclusion, this is what we're getting at.

Q. Well, you could normally.

A. In a sample like, we'll go back to the old example here, B and D, I look at it and I say, exclusion, you want me to say how likely that's an exclusion?

Q. Yes, how likely is this an exclusion?

A. It's an exclusion.

Q. It's an exclusion period, a hundred percent?

A. It's absolute, and then when I go to the next probe, I'll show you again. At any one point at that probe where I got a match, it's not going to diminish the impact but it's not going to say, well, it's four fifths of an exclusion, four of them excluded, one match, I think that's what you're getting at, that doesn't diminish that at all.

Q. All I've been getting at, is you can't eventhough this constitutes a match, because visually it's the same, you admit that you don't know whether those base pair lengths are the same or not?

A. Which is why I don't say they're the same.

Q. And you don't know whether or not they come from the same individual. There's a chance that they don't?

A. When you have a match like that, that's why I say, it's consistent with coming from the same individual.

Q. Consistent, right.

A. And we put numbers like one in fifty to that consistency.

Q. I want to get back to the uselessness of mixed samples or mixed runs, because now we know they're

not useful because contamination and degradation causes band shifting?

A. That's only one reason.

Q. What's the one?

A. No, that's only one reason.

Q. Yes, well, let's take it a stage --

A. That's a logical reason, there's practical concerns as well.

Q. But that is one reason, that's a valid reason, We now know that degradation and contamination causes band shifting?

A. Can cause band shifting.

Q. Can cause band shifting. To what degree?

A. Those are things you can't predict. It's not going to move bands, it's not going to create the picture that I just showed you in Lane B and Lane D.

Q. Are you able to determine how much band shifting was caused by either degradation or the contamination through your monomorphic probe?

A. I can tell you approximately the magnitude of the band shifting, I can tell you the direction of the band shifting through the use of monomorphic probe. I can't tell you if it's twenty one base pairs or twenty six base pairs.

Q. But percentage wise you have a rough estimate?

A. If you ask me to comment on the band shift of a particular fragment I may be able to through the use of monomorphs give you an idea of the direction and magnitude, not precisely but an idea.

Q. Even your monomorphic probe to adjust for band shifting or to recognize band shifting, is that consistent and reproducive?

A. The monomorphic probe?

Q. Yes.

A. To recognize band shifting?

Q. To recognize band shifting, how valid is it?

A. It was in fact used to characterize and demonstrate band shifting in this paper where you have all the variables controlled, without ethidium bromide the monomorphic probe gives you --

Q. Even that has not had its rigorous testing in the scientific community to either accept or reject it, has it?

A. The experiments were done rigorously, the peer reviewers had no problems with the science and it's published. And it's been in publication for quite sometime and I haven't heard any dissenting views. It has gone through the normal peer review and I think the experiments were done rigorously, and they reflect reality.

Q. And who pays attention to these peer reviews, just the forensic science of DNA testing or everybody in general?

A. The journal is called Biotechniques and the journal is available to anyone who wants to buy it. In fact the United States subscription is nothing, so a lot of people -- it's one of the journals that has one of the higher subscription rates and it's in no way limited to forensic scientists, molecular genetists, and molecular

biologists in general, it's a technical magazine for how to work with DNA and how to work with proteins and how to work with biological molecules. Which is why I had to put forensics in the title to focus that audience.

Q. What other things or factors can cause band shifting besides degradation and contamination of the sample?

A. We've covered two fairly global causes there, do you want the sub causes of that?

Q. No, no, not --

A. Contaminated with what --

Q. The different kinds of contamination that would cause different degrees of band shifting?

A. Well, certainly any dye that mimics the action of something like ethidium bromide, so dyes that either bind or intercalate between the strands of DNA I would predict could mimic these factors.

Q. The viscosity of the gel?

A. The viscosity of the gel?

Q. Could that cause band shifting?

A. I never really heard the phrase, viscosity used.

Q. Well, maybe I'm using an improper term.

A. When I think of something viscous I think of honey or something like that, a thick liquid, the gel is actually solid.

Q. I'm thinking of the thickness or the ability of -- at which viscosity, the ability it will run itself or something will run through it?

A. So you're talking maybe the concentration of the gel?

Q. Concentration, if you want to use that word, that could cause -- be a factor in band shifting?

A. You could have band shifts be minimized or increased depending on the concentration of your gel, the length of your gel, your electrophoretic conditions. Again, that is where I was harkening back to the FBI's procedures. It's not identical to us, in fact, although the gel dimensions and things are the same, there's different types of gels that they use, different manufacturers, that's just one example there. You can call it gel viscosity or gel supply or gel concentration, you may see what I call significant or up to six percent band shifts, the way we were doing it, they tried to replicate a lot of these experiments in their system, with some minor adjustments and those shifts were minimized.

Q. You've had -- you say up to six percent band shifting.

A. This particular paper when we did the control experiment, to demonstrate band shifting, to try to understand causes of the band shifting in relation to ethidium bromide, six percent was the maximum in this particular set of experiments.

Q. I am going to try to move away from this topic. To use an example, VD-51, again, two bars which I have at roughly 5.2 percent apart from one another. Now, if you had two bands, one that was measured at a thousand, and say, the other one was measured at nine hundred rather than ninety fifty, it would be well outside your matching window?

A. Correct.

Q. It would be roughly ten percent out rather than 5.2?

A. That's correct.

Q. And on your monomorphic probe, your band shifting states that it's shifted maybe two percent.

A. Okay.

Q. That would still not be enough to bring you into your matching window?

A. I wouldn't try to correct -- again, you're playing Lifecodes.

Q. I'm playing Lifecodes system.

A. How I understand it?

Q. That's improper.

A. I don't use that system and I don't prescribe by that logic.

Q. Well, is it logical or illogical?

A. For the fragment sizes you're doing there, it's not good scientific practice to try to correct that. It certainly isn't going to do your client any favours. You're trying to force a match from something that visually doesn't look like a match, nor does the computer size it as a match. The prudent thing to do is to call it inconclusive, whether you think it's a band shift or not.

Q. Okay, then, from what I understand is that if you can visually see that there is a difference, regardless as to how close they are, the computer says how close they are, if you can visually see a difference, you will call it inconclusive, is that right?

A. The point is and I know this through both extensive work with pristine samples and casework samples, is that if my eyes tell me that these things are not the same, the computer is going to tell me the exact same thing. Conversely, my eyes will often, not often but my eyes can sometimes tell me that these things look bang on, the computer will sometimes tell me I don't think so, they're outside my window.

Q. So in those cases you rely on your eyesight and the computer is out to lunch?

A. No, as a scientist and between you and me, or anyone who wanted to know, my opinion would be that we're still dealing with a match. As somebody presenting that data to the court, it's outside of the criteria, I call it inconclusive, eventhough I'm convinced it's still a match.

THE COURT: Haven't we spent just about as much time on that topic as it warrants, Mr. Furlotte?

Q. Now, I understand that contaminated samples or contaminated probes or controls may produce extra bands on the autorads which can cause different scientific opinions in the interpretation of the autorads? Am I to understand that --

A. Which one of those --

Q. -- you've eliminated that problem?

A. Which one of those, you've listed a number of things there that would give spurious bands.

Q. Okay, let's just go back -- let's start with contaminated samples.

A. Correct.

Q. Can they cause extra bands on a autorad --

A. Define --

Q. -- in a lane, say, you're going to get three or five bands instead of two?

A. You'd have to define the nature of the contamination. Environmental contamination, such as mixing household cleaners or things like that, you're not adding any DNA to the sample, you're not going to alter the patterns that you get, you're not going to create extra bands.

Q. You won't alter the patterns that you'd normally get from the human DNA, but you'd just end up with extra bands, is that it?

A. Other than -- other than what we've been talking about, realizing the fact that some of these factors can cause band shifts. The same factors, environmental contaminates, increasing salt, et cetera aren't going to take a two band pattern and make it a four band pattern, not in my experiments.

Q. Not in your experiments.

A. That's a fact.

Q. But you will admit that contaminated samples can give you extra bands?

A. If I mix two different DNA's, so I have contaminated one of those DNA's, actually I contaminated both by mixing them, say, a DNA sample of multiple origins, if you assume it's a single origin, you're dealing with a contaminated sample, if you then hybridize with a probe, the probe is going to detect both

samples and you'll get extra bands, they're not extra, you're just detecting what you're analyzing.

Q. Now, could some of those extra bands be non-human?

A. If you have gross amounts of non-human DNA in your sample and I showed a quantification sample yesterday where probably ninety nine percent of the DNA was non-human. I detected both the human band that matched the victim and I also detected a blackening or a smearing of bands below that, non-specific hybridization to a bulk of DNA that was non-human, not a band, a smear, a black smear.

Q. So when you read an autorad, it's -- you're saying it's not difficult to distinguish between human DNA bands and bands that are caused by non-human DNA?

A. We call that non-specific hybridization, you just have so much of this foreign target DNA there that a small amount of probe binding to it, relative to your human signal will be significant, you can detect it. The thing is, it's non-specific, you go to the next probe and you'll see the same smear, it has nothing to do with the probe, it has to do with subjecting that target to radioactivity.

Q. Why does the probe stick to this, it's a honing- isn't it a honing device for specific base sequences in human DNA?

A. We talk in absolutes. There is nothing absolute in biology, not one hundred percent of those

probe molecules are going to go to one hundred percent of the target molecules. There's going to be a lot of excess probe floating around in that bag, some of it will go on the membrane, sometimes you get a blotch, sometimes it will bind non specifically to background DNA and you get a smear in the lane, you don't get a non-specific band, you get a smear, these are things that as an analyst or anyone familiar with hybridization are factors that -- these types of samples or even pristine samples, depending on how you analyze them, you can have.

Q. Then if you got extremely light bands in a lane, sometimes it might be difficult whether the probes are hybridizing to human DNA or just something else that's there, some contaminate?

A. Some contaminating, non-human DNA.

Q. Yes.

A. If you had extremely faint bands in the lane and what, you'd likely get if it's non-human DNA, what I've seen in my experiments, not discreet bands, you get an increased background in that lane.

Q. I understand there's also sometimes the probes themselves are contaminated?

A. The probes?

Q. Yes.

A. There is --like anything you buy, there's always the potential if someone else made it or if you made it and you're incompetent, they could either mix two probes together or send you the wrong probe or some sort of scenario like that. The

point mixing two probes together is a form of contaminating the probe. And then you sell it to somebody and he uses it, yes, he's using a contaminated probe. There's controls that monitor those types of things.

Q. You have controls to find out whether the probes you buy from the different companies are contaminated or not?

A. Yes.

Q. What kind of controls do you have?

A. On every experiment you analyze a male and female control DNA and you know the pattern that you will get with that particular probe. If that sent you that probe contaminated with another probe, I'll get that pattern plus whatever that other probe is supposed to hybridize to. I don't get the expected result, hence the probe is contaminated.

Q. So when you say a probe is contaminated actually you're getting a mixture of different probes, is that what you're getting in the batch?

A. I've never received a contaminated probe. But again in Castro, when discovery or this is how I believe it worked, when discovery was made and they started going through lab notes, they realized that Lifecodes at one point in their operation had contaminated a probe and sold it to somebody.

Q. And you still get -- the R.C.M.P. when you were there, you were buying probes from Lifecodes?

A. We purchased one of our probes from Lifecodes. and again, tested it, tested each lot ourselves

and tested it in fact as an internal control in each experiment.

Q. Which probe was that that you bought from Lifecode?

A. D17S79.

Q. D17S79?

A. They're the sole supplier of it, whether you like Lifecodes or not, if you want to use that probe you have to buy it from them.

Q. Would you agree that if you discovered that a probe had been contaminated that the proper thing would be to discontinue its use right away?

A. If I did the appropriate test and demonstrated that it was contaminated I wouldn't use it in any study that I was going to try to interpret the results, I wouldn't use it in casework, I wouldn't use it in population --

Q. You wouldn't try to interpret the results?

A. I'd send it back and I'd ask for the product to be -- a new vial to be sent to me. I'd certainly bring it up to the company exactly what I found and why I believed it was so.

Q. Did I understand your direct testimony correct that you were able to analyze your DNA to find out if there was any bacterial contamination?

A. I used --

Q. The probe that you personally developed to detect whether human DNA is there and how much?

A. I used bacterial as an example, the correct thing would be to analyze specifically how much human there is and whatever else is there, unless you know something about the history of that

subject, you're just speculating what it is. I use -- I'm dealing with something, say, that comes from a rectum as was that example, bacteria is a good guess for the non-human DNA. A poor guess would maybe gorilla DNA.

MR. FURLOTTE: My lord, how late do you intend to go on?

THE COURT: Oh, nine o'clock, how long are you going to take?

MR. FURLOTTE: I can guarantee you, I won't be finished by nine o'clock.

THE COURT: Well, I was sort of hoping you might be approaching the end of this. But you're going to take some time yet, are you?

MR. FURLOTTE: I think I advised my lord when I asked for an adjournment that I had a thousand questions for these witnesses and I don't think I hardly covered a thousand yet.

THE COURT: You haven't used a thousand because you've repeated some of them quite frequently. I don't mean to be critical but I--

MR. FURLOTTE: No, but I have to get an understanding, like I say it's difficult for Dr. Waye and I to communicate on the same level. I have to try and understand this stuff as much as possible, so I can present a half decent argument at the end.

THE COURT: Well, I think we'd better adjourn now, the Crown don't feel desirable to press on any longer tonight, you would prefer to adjourn now, you must be tired?

MR. FURLOTTE: Well, I'm getting tired. I could spend three hours here and probably get about an hour's work that I could do tomorrow because of the tiredness, it just doesn't work, it's called burnout.

THE COURT: Well, if you promise not to get your second wind overnight, we'll adjourn now until 9:30 and go on then.

What is the -- you will want an opportunity to have re-examination?

MR. WALSH: Yes, my lord.

THE COURT: Briefly, hopefully.

MR. WALSH: Up to this point in time I wouldn't expect that my -- up until this stage I wouldn't expect my re-examination would be very long. I tell you what is concerning me, my lord and I would ask the Court to give consideration to it. is that as I've pointed out, I have Dr. Kidd coming and he must get on the stand Monday morning, because it's absolutely imperative, there was another telex today, that he be able to leave Tuesday evening. As a result it's important for the evidence of Dr. Bowen to be in, in advance of, the case specific evidence go in before Dr. Kidd. I am going to ask the Court to give some consideration to sitting on Saturday. So that we will b able to get through Dr. Waye and Dr. Bowen, so that on Monday morning Dr. Kidd could begin his testimony.

THE COURT: Well, how are we -- you say you may have an hour at best, a window, give me a window?

MR. FURLOTTE: I say there is no way that I can be finished by nine o'clock. You suggested maybe I'd be finished at nine.

THE COURT: Oh, well, I--

MR. FURLOTTE: I'm not suggesting that my cross examination is only going to take another three hours and far from it. I don't have a clue how long my cross examination is going to take. As I told Mr. Walsh --

THE COURT: Presumably, you have a plan, there are certain things you want to bring out in cross examination of this witness.

MR. FURLOTTE: As I tried to explain to the Court when I asked for the adjournment to finish preparation on this that I had organized all my material and I took it and I condensed it down into these brown volumes here, and I would have liked to have had more time to condense it again to narrow my questions down to save a lot of time in court. But since I haven't had that, then I am going to have to fumble through, I think I warned the Court when I asked for the adjournment that it would take considerable -- the court procedure was going to take considerable amounts of time because I don't consider myself to be adequately prepared.

THE COURT: Well, your hope of getting Dr. Bowen on tomorrow doesn't seem very good, Mr. Walsh.

MR. WALSH: No, it doesn't, my lord, but I had Saturday, I'd have a chance of putting him on and I expect once I can get him on the stand, I

can get enough evidence in that when Dr. Kidd testifies on Monday morning, it will be a logical progression. I could always -- in that eventuality stand Dr. Bowen aside until after Dr. Kidd testifies. He's the one person, my lord that I'm fixed to a time slot with him. I have no cushion available.

THE COURT: Dr. who is it on Monday, Kidd?

MR. WALSH: Dr. Kidd.

THE COURT: How long is his direct examination likely to take?

MR. WALSH: My lord, again, at the risk of being wrong, I would hope that I would be able to complete his direct examination within a half a day. You know, there's not going to be any need for the Crown to redo a lot of what Dr. Waye has done and that is the biology lesson, the technique but it will important for Dr. Kidd to comment or give opinions on some of the aspects. I am hoping, never having done this before, I'm hoping that I can do it in half a day. That will allow Mr. Furlotte sufficient time should he decide to -- it will give him lots of time to cross examine Dr. Kidd.

THE COURT: Well, I mean -- surely, there will be another day and a half that he would be available, if necessary, well, surely, cross examination couldn't possible take a day and a half.

MR. FURLOTTE: At this time, I can't see myself being less than another full day with Dr. Waye,

and then again, it might be longer than that, too, there's no way I can tell.

MR. WALSH: Perhaps I would then ask the Court if it would consider Saturday.

THE COURT: Well, I think we should, I think that's a fair request, Mr. Furlotte, if we sit on Saturday. As a matter of fact Mr. Ryan had mentioned it this morning to me, the possibility of sitting on Saturday on the telephone. I have -- earlier, I haven't mentioned it or discussed it with anyone, I did feel that, I knew the Crown's sequence of witnesses was being thrown out by delaying two days this week. And I thought that perhaps that time could be made up where you could be put back on program by sitting on Saturday, I hadn't brought it up to anyone.

MR. WALSH: I had it in mind, my lord, anything. that we could do to facilitate the calling of the evidence. I have no problem with sitting on Saturday.

THE COURT: You've got Dr. Bowen here, have you --

MR. FURLOTTE: The only objection I would have to sitting on Saturday, it takes one more day away from my ability to prepare properly and adequately for this trial.

THE COURT: Well, I don't want to get back and harp on it but we're still four and a half months from the time when it started, as a matter of fact it's five months now.

MR. FURLOTTE: I would like to point out, my lord that the Bourguignon that the defence had nine months to prepare for his and I only got half his time.

THE COURT: How long were you cross examined on the Bourguignon case, Dr. Waye?

WITNESS: On the voir dire?

THE COURT: Well, yes, how long did the voir dire take, it only took four days was it, altogether, all of the witnesses, I don't know how many there were?

WITNESS: For DNA, I believe it was a week.

THE COURT: A week and you testified, did you testify for more than a day?

WITNESS: I testified in direct for a day and I believe two and a half days in cross.

THE COURT: In cross examination?

WITNESS: Or one and a half days, I can't quite recall.

THE COURT: And then you were -- well, everything was admitted essentially except certain population statistics evidence apparently at trial. You testified at trial there, did you?

WITNESS: Yes.

THE COURT: How long did you -- at the trial, the DNA evidence at trial didn't take more than two days, did it, altogether?

WITNESS: Direct and cross were two days, yes.

THE COURT: Direct and cross. Were you the only witness, were there other witnesses, were there?

WITNESS: In the voir dire there was one more crown witness on statistics and the defence had a witness as well.

THE COURT: And at trial you were --

WITNESS: I was the sole witness for the DNA.

THE COURT: You were the sole witness. But the defence witness testified at trial as well?

WITNESS: No, he did not.

MR. WALSH: My lord, I may have a suggestion to offer to the Court and to Mr. Furlotte. The importance of getting Dr. Bowen on is that Dr. Bowen is going to introduce the case's specific evidence, he did the testing and he's going to introduce it. What he would be introducing would be the autorads, the actual results of the test. Now, what we could perhaps reach a compromise and that would free up --

MR. FURLOTTE: Maybe half a day.

MR. WALSH: Well, we could free up, Mr. Furlotte perhaps is to mark -- enter the autorads and I have prepared a list as I indicated at the opening in which I have indicated what lanes go into what -- what substance applies to what lanes. Now, mind you, this is for the voir dire only. Then, Dr. Kidd would be actually to actually testify with respect to the autorads and Dr. Bowen would follow Dr. Kidd and then Mr. Furlotte would have a right to cross examine Dr. Bowen on his testing. But since the autorads as I understand it, are a memorialization of the

testing procedure and he has access to Dr. Bowen's notes and things of that nature, Dr. Kidd could talk about the case specific evidence and then we could follow it with Dr. Bowen.

THE COURT: By agreement or by calling Dr. Bowen briefly to introduce them.

MR. WALSH: I could either call Dr. Bowen briefly to introduce them or just enter it with agreement and then we could do it --

MR. FURLOTTE: What if we put on Dr. Waye tomorrow morning, we put on Dr. Bowen in the afternoon to get done what you want to do and we'll stand Dr. Waye aside for cross examination and have Dr. Kidd on Monday and then after Dr. Kidd is finished, I continue on with cross examination of Dr. Waye.

MR. WALSH: See, Dr. Waye is going to be recalled but he has commitments, Dr. Waye has commitments he wouldn't have expected to be here over the weekend, he's not expected to be recalled back until the end of next week or at least the middle of next week.

THE COURT: Let's do this, we will go on with Dr. Waye tomorrow morning, you get as far as you can with him tomorrow morning. Tomorrow afternoon we will put Dr. Bowen on, you do all your -- why don't you do all your direct examination of Dr. Bowen tomorrow afternoon. On Saturday morning we will continue and hopefully conclude with -- I don't know what that does to Dr. Waye's family life, what it does with his family life or weekend plans. Hopefully, we

could perhaps finish with Dr. Waye on Saturday and that would be the end of his evidence at this stage.

MR. WALSH: Perhaps if I could have one more suggestion, there might be something that we could agree on. If, for example, we went --

MR. FURLOTTE: You planned on bringing Dr. Waye back next week in the middle of the week anyway? I probably wouldn't be ready for him until that time anyway once we have Dr. Kidd on Monday.

THE COURT: Why not complete all your cross examination at that time, defer it?

MR. FURLOTTE: There is no guarantee I can.

THE COURT: Pardon.

MR. FURLOTTE: There is no guarantee I can complete all his testimony even if we sit Saturday.

THE COURT: Oh, no, no but I mean why not let it go, why don't you let Dr. Waye come back you're going to call him again after Dr. Kidd has testified.

MR. WALSH: Yes, perhaps what we could do if we could reach this compromise. Since Dr. Bowen is planning on being here throughout, Dr. Waye, you know, he has other commitments, if we could finish, at least this part of the cross examination either today or tomorrow morning or noontime tomorrow.

MR. FURLOTTE: No way, I am going to have at least another day.

MR. WALSH: He's going to be recalled in any event and you could continue your cross examination when he's recalled next week. And that would

give me a chance to put Dr. Bowen on, get at least some of Dr. Bowen's -- get through some of his testimony tomorrow afternoon and he's going to be recalled after Dr. Kidd, that will free up for Mr. Furlotte and he will still have the ability to cross examine both Dr. Bowen and Dr. Waye when they're recalled. And that would facilitate me putting Dr. Kidd on.

THE COURT: It might even be -- how long is Dr. Waye going to be on direct examination in the second phase of his testimony?

MR. WALSH: Again, I would not expect to be very long, I would expect a couple of hours would probably do it.

THE COURT: It might even be that that could be done after Dr. Kidd finishes, in that sequence.

MR. FURLOTTE: I would prefer to finish cross examination of Dr. Waye as soon as Dr. Kidd finishes which will definitely be in the middle of the week anyway.

THE COURT: Well, that's all right, do all your cross examination together of Dr. Waye. Why don't you let him do his two hours additional direct and then do the whole thing, finish this off and do the other thing, because the temptation is going to be awful --

MR. FURLOTTE: I have to see how far I get in this, I don't want you sleeping on his, what I will call, misconceptions too long before I get a crack at him.

MR. WALSH: My lord, I have no problem, again, to facilitate the Court, and with a voir dire and

experts like this, this was to be expected, if we could agree as you indicated to finish with Dr. Waye as far as Mr. Furlotte wishes to go, say, noontime tomorrow, stand him aside, he's stood aside anyway. We can recall him, I would like to recall him about the middle of next week, that would meet Dr. Waye's plans or his scheduling. I would put Dr. Bowen on Friday afternoon, go through Dr. Bowen until -- as far as we can go on Friday afternoon.

THE COURT: Would you suggest might see him through his direct?

MR. WALSH: I'm not sure, I don't think so. But we could stand him aside, call Dr. Kidd Monday morning, go through the direct and cross examination of Dr. Kidd and I would like to call Dr. Carmody and then I'll recall Dr. Waye. Mr. Furlotte-- we'd finish his redirect and his direct -- Mr. Furlotte could finish his cross examination and then I can recall Dr. Bowen.

MR. FURLOTTE: I think I would like to have Dr. Waye back on before you call Dr. Carmody.

MR. WALSH: Before Dr. Carmody.

MR. FURLOTTE: Yes.

MR. WALSH: I'll see what I can do for -- I'll see what I can do, I might be able to work something out that way. I don't want to be committed to that though, because Dr. Waye is -- I have a schedule for Dr. Carmody, I have a schedule for Dr. Waye and I'm trying to juggle a lot of --

THE COURT: Well, we'll hear you on that, Mr. Furlotte and I don't want to get these things jumping back and forth from one witness any more than we have. I would like to get one witness out of the way, but at the same time some regard has got to be had for the Crown's scheduling of these witnesses.

Let's go as far as we are now and the first of the week we'll consider what to do about Carmody and Dr. Waye's completion of his cross examination and so on.

So tomorrow morning Dr. Waye's cross examination is completed or is not completed, is proceeded with, is continued.

Tomorrow afternoon and we may stop about twelve o'clock perhaps, tomorrow is Friday, we'll stop at about twelve o'clock and perhaps one o'clock resume and start with Dr. Bowen at say, one o'clock tomorrow afternoon and that will give you a pretty full afternoon if you want to take it all, and get as far as you can with him, and then we'll go over until Monday morning and do Dr. Kidd on Monday morning and see where we go from there.

So we'll recess now.

COURT ADJOURNS AT 6:10 P.M., MAY 2ND, 1991

DATED THIS 15TH DAY OF MAY, A.D. 1991

I, Nilah M. Amos, do hereby certify this to be a correct transcription of my shorthand of this evidence and proceedings to the best of my skill and ability.

Nilah M. Amos

Court Reporter