VOLUME VIII

IN THE COURT OF QUEEN'S BENCH OF NEW BRUNSWICK

TRIAL DIVISION

JUDICIAL DISTRICT OF FREDERICTON

BETWEEN:

HER MAJESTY THE QUEEN

- and -

ALLAN J. LEGERE

VOIR DIRE held before Honourable Mr. Justice David M. Dickson at Burton, New Brunswick, on the 7th and 8th days of May, 1991.

APPEARANCES:

Anthony Allman, Esq., and John Walsh, Esq.,) for the Crown.

Weldon Furlotte, Esq., and Michael A. A. Ryan, Esq.,) for the Accused.

VERNA PETERSON
COURT REPORTER

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LIST OF EXHIBITS

(COURT RESUMES AT 9:30 a.m., MAY 7, 1991.)

(ACCUSED IN DOCK.)

DR. GEORGE CARMODY RESUMES STAND:

THE COURT: Now, we're all set again, the same counsel present, accused present. Just before you resume cross-examination, Mr. Furlotte, I might just allude briefly to a point that Mr. Walsh had raised yesterday, and that was he pointed out that this witness has been declared an expert in the field of population genetics, I believe it was described as, and I believe the direct examination was confined by and large to the field of population genetics, at least as I appreciated the questions. The objection was raised that perhaps some of the cross-examination might be getting to other fields. Now, it's very difficult, of course, to define the parameters of a field of expertise like population genetics. There's certainly an overflow from - of expertise from one field to another, but once a witness, of course, gets on a stand, even though he's qualified as an expert in a particular field he's fair game then, or at least he's open, I won't say fair game - he's open to cross-examination in any matter at all. You know, for instance, the fact that this witness had been involved in one of the incidents involved in these alleged crimes he could be examined on that, but if opinions are to be sought or views are to be sought in fields other than that for which he's qualified it would first have to be established that he is an expert in that field. I think this was the point - well, I don't know whether this was

the point you were making yesterday but it's related to the point you were making.

MR. WALSH: That is in fact the point I was trying to make, My Lord, yes.

THE COURT: Yes, and I can only say that Dr. Carmody, of course, if he feels that questions are getting outside the bounds of his particular field of expertise, we have to rely on him to say, "Well, look, that isn't within my field", and that sort of puts an end to that type of - that question, unless he can be established as having a broader range of expertise than he has. I'm just making this point generally, this is not in criticism, it's just more of a reminder, Mr. Furlotte.

MR. FURLOTTE: My Lord, I believe the Crown admitted yesterday that Dr. Carmody was - although he wasn't declared as an expert for the purposes of court proceedings the testimony he's given on direct evidence, he's an expert in the field of molecular biology. I believe the Crown has admitted that, in fact, he is an expert in that field also.

THE COURT: Well, is that admitted or - whether it's admitted or not I think the rule is that the Court has to be satisfied that he is and you have to put those questions to him, but go ahead and answer that question.

MR. WALSH: I asked the Court to have him declared an expert in the field of population genetics, period. I didn't ask him to be declared in any other particular field and I didn't develop the other particular fields. If Mr. Furlotte believes that he is, well, that's something certainly I can't change that opinion, but the Crown's point was, as the Court

has pointed out, is he's been declared an expert to give an opinion in a particular field and my understanding is witnesses are not generally entitled to give opinions outside of what the Court says they're allowed to.

THE COURT: Well, that is right, but if you want to ask the witness, are you an expert or do you have expertise knowledge in - or expert knowledge in molecular genetics, was that it, and he says yes, well, that paves the way for your asking opinions in that field.

CROSS-EXAMINATION OF DR. CARMODY RESUMES:

Q. Dr. Carmody, aside from being declared an expert in population genetics I understand you also do work with molecular biology and running autorads such as the exhibits that are in effect at this trial?

A. That's correct, and I think I would feel reasonably comfortable in answering the types of questions you were asking me yesterday. On the other hand, I would take direction from Judge Dickson that if I feel there is something outside my area of expertise which there could conceivably be, I think I'd just answer to that effect.

Q. And I'd appreciate that also.

A. O.K., but I felt that the questions I was asked yesterday I have reasonably good knowledge in the techniques and -

Q. And how long have you been working in these techniques?

A. For at least ten years or whatever. It's just that I don't have personal experience with some of the

difficulties with forensic specimens. I have never run my own case except as I mentioned yesterday, these bullfrog specimens, that would be considered forensic specimens of any sort.

Q. Well, as I understand, neither has Dr. Kidd, but he's also declared an expert in both areas so -

MR. WALSH: Well, maybe we'll leave that to Dr. Kidd.

THE COURT: I won't try to redefine the area of expertise here, I think we'll just go along on a pragmatic basis and if you feel you're getting outside your expertise, you say so.

DR. CARMODY: Thank you, My Lord.

THE COURT: You know, it's like the case of a carpenter who builds a house. He may not know a great deal about wiring a house, he's not an expert, house wiring or electricity, perhaps, isn't within his field of expertise, but he - a carpenter who can build a house is still pretty knowledgeable about wiring houses, and there's an overlapping there that's hard to define. O.K.

MR. FURLOTTE: Yes, I know, My Lord, I was an electrician for 22 years before I was foolish enough to become a lawyer.

THE COURT: I was a house builder before I became a lawyer.

MR. FURLOTTE: Now, Dr. Carmody, I may give you a little - I won't say a hard time, but I may want to deal into the aspect of it being valid to use the Hardy-Weinberg formula and the product rule in this particular case and probably cases in general. I suppose I have a problem because in my undergraduate studies I did an honours program in philosophy and I got stuck on the problems of logic in my courses of logic and I guess basically

philosophy is the study of cause and effect and to distinguish between appearance and reality, and when I mentioned yesterday that I thought maybe the forensic scientists were not using the Hardy-Weinberg formula and the product rule they weren't it wasn't based validity in scientific principles and that they were using that to provide big numbers, O.K., but it's got to be a valid theory and principle, got to be founded on fact; is that correct?

A. Yes.

Q. And I was concerned that because the forensic scientists are coming up with the big numbers, they're using the big numbers to justify the theory, which I thought they were puting the cart before the horse, which is a possibility in my book, so that is what I want to explore with you at least this morning. Now, a statistical probability of one in 10,000 or one in 1,000 is not all that great - we'll say one in 1,000; would you agree with that? You couldn't come to court and say, well, one in 1,000 is - you know, it's probably this person or that person?

A. I would think it would depend on the circumstances, honestly. I don't think you can make an absolute statement about a probability that is it one in 1,000. I think there are circumstances where that would be considered very rare to have one in 1,000, and for example, as I've looked at sort of some of the forensic implications of these things I don't know what probabilities, for example, to use for eyewitness testimony, and I don't know if any of us could put an actual number on that, and I don't

know whether the reliability of eyewitness evidence is greater than one in 1,000 or whether it's one in ten or whether it's one in 100 and so forth, so I'm not sure that I could give an absolute value to whether one in 1,000 is considered rare or not. I think if there were a situation where you knew it had to be one of five people and the probability of these four having done it was one in 1,000 and the probability that the other one had done it remaining of the four was 999 in 1,000, I think I would say there that I would go with the 999 in 1,000, and the one in 1,000 would exclude them.

Q. O.K., but I see this forensic tool being very powerful for police departments, the Crown, and basically our administration of justice if it is valid, but where one in 1,000 in - say if you had a profile that matched, and the probability is - because you couldn't match all five probes, just a few bands here and there, and the probabilities come out as one in 1,000, that would not be all that significant, would it?

A. I would say probably not in most cases if you had DNA evidence, whatever, although numbers like that have been used seriologically, in seriological evidence, in the past, I know.

Q. Well, if for instance - I think it would become advantageous to our administration of justice if it's valid is that if - we'll say for instance there was a gang rape or at least two people had sexually assaulted a woman and in the vaginal swab they found DNA from two different individuals besides the woman, two male intruders, and they

had two accused people and they matched a profile with each accused person and for each the probabilities once you figured it out, the couple of bands that matched each one, they were each one in a thousand. Then you could multiply that again, one in a thousand times, one in a thousand, and get the one in a million, I suppose, to show the greater probability of these two individuals meeting these two matches; that would be correct, and that makes a powerful tool?

A. Yes, I suppose in that case the question typically that would be as you'd look at each individual separately, probably, in that case. I don't want to get into sort of the statistical quibbling about the actual numbers here, but I think in that case you'd probably want to see what the probabilit of a match for this one was and what the probabilit of a match for that one was, and it's, I think probably, a question of looking at those two separately and a question of whether they were both jointly there or both had contributed. Each of these two would probably not come up, it would be a question of looking at each of them individually.

Q. Yes, but like if it was myself and my best friend that were accused and they come up with this profile for the two of us in this victim of a sexual assault, the probabilities would be much greater than one in 1,000 for each of us because we were together, so that I say that amplifies the power of this tool in identifying people in the commission of offences?

A. Again I think in my analysis of it would be that

you would look at the bands from the vaginal swab and you would see whether there were half of those bands that completely matched one of the suspects and you'd then want to say, did the other bands tha were not accounted for in that semen specimen match the other suspect, and you'd want to look at them sort of separately like that.

Q. To begin with, yes.

A. To begin with, yes.

Q. Doctor, to get back to Exhibit VD65, I see like for the Canadian data base and figures you used the 99% upper confidence interval?

A. Yes.

Q. The R.C.M.P. does not normally use that, do they?

A. No, they don't. They don't.

Q. Nor does any forensic lab that you know of?

A. I haven't seen any that have used it. I've seen the calculations done by some experts in testimony in the U. S. where they've used it.

Q. Are they when they're testifying for the forensic lab or for the police departments?

A. I guess they were testifying for the prosecutors in those cases.

THE COURT: I'm sorry, what was that you were referring to?

MR. FURLOTTE: VD65.

A. And in that first column I've calculated what I call the 99% confidence interval of one in 56 to one in 129.

THE COURT: Yes, but what was it you were saying, the R.C.M.P. don't use these parameters?

MR. FURLOTTE: They don't use this.

THE COURT: The parameters, the outside figures.

A. That's right.

THE COURT: Oh, yes.

A. They may in future if I have any -

Q. If you have anything to do with it, eh? I understand there was other scientists agree that at least the 99% upper confidence figure should be used? In other words, what the R.C.M.P. maybe should be coming to court and saying, well, look, we don't know the exact numbers but it could be one in 56 or it could be one in 29 and give those parameters as possibly falling within that area.

A. Yes.

Q. Would you agree with - that would be a more scientific and appropriate way to do it?

A. I feel as a population geneticist and a statistician it conveys better a feeling about the precision of that estimate. I've felt that sometimes people who are not knowledgeable in this area, when they hear a figure of one in 78 feel that there's a precision and exactitude about that that is really not intended, and unfortunately mathematically we don't have a good way of expressing that imprecision without using something that you call a standard error or a 99% confidence level or some other equivalent technique.

Q. No, I understand too that because there are some experts out there in the fields that they feel because of the large size of the matching window of the FBI and the R.C.M.P. that probably a better figure would be to use the 95% upper confidence level?

A. Possibly. I'd say that that almost comes down to a question of taste. I feel that I like the 99%

confidence interval because I feel I can have more confidence in it. I don't mean to be facetious there but that's what it means, it means that over 99% of the time if you redid the sampling you would get a figure that would fall within that range.

Q. So the ones who feel that maybe a 95% confidence level would say - they would say well, it's just when you do it 95% of the time you're going to fall within that range?

A. That's right, and it would be a narrower range, actually, if you did a 95%.

Q. Narrower range or wider range?

A. It would be narrower, actually. It would be narrower than that because in fact you would allow 4% of the time in mine to actually fall outside where theirs was, so in fact as you get down 95% it becomes a narrow range, if you took a 50% it would become narrower, and it keeps getting narrower as you decrease the percentage of your confidence, so that if you allowed me only a 5% confidence interval I would say it's probably like one in 75 to one in 85, something like that is the idea, but if I had a 5% confidence interval, 95% of the time when I redid the sample I'd fall outside it then, and so I wouldn't want to use a 5% confidence range. I mean, that's the notion of this confidence interval.

Q. I'm not sure I understand that. You said if you use a 95 you'd fall outside?

A. No, if I used a 5%, and let's say in the 5% case I might have a very narrow range there, let's say one in 75 to one in 85 for this instead. Then if

I used a 5% confidence interval, 95% of the time I would be making a mistake because my next sample would fall outside that range 95% of the time.

Q. Which confidence level would be more beneficial to an accused person?

A. I think the 99% one. It gives you the widest possible interpretation of where the range could be because you're getting down - as you make that range wider it means that going in the side of becoming more frequent, in this case the one in 56, for example, that is more beneficial to the accused than in the other direction of one in 129.

Q. That's in your end product?

A. In the end product, yes.

Q. But if you use the 95% confidence level, then you would have to use that to begin with and admit that, well, maybe 5% of the time this doesn't even match or it shouldn't fit? There's a 5% room for error, to begin with?

A. That's right, and what I'm saying is that I feel particularly in these cases that you want to take great precautions about making an error. I mean I think the inference that you make here is very critical, you know, the circumstances and whatever are not as easily dismissed and you worry more about making a mistake in these kinds of interpretations than you would in perhaps some abstract experiment I was doing in a laboratory.

Q. What if all the readings that I've done on this and the binning procedure and the product rule and how everybody says how conservative they are and conservatives always benefits the suspect - I can't

understand how they work as sometimes some of us feel that there's room for 5% error because of the 5% matching window. If there's room for 5% error to beging with how can you compensate for that in the end product or how does the bidding system compensate for that room for 5% error to begin with?

A. Well, it compensates by virtue of the fact that the bins that you start off with you know are wider than the capabilities of the technique, so there are more bands counted in that wider bin than would be counted if you used the bin that had a width that was really exactly and precisely the width of your resolution and the technique. That is, these bins typically are in most cases about twice as big as the actual resolution of the technique 95% of the time, so that in fact that bin size is, I would say, really a confidence interval that is much higher than 99%. I know it's hard to imagine getting higher but it's 99.99999% when you take a bin that is twice as big as the 95% window of the resolution technique. I mean, what happens is with these windows that's 95% of the time you're going to be right. If you take something that's twice as big as that, it goes up enormously in terms of your confidence limits there, your confidence in that interval, and so it's conservative in that sense in that the frequency is going to necessarily be higher when you increase the width of that bin than if you took just the size that you know is the resolution of the technique, or it has to be lower because there

would be fewer individuals in there.

Q. That only raises your confidence that you're putting these two bands, although they may show a variation in size in the computer sizings - that just ups your confidence that they belong or they should be put in this arbitrary bin; right?

A. Yes.

Q. And it wouldn't matter if the bin size was just double the size of the window or four times the size of the window?

A. Well, it does because the wider you make that bin the greater the frequency that that bin is going to be in any calculations that you do. See, because you're just encompassing more bands then from the sample from the population as you make that bin wider. It's like saying if you created bins, let's say we had information on everybody's annual income and we lump that together like that, if you made a bin that was from $10,000.00 to $13,000.00 or whatever, there are going to be fewer people in that bin than if you made it from ten thousand to eighteen thousand. You just know that as you make that bin wider there's going to be a greater fraction of your sample in that bin. It just has to be the case that as you make the bin wider you get more individuals falling in that bin and so the frequency of that bin goes up as you make it wider. Taking it to the extreme, if you just had one bin for the whole spectrum that you were analyzing, it has to have a frequency of a hundred per cent, so as I say, as you make the bin wider it has to increase its frequency and by increasing

its frequency, that gives you a number that is going to be more conservative and more - and less likely to exclude - or more likely to exclude the individual.

Q. Yes, but this is where I think that argument is fallacious because if we have two bins out of 200 samples - let's say out of 100 samples, and we'll say the bin is the same size as the window, R.C.M.P. window.

A. All right.

Q. Bin 1 and Bin 2 are both 5%, same size as the R.C.M.P. window, so in Bin 1 out of 100 samples we have ten events, O.K., which is 10%?

A. Right.

Q. Bin 2 we have ten samples out of 100, so we have 10%?

A. Right.

Q. If we combine these bins we have 20 people.

A. That's 20%.

Q. Which is 20%, so that's no real advantage to the individual when it comes to calculations because you have 200 events and you have 20 people in the 200 events -

A. No, you had 100 events, I thought.

Q. Well, there's 100 events -

A. You've got 100 events and ten events in each of the two and you lump them together and you've got 20 events that you're talking about in that case and so it's 20%, and so 20%, if you do the calculations, 20% is one in five, 10% is one in ten, so by using a one in five, that's more to the advantage of the accused, because saying that's

there's a one in five chance of a match is less - is more frequent than one in ten.

Q. Right, I understand that. Now, if we go back to VD65, like, the R.C.M.P. does not use their upper confidence - 99% upper confidence level?

A. No, they use the best estimate which is the one in the middle.

Q. So across the top for D1S7 you found that they were all within that confidence level.

A. When I looked at other populations, yes.

Q. But has the R.C.M.P. - you know, the R.C.M.P. does not use that so in fact Minnesota falls outside of the - in Canada it's one in 78, Minnesota it's one in 76.

A. Right, and there's no statistically significant difference between those two numbers.

Q. But there would be - if you just used the one in 78, the FBI is one in 96, which would be definitely way over, or outside? Let's say we're not dealing with the confidence interval here, because the R.C.M.P. doesn't use it and I just don't feel it's right for you to come -

MR. WALSH: Objection, he's making a statement.

MR. FURLOTTE: Is it right for you to use this upper confidence limit to try and show that the FBI is not outside of - or not outside statistically or proportionately or substantially, whichever term you want to use?

A. I think it's a perfectly legitimate statistical inference to make.

Q. Because you believe in this 99% upper confidence?

A. I think that's a completely accepted statistical

tool is to use -

Q. I agree with you, you're not going to get into an argument with me on that one.

A. And I've had - well, I'd be willing to defend that before any expert that in fact it's a legitimate technique to use, and I would say to show me that one in 78 is different from one in 96, the only way to show that is to use some statistical test.

Q. The only thing I'm concerned with is if you're going to come in and use these comparisons to show that there's no significant difference between the R.C.M.P. and the FBI you should be sticking with their system of analysis and not creating your own.

A. Well, I feel I have the privilege, not being a member of the R.C.M.P., to do what I want with these. I mean, these are defensible, legitimate statistical techniques that I've used and I haven't asked their advice as to whether I could use it or not use it. I'm using it because I know it's correct.

Q. And I have no qualms with that.

A. The fact that they don't use it, I think, is their loss.

Q. My position is that if the FBI does not want to use the upper confidence limit, if the R.C.M.P. does not want to use the upper confidence limit, then it's probably unscientific and improper to come to court in this instance and try to say there's no statistical difference if we use the upper confidence limit.

MR. WALSH: Is that a question?

THE COURT: Yes, are you asking his opinion on that?

Q. Would you think that that would be scientific and proper for them to do that?

A. I think if they wanted to use some statistical test that used the upper confidence limit, I think that would be proper for them to do that. I don't think that because they have not published that in any of their publications that I've seen or internal documents that they might have doesn't make it invalid. I think it's just that they haven't used it. I think that in order to say that one in 78 is different from one in 96, for example, one has to do some statistical test, and to my knowledge they haven't even considered that. I think so far as I know I'm one of the first people that has done this kind of analysis.

Q. If the R.C.M.P., and the FBI, since they do not use the upper confidence level, O.K., so let's go on the premise that it shouldn't be used for these comparisons, the FBI compared to the R.C.M.P., the FBI is one in 96 for D1S7, the R.C.M.P. is one in 78. Numbers-wise that would be of statistical significance?

A. No, it wouldn't.

Q. Even if you're not using the upper confidence limit?

A. It would not be significantly different no matter what statistical test you used, I would argue, but you don't have to use confidence limits to do a statistical test. I can name five or six tests that you could use to see whether in fact one in 78 is significantly different from one in 96, and it would depend on the size of your sample, for

example. and there are T-tests, there are non-parametric median tests, there are a number of tests that could be done. My point in doing this is to try and indicate and convey in what I thought was a reasonably simple way the fact that when you state a number as one in 78, that does not have the precision that it seems to have, that it does not really mean that it couldn't be one in 79, it couldn't be one in 75, that in fact when you say that one in 78, because of the fact that that's derived from a finite sample and the finite sample is composed of roughly 750 individuals, that number does not have a precision that might be indicated by saying it's one in 78. It will fall with 99% confidence within that range. You could also express it as a standard error of that estimate, you know, as a number of techniques, but that one in 78 is not a hard and fast number that couldn't vary from another sample, whatever. That's what I'm trying to convey there.

Q. Yes, and I recall putting a similar type question to Dr. Waye and the Crown Prosecutor can correct me if I'm mistaken.

MR. WALSH: Well, again, the Crown Prosecutor has a decent memory but unless he's prepared to quote that verbatim and is assured that that is in fact what Dr. Waye has said, then he's in a dangerous game, because I certainly can't give you verbatim everything Dr. Waye said over the last three days last week, so if he's going to put that question, My Lord, I don't want to have the responsibility of objecting or not objecting and thereby taken to accept the statement he says Dr. Waye made.

THE COURT: Yes, well, let's hear what you -

MR. FURLOTTE: As I understand from Dr. Waye when I asked him a question about the confidence level of when you have a number, say, like one in 78, I used the example of, say, one in 50, and he said like yourself, it would all depend on how big your sample size was, the greater the sample size, the greater confidence level?

A. And that results in a smaller - the 99% confidence level would get smaller as the sample got up. If you had a large enough sample, and it might have to be a couple of billion, you could get that estimate of one in 78 to have a 99% confidence interval of like, say, one in 75 to one in 81 or something like that, if you have a large enough sample.

Q. Dr. Waye gave me the figures that, well, yes, one in 50, and I asked him how much would it have to vary before it would be statistically significant, and he thought, well, because of the number in the R.C.M.P. data base that anywheres from one in 48 to one in 52 would be within the range. Maybe anything outside of that would be of statistical significande and he gave the example like one in 26 would definitely be way out, so I'm just wondering here from one in 78 to one in 96, according to the testimony he gave, that may be way out and of statistical significance.

THE COURT: It's just not clear to me why you bother to refer to what Dr. Waye said. I mean a lot of these questions that you're asking, Mr. Furlotte, might perhaps be better saved for argument, really. What you're trying to do really is argue or present

argument, aren't you?

MR. FURLOTTE: No, I don't think I'm trying to argue, I just want to give Dr. Carmody the benefit of, I suppose, what I know about this or what I've been told by other experts, experts by the R.C.M.P., and most expert witnesses, they base their opinions on opinions of other scientists in the field and they like to take everybody's opinion into consideration and -

THE COURT: Well, are you suggesting Dr. Waye really was saying the same thing as Dr. Carmody is saying now, was he not?

MR. FURLOTTE: No, I'm concerned there now because Dr. Carmody is saying there is no significant differenc between one in 78 and one in 96, and I'm suggesting that, you know - you know, he says it depends on the size of the data base, those polled, and according to Dr. Waye the numbers polled, he'd put them down at a very narrow figure, the span would be, say, 48 to 52.

DR. CARMODY: Well, I've done the calculations and that's what I come up with. I don't know what Dr. Waye's calculations or statement was derived from, I wasn't privy to that. I would stand by this as accurate and be willing to have it criticized by anybody.

Q. Is the reason that you're saying there's no statistical significance in these - difference in these two numbers, is that because you've done the calculations and your end product showed that you had a nice big number?

A. No, that's not the basis of it. I'm partly - and

to just start cut in each individual locus calculation, I just wanted to make sure myself what the precision of that estimate was. I really before I did the calculation, I only had a kind of impression as to what it might be, and when I did the calculations this is what I get, and I did that because I wanted to know what the precision really was when you came up with a number of one in 78 based on the sample sizes and the data base that I've been working with, and I didn't have a seat of the pants feeling for what it might be, and these are the numbers and I can defend the calculations, I think, to any statistician.

Q. O.K., and on D2S44, again the difference between the R.C.M.P. is one in 59 and the FBI is one in 70. Of course, the first one was not statistically significant and neither would that one?

A. That's right.

Q. And in D4S139, R.C.M.P. one in 68, FBI one in 98.

A. Right.

Q. Again your opinion -

A. It falls within that 99% confidence interval.

Q. And the D10S28, R.C.M.P. -

A. It's one in 108, one in 92 -

Q. FBI one in 92?

A. Right.

Q. And D17S79, R.C.M.P. one in eight, FBI one in 11?

A. Yes.

Q. None of these have any statistical significant difference because you used the 99% upper confidence limit?

A. Not strictly, and it's not the confidence interval that really tells me that they couldn't be differen I know that the tests, though, that one would do, typically in these cases you use what's called the T-test, that looks at the overlap between any two estimates in terms of their confidence intervals, and I would say - I haven't done that actual test, but because of the fact that these numbers that I derived from the FBI data fall within that interval. If I did a T-test they're unlikely to be different from one another.

Q. Now, I may be wrong but I thought I understood on direct evidence when you were answering questions from Mr. Walsh that you found there was some statistical differences in bin frequencies between the R.C.M.P. and FBI?

A. Yes, there were.

Q. But not significant difference in the product? Once you used the product rule there was no significant difference?

A. That's right.

Q. And that was basically because you got the big figures?

A. Well, I got big figures but it was because the figures that I got in both cases were within the range of variation one would expect. Whether they were big or small, if they were going to be within the range that one expects they would not be significantly different. It wasn't because they were large that they were not necessarily significant.

Q. And I believe your comment was that the difference in the high numbers, say one in five million or one in ten million, you're only looking at 100% difference, that can be deceptive -

A. It can be because - could I just -

Q. That there was no real significant difference because the smaller numbers still gives you a very rarity - very rare?

A. Well, that's right, but it's because of the fact that I think I earlier tried to explain that that final number which is the result of doing the probability of 2 PQ calculation at each locus and then multiplying that through for five probes sort of amplifies the effect of the variation at each one of those intermediate preliminary steps. If each of those - for example, at the D1 site, if you had a 99% confidence interval of one in 56 to one in 129, which is less than - you know, I mean, you're going from one to 78 to one in 129 or one in 56. That's not doubling that number or halving that number, but if you do that for each locus it increases the span of the confidence interval and the size of the confidence interval that's going to be the net result of multiplying all those things together, and I think I tried to use the example of if you multiply five times five times five times five you'd get a certain number, and if you just took a difference of one and multiplied six times six times six times six, you'd get a number at the end that is much different than just one digit which was just the difference in each of those.

Q. Yes, I believe you explained that.

A. It amplifies out like that.

Q. You explained that yesterday.

A. And so that amplification effect, actually, it's not really the fact that these are that rare or the size of the numbers are that large, is the effect of doing all those intermediate calculations that causes that range to be much broader like that at the end.

Q. And I believe you also testified on direct examination that you said once you get over the figures of one in 100,000 or one in 200,000, then there's really no significant difference?

A. Well, again I recall saying that. I think it will depend on the sample sizes involved. If you have extremely large sample sizes you can get greater precision and it's always a trade-off as to how large a sample you can get to get the precision down. It becomes a practical limit to how large that sample can be ultimately in terms of cost and so forth.

Q. And so do I understand you to say that if you were going to run a profile through one data base and you got the figure one in 100,000 and then you run, say, the R.C.M.P. data base, and then you run that same profile through the FBI data base and you got one in ten million, that there would be no real significant difference?

A. You said one in 100,000 and one in ten million? Again I'd have to use the sample sizes and actually do a statistical test in that case, because one in 100,000 and one in - was it ten million you said?

Q. One in ten million.

A. Ten million - that that's a hundredfold difference and I'm not sure that at a hundredfold difference wouldn't be statistically significant. I think in terms of the forensic implications, and from my understanding of court room evidence, that if a number were one in 100,000 or one in 100 million, to me it wouldn't convey that much difference in the weight of the evidence, personally, and I think in many minds it wouldn't.

Q. If they were both valid?

A. If they were both valid, yes.

Q. In other words, if it was valid to use the product rule, then there would be no real significant difference?

A. Well, again, if you want to take it back to a statistically significant difference, indeed there might be, and you'd have to do the tests based on the actual sample sizes that the two estimates were based on and there might be - given the sample sizes, there might be a statistically significant difference of things that are in the magnitude of a hundredfold different, but I guess I'm saying as a non-statistician when you say that the probability of something is one in 100,000 and you say one in a hundred million, to me in terms of court room evidence they're both pretty convincing.

Q. I'd like, Doctor, for you to forget that this has anything to do with court room evidence and this is purely scientific.

A. All right.

Q. As a pure scientist forget about forensic evidence altogether, just your population genetics and your natural field, if you saw this difference between two studies in population in two different areas of the country would that ring any bells to tell you that, geez, maybe we have substructure here, and significant substructure?

A. Well, it might, but I couldn't just look at the numbers in isolation again, and I know it sounds like maybe I'm retreating to this point again and again, but the significance between two numbers can only be determined by looking at the size of the sample that each of those numbers were derived upon, and to do a bona fide statistical test on that. If the size of the samples that those two numbers were based upon, regardless of whether there was structure, substructure, whatever, if those two samples were quite small, then those two numbers would not be significantly different. If the numbers in the samples that those numbers were derived from were large, and by that I mean considerably larger than typically the samples that we have before us, they would be significantly different.

Q. You mean the samples we have before us like the R.C.M.P. data base and the FBI data base?

A. One in 750.

Q. That's a significantly small -

A. It would depend. I'd have to do the calculations.

Q. I think you mentioned something like, what, 50,000 yesterday it would take sample size to prove substructure?

A. If I had to do an experiment, as I was saying, where you would have to look at individuals and both their parents and so forth, my feeling is you would have to have a sample of at least 50,000 to show some significant linkage disequilibrium in that case. I would think you would need very large samples. It may well be, and I haven't done this test, that in fact one in 100,000 and one in a 100 million or 10 million, I've forgotten what the figure was, would be significantly different statistically. I really can't give you a correct statistical answer on that, I don't know.

Q. With all the studies you've done so far and all that you've gained from it either through the last court experience, this court experience, and your studies, is there reason to believe that there just might be substructure out there?

A. I think there's some evidence in some populations, particularly as I mentioned earlier, black populations in the U. S. definitely show the substructure, and I know some studies done sort of in smaller populations, Yanomana Indians down in the Amazon Basin and so forth, there is some indication there that there is some substructuring. I don't feel from the analysis that - and the analyses that I've seen on Caucasion populations, that there is going to turn out to be significant substructuring. That's my opinion at this point in time.

Q. But it is possible?.

A. Oh, it is possible.

Q. But I suppose now we'll get back for the purpose of

forensic evidence. For the purpose of forensic scientists the task to prove that there is no substructure out there would be enormous on them, I would say. It would probably set the availability of this type of forensic evidence back a couple of years if they had to go back and prove there was no substructure?

A. If they had to get much larger samples, if they had to get much larger samples and so forth, it would certainly take time to generate that data, yes.

Q. Now, you mentioned yesterday that if for some reason you were to take another sample from the same population you would get the same bin frequency in another area of the country, you should get the same bin frequency?

A. Very close to it, yes. I mean, that's what the studies done on the Vancouver, Ottawa, Canadian Forces Base in Kingston would tell me, yes.

Q. Do you know a Dr. Hartl?

A. Yes, I do.

Q. And how would he rate in the scientific community in his profession?

A. Rates very high, I would say he rates very close to Dr. Lewontin.

Q. Are you aware that he did a test on the FBI rebinning data base?

A. I know he did some work, I don't remember all the details of it.

Q. Do you recall what his conclusions were?

A. Well, I know that he was of the opinion that they needed more samples and they needed more information to be able to do further tests before this kind of

data should be used forensically. I think that's a fair summary of what he said in the document that I saw.

Q. And I understand that the affidavit of Dr. Shields that you were given a copy of, I believe Dr. Shields refers to that experiment or test done by Dr. Hartl?

A. I think it does. I don't recall for certain but I think it does.

Q. Do you know whether or not the bottom line of Dr. Hartl's analysis and study into the FBI data base on the different runnings that he found that there was a statistical significant difference in the rebinning even though they conducted their rebinning on the same FBI agents?

MR. WALSH: My Lord, at this point we're into a dangerous game here Mr. Furlotte is playing. I'm going to from the Crown's point of view base an objection on the fact that the Crown would insist that Mr. Furlotte put the exact statement made by Dr. Hartl to Dr. Carmody, and Dr. Carmody can address the exact statement. What Mr. Furlotte is doing is giving his version of what Dr. Hartl says whether or not he has the report, what the report is, Dr. Carmody has pointed out he's not sure of all the details of it, so certainly Mr. Furlotte could put the exact statement Dr. Hartl made so -

THE COURT: I think, Mr. Furlotte, that's a fair comment that Mr. Walsh makes. Surely if you're going to attribute statements to Dr. Hartle you should tell us precisely what those statements are.

Q. Did you read Dr. Hartl's report?

A. I did read Dr. Hartl's report a number of months ago, yes.

MR. WALSH: I would like to know what report that is and what the details of it and where this report was filed so we understand if Mr. Furlotte and Dr. Carmody are on the same wavelength.

A., The report that I'm referring to that I read I believe was a report that Dr. Hartl submitted to a case in Ohio, I think it was the Yee case but I don't keep the case names carefully remembered in my mind, but I know it was a case where both he, Dr. Lewontin, Dr. Kidd, and a number of other experts testified, and I know it was in a - I guess they call it a Frye hearing in the United States and I know the judge concluded that in fact what Dr. Hartl and Dr. Lewontin were saying to the court was not taken as advice by the court, in fact and they felt that Dr. Kidd's testimony overruled or outweighed what Dr. Hartl and Dr. Lewontin had said in that case.

THE COURT: Mr. Furlotte, if you have a proposition that Dr. Hartl enunciated in some report, why don't you put the proposition without attributing it to Hartl or to anyone else to the witness and say, do you agree with this or don't you agree, and if he says he doesn't agree, then ask him why. It's not of any significance to us whether Hartl said it or Lewontin or anyone else.

MR. FURLOTTE: O.K., I will be probably getting into that later on. I just felt it was necessary to touch on that subject at this point in time.

THE COURT: I would think, actually, that it would benefit

you more if you wanted to show that there were people like Hartl who agreed with Lewontin and so on that if - through your expert, perhaps Dr. Shields, if he were to say, well, I'm agreed with in this proposition by so-and-so, Hartl, Lewontin, so-and-so, but you can put the proposition to this witness and -

MR. FURLOTTE: I don't mind the Crown's expert witnesses having different opinions than my expert witnesses, that's not only fair game, it's good science, as I'm sure Dr. Carmody would readily admit, but -

THE COURT: Well, I'm thinking primarily of the time we're taking in some of this thing, and the fact that you may not be accomplishing very much really -

MR. FURLOTTE: Well, I expect to touch back on that later on in my cross-examination and I'll -

THE COURT: Of other witnesses, yes.

MR. WALSH: My Lord -

MR. FURLOTTE: Otherwise I have to go fishing through all my data here and records.

THE COURT: Well, thank God no one gave you an Encyclopaedia Brittanica, Mr. Furlotte, because you might have started at the letter 'A' and cross-examined each of these witnesses right on every subject through from 'A' to 'Z', but surely you don't intend to go through every case that's ever been decided on DNA and ask this witness's opinion on every possible issue that's arisen in those cases.

MR. FURLOTTE: I do not intend to go through every case and every issue that was handled in every case, but I do intend to go through every issue, and there are many of them.

THE COURT: Well, if you have a proposition that Hartl has stated in some case or in some article and you want to put that proposition to this witness without attributing it to Hartle or to anybody else and say, do you agree with that proposition, and if the witness says no you can ask him, why don't you. or if he says yes you can say, why do you, and period, that's it, but there's no point in your arguing with a witness trying to convince him that his opinion is wrong. Did you have something to add, Mr. Walsh?

MR. WALSH: Yes, My Lord, just so you understand why the Crown is basing its objections at these points in time. The cases Mr. Furlotte referred to in Yee and cases like that where the expert witness's testimony is summarized by the trial judge, his interpretation of the expert witnesses is there and Mr. Furlotte can make what use of it if he wants, but the danger is - and certainly scientific articles and journals that he wants to refer the doctor to and read out of, you know, that's quite proper, but what Mr. Furlotte is going to start doing, I expect, and he's just started, is in some of these American cases experts have filed reports for particular cases. Now, if he wants to use those reports and refer to them, you know, that is understandable and it's proper, refer to a section so the doctor knows exactly what it is he wants him to comment on as opposed to Mr. Furlotte's interpretation, but there's one added complicating factor, Mr. Furlotte is aware of it particularly with Dr. Hartl, and Dr. Hartl has circulated a

letter in the United States where he's upset by the use by defence lawyers, or by anyone in that fact, of his report - bootlegging his report from case to case to case as if it's the standard for each case, and I have actually provided a copy of the letter to Mr. Furlotte because he asked me permission to enter all these different expert's reports that have been filed in different cases in the States. I have a copy of a letter Dr. Hartl sent to a lawyer in the States indicating his displeasure with having his report bootlegged in that fashion, so I've given it to Mr. Furlotte and he knows Dr. Hartl has taken objection to his report filed in one particular case being sent from case to case to case.

Now, if he wants to do it in any event, fine, but I would like - from the Crown's point of view like him to specify the actual statement he wants the doctor to comment on as opposed to this generalization that is causing us the concern.

THE COURT: Well, I don't feel any obligation to protect Dr. Hartl's copyright.

MR. WALSH: No, My Lord, but -

MR. FURLOTTE: Once Dr. Hartl submits a report in affidavit form as Dr. Fields did, then that becomes the property of the court and -

THE COURT: Well, we're not concerned with that aspect of it. The aspect I'm concerned with is if you're going to put a proposition to this witness, put it concisely, and I don't care whether it comes from Hartl or who it comes from.

MR. FURLOTTE: Well, I agree, and I intend to do that later

on whenever I get into my documents. I'd just like to get rid of his direct examination and - now, Dr. Carmody, you stated that the scientific procedure used in forensic science, you said it's accepted - the current standards are accepted by the people who are using it. Is there a difference between the way the forensic people - is there a difference of opinion in the way the forensic people are using their experiments? I realize that it's accepted within their community, forensic scientists, but is what they are doing, the forensi scientists, accepted within the general scientific community?

A. In my opinion it's generally accepted. I know - and it's difficult, I've never seen a sort of ballot taken or whatever, which I think you'd have to have done to really indicate that. I am aware o a number of publications where people, population geneticists, illustrious population geneticists, if you will, have disagreed with using these data bases and have expressed some - that there should be some further precautions and a delay made before this evidence can be used reliably, but I think that there are a number of people, and I include myself in that, who feel that it is the proper time and these data bases are large enough and we're not finding a significant substructuring and we should go ahead and use it.

Q. Now, when you say the term generally accepted, like you say, you don't know the numbers, so we can't go and say the majority accept it, but generally accepted meaning there's enough people

out there in the community that does accept it, that maybe therefore it's reliable?

A. That's what I'm saying, that's my opinion, yes.

Q. But you would admit that the scientists who excel in their fields of population genetics like Dr. Hartl, Dr. Landers, Dr. Lewontin, they would rank maybe the top three, would they not?

A. No, I wouldn't say that because I would say an equal number of illustrious outstanding population geneticists who feel quite comfortable with it, an I would include Dr. Kidd, I would include Dr. Weir I would include Dr. Clegg, and I could name as man as you might name on the other side, so to speak, so I would not agree that the most illustrious ones are all on the one side and the lesser people are all on the other side or whatever.

Q. How do you think this issue should be properly resolved?

A. I think the scientific issue needs to be resolved by further experimentation, further work, further gathering of data, and by people actually designin new statistical approaches that heretofore have not been applied to data like this.

Q. Would you say that a judge or a jury of 12 common people are poor people to resolve this issue?

A. I would say a jury, certainly. I think these kind of hearings have been held in several dozen states in the U. S. I know that this is not the first time the issue is being presented before a court in Canada. I think it's possible for courts to decide this issue, I wouldn't say that the issues need to be decided by a jury, but I think they can be presented in a reasonably simple enough way that

the issues are coming out and I think a court can make a decision.

Q. Would a jury be able to decide whether or not it's reliable?

MR. WALSH: My Lord, again, I don't understand the relevance of this and -

THE COURT: No, I don't think that's a fair question to put to this witness. He's not an expert in justice. None of us are, I guess.

MR. FURLOTTE: That's the first time we agree, My Lord.

THE COURT: At least he hasn't been qualified as an expert in justice, I'll put it that way.

Q. Now, I believe you had testified on direct yesterday that you said that you can get deviations from the Hardy-Weinberg and product rule in ethnic groups, and I believe you also mentioned geographic areas?

A. In the case - well, we've found significant differences in the bin frequencies in blacks and Hispanic populations that have been looked at in the United States. Nobody has yet shown that there is deviation from Hardy-Weinberg equilibrium - the Hardy-Weinberg equilibrium equation or linkage disequilibrium, in fact, in these populations that has not been shown.

Q. And that has not been shown amongst blacks?

A. It has not been shown amongst blacks.

Q. And I believe you mentioned non-random mating?

THE COURT: Mr. Furlotte, you're reminding the witness that he has testified about all these points. Why go over them again? I mean if you're leading up to a particular tack against some particular opinion,

come right to the point and say it, but why have the witness restate all this evidence that he gave yesterday? It's just total repetition.

MR. FURLOTTE: My Lord, I think this would be a proper time for a break as I have another area to -

THE COURT: It's quarter to eleven, let's break here for 15 minutes.

(RECESS - RESUMED AT 11:05 a.m.)

(ACCUSED IN DOCK.)

THE COURT: O.K., Mr. Furlotte.

MR. WALSH: My Lord, before Mr. Furlotte continues his cross-examination, Mr. Furlotte asked me at break if I would obtain the sizings for the band fragments that were found in this particular case. As Your Lordship remembers, the sizings are the measurements that are made after the visual match, they look at the band sizes by base pairs to back up the visual match. That's the computer quantification. Mr. Furlotte has been given copies in part of the discovery of the sizings, and we certainly have no objections to actually entering the sizings into evidence. I would have done that through Dr. Bowen and in fact copies are being made right now of Dr. Bowen's originals should the Court wish the sizings to be entered at this point in time. However, I wish to go on the record as again it goes into the fields of expertise. I can only assume that Mr. Furlotte wants the sizings entered at this time so he can cross-examine Dr. Carmody on the sizings. It's the Crown's position

that we're now into the field of the RFLP technique and that particular aspect of it, and Dr. Carmody has not been declared an expert or the Crown has not sought to have him declared an expert in the field of RFLP technology or DNA technology in testing procedures. He is here as a population geneticist. My understanding is in the field of population genetics to be cross-examined on the actual sizings is really outside the field and what Dr. Carmody is doing is actually looking at the statistical significance associated with any such match and the sizings are part of the match criteria. Again the Crown takes - with the utmost respect to Mr. Furlotte's position, we believe he's fishing, on a fishing expedition, and he's going to have the opportunity to cross-examine Dr. Bowen on that particular aspect and hopefully Dr. Bowen will be declared an expert within that field.

THE COURT: Well, we'll have to rely - without hearing Mr. Furlotte, I can only say that we will have to rely on the witness's good judgment in assessing his own expertise and if he feels that questions are being asked which fall outside a reasonably wide interpretation of what population genetics is about, then the witness will undoubtedly say so and that will be the end of that. So, Mr. Furlotte?

MR. FURLOTTE: My Lord, I don't think the Crown has too much to worry about because everything he's assumed is - well, at least 90% of what he's assumed is dead wrong, that's not my intention of having the sizings put into evidence at this time.

THE COURT: Good, solves everything.

MR. WALSH: Yes, I apologize to the Court, I just - Mr. Furlotte asked me at break could I get the sizings entered as he wanted to use them on cross-examination. Obviously I jumped to a conclusion that he was talking about the man he had on the stand and he was cross-examining at this time. If that's not the case, then I apologize for wasting the Court's time.

THE COURT: In any event, obviously it's a matter that would be better left for cross-examination of Dr. Bowen.

MR. FURLOTTE: Doctor, I was wondering if it would be possible for you to do some calculations for me as to what the frequency would be of different individuals or different profiles that were taken by the R.C.M.P.

A. O.K., if I could get my notes -

Q. Sure. Do you have a calculator?

A. I have a calculator here, yes.

MR. WALSH: He's asking me for the sizings and I was wondering if the Court would rule as to whether or not we're going to use the sizings at this point in time or not. That's the point I made when I stood up -

MR. FURLOTTE: O.K., My Lord -

THE COURT: Mr. Furlotte, you just said you didn't want the sizings. Do you want them?

MR. FURLOTTE: I want the sizings, I need the sizings so that Dr. Carmody can verify that certain matches do fit into the same bin and which bin they fit into in order for him to do his calculations.

THE COURT: Let's put the sizings in. You're prepared to do that, Mr. Walsh?

MR. WALSH: Yes, My Lord.

THE COURT: Let's put them in and then if Mr. Furlotte gets outside or the witness gets outside the defined parameters you can take objection at that time.

MR. WALSH: My Lord, then I wish to enter these in at the hearing. They are headed - there's documents - I believe it would be best to mark each one separately, My Lord.

THE COURT: All right.

MR. WALSH: Each consists - well, perhaps I'll just go one at a time. This document has three pages. It's headed, Calculated Fragment Lengths (log model). I would move to have that -

THE COURT: That would be VD66.

MR. WALSH: This document has the same heading, it has three pages.

THE COURT: Do they pertain to - what, different people or situations or what?

MR. WALSH: Yes. I was just trying to think, My Lord, how the best way to describe it - perhaps what I'll do is if we could have them each numbered and then I could put them in a package in terms of numbers one through something pertaining to a particular area.

THE COURT: All right, VD67.

MR. WALSH: Same heading, three pages.

THE COURT: VD68.

MR. WALSH: Same heading, three pages.

THE COURT: VD69.

MR. WALSH: Same heading, three pages.

THE COURT: VD70.

MR. WALSH: Same heading, three pages.

THE COURT: VD71. VD72.

MR. WALSH: Yes, same, three pages, same heading, and same heading, three pages.

THE COURT: VD73.

MR. WALSH: My Lord, if I may take the liberty of just explaining perhaps we could identify them a little better.

THE COURT: All right.

MR. WALSH: The documents that have been marked VD66 through and including VD73 are copies of the sizings conducted with respect to the autorads that are set out in VD - that are marked VD55, the first section of VD55. That is the section dealing with gel #1, membrane #1. In particular, VD66 relates to the sizings of the DNA probe D1S7.

THE COURT: 55, did you say, or 66?

MR. WALSH: 66, that's the first document.

THE COURT: Oh, 66, yes. Relates to what?

MR. WALSH: Relates to the sizing of the DNA probe, D1S7. VD67 relates to the DNA probe D2S44. VD68 relates to the DNA probe D4S139. VD69 relates to the probe D10S28. VD70 relates to the probe D16S85. VD71 relates to the probe D17S79. VD72 relates to the probe D7Z2, and VD73 relates to the probe DYZ1. As I say, My Lord, those sizings relate to the exhibit autorad VD55, and the first section of VD55 relates to gel and membrane #1.

Now, My Lord, I'd continue.

THE COURT: Yes.

MR. WALSH: I wish to have marked a document that's headed Calculated Fragment Lengths (log model) two pages.

THE COURT: That would be VD74. Can you tell us - can you

tell readily there what probe that refers to?

MR. WALSH: Yes, My Lord, VD74 relates to probe D1S7. Perhaps I could do it right at the outset.

THE COURT: Yes.

MR. WALSH: The next series of documents that I will be marking or will be marked, including VD74, relates to the autorads set out at VD55, the second part of VD55. That is the autorads related to the second gel, second membrane. VD75, then, My Lord, would be the same heading, two pages, and it relates to the DNA probe D2S44.

THE COURT: VD75, right?

MR. WALSH: Yes, My Lord. Calculated Fragment Lengths (log model). The next document with the same heading, two pages, relates to the DNA probe D4S139.

THE COURT: That's VD76.

MR. WALSH: The next document relates to the same heading, D10S28.

THE COURT: VD77.

MR. WALSH: The next document, same heading, My Lord, two pages, related to DNA probe D16S85.

THE COURT: VD78.

MR. WALSH: The next document, same heading, two pages, related to the probe D17S79.

THE COURT: VD79.

MR. WALSH: Another document, two pages, same heading, related to DNA probe D7Z2.

THE COURT: VD80.

MR. WALSH: And the last document in this series is two pages headed Calculated Fragment Lengths (log model), DNA probe DYZ1.

THE COURT: VD81.

MR. WALSH: Now. My Lord, I have an additional three sizings. These three sizings will relate to VD55, gel #1, membrane #1, the first section of VD55, the autorads contained in there, and these sizings are related to the reprobings that are set out in that particular exhibit. The first one is headed Calculated Fragment Lengths (log model), and it relates to DNA probe D4S139.

THE COURT: That would be VD82.

MR. WALSH: The next one, same heading, related to DNA probe D16S85.

THE COURT: VD83.

MR. WALSH: The last document of that series, same heading, relates to DNA probe D17S79.

THE COURT: It will be VD84.

MR. WALSH: The last document I have on sizings to enter at this time, My Lord, is a reprobing. It's related to the autorads set out in VD55, the second section dealing with the second gel, second membrane. It's entitled, Calculated Fragment Lengths (log model), and it relates to the DNA probe D16S85.

THE COURT: So that would be VD85.

MR. WALSH: Those are copies, My Lord, of the originals in Dr. Bowen's control. I believe Mr. Furlotte will agree to the entry of the copies of -

MR. FURLOTTE: Yes, My Lord.

MR. WALSH: Those constitute the sizings, My Lord, the total number of documents constitutes the sizings related to the autorads made in relation to the first membrane and in relation to the second membrane.

THE COURT: Fine. In accepting them into evidence, now, I'm not retreating from my earlier observation that

MR. WALSH: Now, My Lord, I have an additional three sizings. These three sizings will relate to VD55, gel #1, membrane #1, the first section of VD55, the autorads contained in there, and these sizings are related to the reprobings that are set out in that particular exhibit. The first one is headed Calculated Fragment Lengths (log model), and it relates to DNA probe D4S139.

THE COURT: That would be VD82.

MR. WALSH: The next one, same heading, related to DNA probe D16S85.

THE COURT: VD83.

MR. WALSH: The last document of that series, same heading, relates to DNA probe D17S79.

THE COURT: It will be VD84.

MR. WALSH: The last document I have on sizings to enter at this time, My Lord, is a reprobing. It's related to the autorads set out in VD55, the second section dealing with the second gel, second membrane. It's entitled, Calculated Fragment Lengths (log model), and it relates to the DNA probe D16S85.

THE COURT: So that would be VD85.

MR. WALSH: Those are copies, My Lord, of the originals in Dr. Bowen's control. I believe Mr. Furlotte will agree to the entry of the copies of -

MR. FURLOTTE: Yes, My Lord.

MR. WALSH: Those constitute the sizings, My Lord, the total number of documents constitutes the sizings related to the autorads made in relation to the first membrane and in relation to the second membrane.

THE COURT: Fine. In accepting them into evidence, now, I'm not retreating from my earlier observation that

based on the circumstances as I know them it may be that Dr. Bowen is a more correct witness to be cross-examined on these sizings, in any detail, that is, than perhaps the present witness.

MR. FURLOTTE: I have no intention of cross-examining Dr. Carmody on the validity of the sizings. He would be in no position to form such an opinion, I don't think.

THE COURT: All right.

MR. FURLOTTE: Doctor, the reason I wanted these sizings in was I have asked Mr. Shields to do something for me which has not been done yet and I would like you to do the same thing in court. Basically I can just fill you in on the reasons for it.
I found when I did my cross-references in studying the reports that I found in the profiles that Mr. Legere in his profile, that he shared three bands with another suspect. He shared three bands with one of the victims, and he shared four bands with another victim, and those two victims happened to be sisters, and I'm concerned because he shared as many bands with one of the sisters as the two sisters did, and I'm going to want you to calculate the frequency. What would the probabilities be of Mr. Legere finding somebody out there in the community who shared those number of bands with him?

A. O.K.

Q. Do you understand what I'm trying to do?

A. Yes, I understand.

Q. Now, hopefully we can do this in an orderly manner. I was hoping to have more time to have this better

prepared for you in cross-examination but for reasons I know of I wasn't able to do that. In probe D2S44, if I can find the sizings for that one -

MR. WALSH: On what gel?

MR. FURLOTTE: On gel 1, 1989.

CLERK: VD67.

MR. WALSH: My Lord, I wish to point out just from a technical point of view Mr. Furlotte is putting a question to the doctor based on what he says is his findings, Mr. Furlotte's findings. I have no objection to him putting it in the form of a hypothetical, but it would be dangerous if somehow we were proceeding on the basis that in fact what Mr. Furlotte said is correct. That would mean that Dr. Carmody would actually have to look at each individual sizing and do a matching in order to be assured that that is in fact correct. I have no objection to him putting it in the form of a hypothetical.

MR. FURLOTTE: That is why I need the sizings into evidence, so he can verify my findings.

MR. WALSH: Well, no, My Lord, again I apologize, to verify his findings - Mr. Furlotte is asking Dr. Carmody to make a match. He's going in the back door what we've talked about this morning he can't go in the front door.

MR. FURLOTTE: No, but I don't think this has anything to do with a match. This has to do with just the binning and it's a matter of statistical calculations as to the frequencies.

THE COURT: Does the witness have copies of these sheets

here, these -

DR. CARMODY: In fact, My Lord, if it would help, and it might cut through some of the legal questions here, I have my notes and I have in my notes the size of the bands that I used in my calculations and I thin for purposes, as I understand it, what you'd like me to do, that should be sufficient. I mean I can read out the sizes that I used in my calculations which were taken from Dr. Bowen's notes that he provided a copy to me, and these are the numbers and the sizes of the bands that I used and that Dr. Bowen used to do the calculations that have been submitted to the Court so far, and so unless there is some discrepancy, which I don't believe there is, if I do the further hypothetical calculations that you wish me to do based on the numbers that I already have, it might be the simplest way to proceed.

THE COURT: Yes, that would short-cut it. That would seem to be satisfactory. If you want to read out your sizing figures and you could check them at the same time if they're the ones you used.

MR. FURLOTTE: O.K., what I did, My Lord, is I broke down and drew my own categorization of the different sizings of Mr. Legere's DNA and the different gels and the different sizings of the DNA for that probe of the different people, the known people who were in the different gels, and since they're all in one sheet Dr. Carmody could cross-reference the sizings put in by the Crown with the sizings I have on the sheets and then if he has it all before him it might be easier for him to calculate whether or not they would fit in the same bin.

THE COURT: Have you a copy of that?

MR. FURLOTTE: Yes, I could put one copy into evidence.

MR. WALSH: My Lord, again, I appreciate - just putting things that he prepared into evidence, if that's the case I have some pretty nice things I have prepared that it might help the prosecution, it might not be quite proper, but I don't mind Mr. Furlotte putting something to the doctor and asking for his opinion on it but he's doing it in a backhanded way that I find confusing, I'm having a hard time following exactly what he wants to do here.

MR. FURLOTTE: I just thought I'd try to shorten it up by doing this.

THE COURT: Let's not put that in evidence. I think we're opening the thing up unduly if we put your notes in evidence.

MR. FURLOTTE: O.K., Doctor, I will show you Exhibit VD67.

A. O.K.

Q. And can you tell me what that is?

A. This indicates the calculated size of the base pairs from a particular autoradiogram that Dr. Bowen ran on the - it's marked the first of December, 1990, although the autogram I think is dated - if I could read the coding on that - well, I can't read the coding, I don't know what that coding means, actually, but it's for the D2S44 locus and in various lanes where different forensic specimens were run there are the estimates of the molecular weight for each of the bands in the lanes

Q. O.K., in lane 3 which is, I believe, Exhibits 56A and 69A?

A. That's correct.

Q. And that is reportedly hair from the suspect, Mr. Legere?

A. Correct.

Q. I'm not sure if it's marked on that.

A. It's not but I recognize the code 56A, 69A, yes.

Q. And his molecular band readings were what?

A. 2,918 for the base pairs for the higher molecular weight band and 2,094 base pairs for the lower molecular weight band.

Q. O.K., for my purpose what I want you to do, we're only going to concentrate on the higher molecular weight band, 2,918.

A. Right.

Q. In lane 2 for a suspect -

A. Yes, the higher molecular weight band was 2,919.

Q. 2,919?

A. Right.

Q. And that would fit in the same bin as -

A. That would fit in the same bin as the 2,918, they would both be so-called bin 13.

Q. Now, lane 4, which is an exhibit from Donna Daughney?

A. Yes.

Q. Exhibit 115B?

A. Yes.

Q. And did she also have -

THE COURT: Exhibit what?

A. This is Exhibit VD67, you're talking about?

Q. Yes, Exhibit VD67 but -

THE COURT: Yes, but what was the Daughney specimen?

A. Oh, it's 115B, I take it. It's lane 4.

Q. And she has a band reading of 2,965?

A. Yes, that's her smaller band, yes.

Q. And that would also fit into the same bin?

A. That would fit into - I just have to check here to be certain of that, 2,965 - yes, that would fall into bin 12. Actually, that would fall into - wait a minute here - 2,965 falls into bin 12. Oh, I know the reason, I'm looking at the wrong information here, it's not making sense to me. Statistics won't help you when you're looking at the wrong information. That's in the same bin, bin 13, yes, that's correct.

Q. So far all three readings from the suspect in lane 2 from Mr. Legere and from Donna Daughney, they all fit in bin 13?

A. They all fit in the same bin and if the next part of it is what the frequency of the bin, I could tell you that.

Q. Well, we'll get into that after, and then in lane 5 which is Donna's sister, Linda, she has a reading of -

A. 2,963, that's lane 5, the specimen number is 140A. She also has a band at 2,965 that would be classified in the same bin, bin 13.

THE COURT: 2,963.

A. 2,963.

Q. That's for lane 5?

A. That's right.

THE COURT: That's the higher band?

A. That's actually the lower one, My Lord.

Q. She only has one band that fits into lane 13, right?

A. Yes, her other band is 38, that's in a very different band, and -

Q. O.K., I'm only concerned with lane 13 and the bands in that range.

THE COURT: And in lane 4, Donna Daughney, 2965, that was the lower or higher? Lower band again?

A. That's her lower band, it's a smaller molecular weight.

Q. Now, if we go down to - we'd have to go down for this purpose to lane 21?

A. Yes.

Q. Which is the human cell?

A. Right.

Q. And would both those bands fit into lane 13?

A. 3038 - 3038 falls into a different bin, but 2810 falls in the same bin.

Q. 2810 falls in the same bin, O.K.

A. No, sorry, 2810 falls in bin 12, so neither of those two fall within bin - wait a minute. 2810 is below that and 3038 is above it, but they're both reasonably close to the borders of that bin.

Q. They would both be within the 5.2% matching room of Mr. Legere?

A. They are near the border of the bin. I'd have to do a calculation in terms of the match and I would say here that in terms of calling a match that's not my area of expertise and I'd be a little bit reluctant to say that those would be seen as the same band on the gel, and I don't think they would be called a match but I could be wrong there, so I would say at this point if I were being asked whether I would call these a match, that's outside

of my area of expertise, My Lord. I can say whether they fall in that bin or not. These two do not strictly fall within the bin. I concede that they're on the bin boundary or near the bin boundary and near enough to the bin boundary that in terms of calculations you would take that into account, but in terms of calling them a match, I think that's out of my area of expertise.

Q. Now, there's no way you can find that on the data before you but maybe the Crown will admit that in the gels that I have received or the R.C.M.P. have done in this case, as far as for gel 1 of which there are sizings of different people and - how am I going to state that - maybe I'll try and leave it out for this purpose. It makes the miniature data base a little smaller but on gel 1 I believe you might find lanes for seven known people? Well, yes seven distinct people rather than evidence?

A. I have to confess that I'm not that familiar with the coding of what these specimens pertain to in terms of this column, and I don't know how many different individuals -

Q. O.K., maybe I could go over it with you?

A. O.K.

Q. Lane 2 is Exhibit 157A?

A. Yes.

Q. And I believe the Crown will admit that that is from a known suspect?

MR. WALSH: If Mr. Furlotte would like to agree that - consent as to who those lanes belong to, I have no problem, My Lord. I'm concerned about where we're going, that's the only thing. I'd just like to know

where Mr. Furlotte is going in relation to Dr. Carmody's expertise. Dr. Carmody is saying, I'm not familiar with these things. Now Mr. Furlotte wants to educate him on that and I'm just concerned that we're way off what Dr. Carmody actually does or is here for.

MR. FURLOTTE: He's a statistician, he's a population geneticist, and I want Dr. Carmody to compare the pattern as well as we know it within the Newcastle area in comparison to what the pattern is in the general data base.

THE COURT: Well, I think it might facilitate things, perhaps, if these exhibits were identified by suspects or whatever. Are names of suspects going to come out in this thing or -

MR. FURLOTTE: Not in the voir dire anyway.

MR. WALSH: Yes, I believe, My Lord, in VD55, if I'm not mistaken, if I may approach, My Lord -

THE COURT: Yes.

MR. WALSH: In VD55 we've set out for the purposes of the voir dire to make reference easier. We have set out the -

THE COURT: Aren't they A, B and C?

MR. WALSH: Yes, but we've also identified them by name to make it - to prevent cross-referencing every time that you look. That should be a pretty good indication of who belongs in what there.

THE COURT: Well, there's only one name that I see here that - other than those of alleged victims and the accused on this first page here.

MR. WALSH: Yes, My Lord.

MR. FURLOTTE: There's only one other suspect run on that gel.

THE COURT: Are there any objections to using surnames of suspects?

MR. WALSH: Oh, no, I certainly have no -

THE COURT: Well, Murphy is the name.

MR. FURLOTTE: O.K., I know Murphy's name.

THE COURT: All right, we'll choose Murphy if you want to use it.

MR. FURLOTTE: So in lane 2 is a suspect named Murphy. Lane 3 is the accused, Mr. Legere. Lane 4 is Donna Daughney. Lane 5 is Linda Daughney, and Lane 6 is the female fragment of Nina Flam.

A. Yes.

Q. Then we have to go to NM in lane 20.

A. All right.

Q. NM, who is, I believe, a member of the lab in Ottawa, and then we have the human digest cell.

A. All right.

Q. The control digest, human cell.

THE COURT: What is that lane 20, the last one?

MR. FURLOTTE: Lane 21, the last one.

THE COURT: Lane 21, the male control?

A. Yes, it's just called human cell on this sheet.

Q. So that would be what, seven people altogether?

A. Right.

Q. And the last two for your purpose, they are not from the Newcastle area but rather from, I would assume, Ottawa, so out of -

THE COURT: Well, the witness is saying he doesn't know where they're from.

MR. WALSH: And this point about the Newcastle area, we're being deceptive again and not intentionally, I kno

Mr. Furlotte is not being intentional, but we're dealing with individuals from Chatham, individuals from Newcastle, and we're dealing with individuals, I assume, that are not from Chatham or Newcastle. If Mr. Furlotte's idea here is to develop some kind of a mini data base, I mean, we have to have some kind of correction in terms of what we're actually dealing with.

MR. FURLOTTE: If you want to expand it to New Brunswick, I have no problem with that, it's just for a matter of demonstration.

THE COURT: All right.

MR. FURLOTTE: So I just wondered if you could calculate what the frequency is of these bands occurring in the whole data base, what would the frequency of these bands be?

A. All right, the band you were asking me about in the case of lane - or lane 2, rather, is the one that was 2918 base pairs?

Q. Yes.

A. And that was falling in bin 13 so the frequency of bin 13 in the R.C.M.P. data base that I used and that Dr. Bowen used, there were 166 bands in that bin and the total size of the number of bins in that data base was 1712, and so the frequency of that bin is .09696.

Q. Which would be one in what percentage?

A. In terms of that rounding off what you do is you divide .09696 into one and that comes out to be, in rounded terms, one in ten, so that means that 10% frequency of that bin. I can refine that here with just doing the calculation of dividing .9696 into one and that actually comes out to be one in

10.31353.

Q. O.K., now, in the people from Newcastle area, which is lanes 2, 3, 4, 5 and 6, that's -

A. 2,3,4,5 and 6.

Q. That's what, five people?

A. Those are five different people, yes, although two of them are related, known to be related.

Q. And what is the frequency there?

A. Of that same band?

Q. Yes.

A. I presume you're asking. I have to go back again so there's a bin 13 in lane 2, there is a bin 13 in lane 3, there is a bin 13 in lane 4, there is a bin 13 in lane 5, there is a bin 13 in - there is not a bin 13 - let me see, I guess there's not a bin 13 in lane 6, so now, what was the question?

Q. What would be the frequency for the known five people that we have from Newcastle?

THE COURT: Let's say New Brunswick, you agreed to say New Brunswick.

Q. All right, New Brunswick.

A. O.K., based on this sample of five people, that band occurs four times in ten; it would be 40%. That's if - there are ten bands there and four of the bands are falling into that bin, so the frequency of that bin in these five individuals which produced ten bands, so there's four of those bands of the same kind in a sample of ten, it has a 40% frequency in that sample.

Q. And that would be - that would become a fourfold or -

A. That is four times higher than the - or a little bit more than four times higher than .09696.

Q. If that were to hold true for all of Newcastle would

that be a significant difference?

THE COURT: All of New Brunswick.

MR. FURLOTTE: Or all of New Brunswick, I'm sorry.

A. If that were to hold true in a larger sample from all of New Brunswick that would be a significant difference for the frequency of that bin. If I did the statistical comparison, though, based on the sample of ten bands and I compared that to the .09696 based on a sample of 1712, I haven't done the calculations and I couldn't do it spontaneously here, but I'm quite certain that there would be no statistically significant difference because this is a - I might use the term, pathetically too small sample.

Q. I would agree that it, you know, might be.

A. It would be the equivalent of having asked five people who they're going to vote for in the next election and say well, if four of the five said they were going to vote for the Liberals in the next election and you compared that to a sample of a thousand taken across Canada, it would have no statistical validity or accuracy or useability.

Q. It may carry little weight.

A. Carry very little weight, very little weight. I would consider it hearsay evidence.

Q. I'll show you Exhibit VD70 which is - I assume is the sizings probes of D16S85.

A. Now, I'm willing to go through this but as I understand it, in none of my calculations have I ever referred to this particular probe, but we can go through it.

MR. WALSH: The doctor has made a good point, My Lord, that particular probe has not been used in the

calculations that have been generated in this case. Dr. Carmody's statistical evidence, that probe was not used in the actual comparisons or in the actual generation of any figures. We're into a situation where Mr. Furlotte - the doctor has pointed out that Mr. Furlotte is into a pathetically small data base that from my understanding from the doctor would really have no statistical weight, so we're doing that, and on top of that he wants to get into the questions on probes that we haven't actually used. It just would seem to me that Dr. Carmody's time could be better spent.

MR. FURLOTTE: I think I should be the judge of how Dr. Carmody's time is better spent than the Crown Prosecutor.

THE COURT: I'll be the judge and I'll say his time will be spent on one more. Pick out your best one and we'll do one more.

MR. FURLOTTE: Well, we have that one now. I'm concerned about the band of Mr. Legere in lane 2.

A. Lane 2, all right.

Q. O.K., the size 1015?

MR. WALSH: Mr. Who, did he say, in lane 2?

A. Well, this is lane 3, sorry, it's called lane 3, it's the second lane indicated here. There is a 1600 base pair and a 1015 base pair band..

Q. And what bin number would that fall into, the 1015 base pair?

A. Which one did you ask?

Q. 1015.

A. That falls into the very first bin, that's bin #1, we would call it.

Q. O.K. Now, if we go to lane 2 are there any band sizes that will fall into bin 1?

A. Now, when you say lane 2, I think you mean lane 4 here?

Q. No, I mean lane 2 up here.

A. Lane 2. Two of those three bands, and that's a so-called three-banded pattern, would fall into that first bin. Now, I don't know if this has come up in any previous testimony but this is a case where an individual has three bands, which is quite rare in Caucasian populations, and these can be used in the way that we're using them but they're typically treated as unique when these data bases are constructed. I'm just pointing that out, I don't think it's going to make much difference in what -

Q. Would it be conservative for the Crown's purpose just to take one of those bands and put it in bin 1 or is it all right to put the two of them?

A. Well, there's three of them there and you have three possible choices, I suppose, to what to do. One approach would be to take all three bands, but biologically it's not at this time certain why some individuals have three bands, and so because of that because there isn't a good biological basis for knowing why an individual has three bands, these are typically not used - and my understanding is these typically are not used to enter into the data base, but I can do the calculations if you so wish and if you want me to take two of those three, I'll take two of those three.

Q. O.K., well, we'll take two of them. Maybe we better calculate as we go as to how many bands we're adding up here.

A. O.K.

Q. Do you have paper there, Doctor?

A. I have paper and I have a pencil, yes, or a pen.

MR. WALSH: My Lord, could I make a suggestion that might help Mr. Furlotte? My suggestion would be that we could break for lunch. Perhaps Mr. Furlotte could ask the doctor during lunch, sit down with the doctor, if I'm not imposing, sit down with him and ask him to calculate the bands, refer to the bands, ask him to calculate them, and then when we come back into court it may prevent the time of the doctor actually trying to work these calculations out in the court room.

MR. FURLOTTE: Well, we could go through this calculation, then break for lunch.

THE COURT: This is the last one, so let's finish this one.

A. I don't think this will take too long, My Lord.

Q. No, it shouldn't take all that long.

A. Right, O.K., so in that first lane, the so-called lane 2, there are two bands that fall in that bin, two out of three.

Q. Lane 3?

A. In lane 3 there is one band out of two.

Q. Lane 4?

A. Lane 4, there are two bands out of two.

Q. Lane 5?

A. Lane 5, there's one band out of two.

Q. Lane 6?

A. Lane 6, there are two bands out of two.

Q. O.K., and can we calculate the frequency on that?

A. All right, we have a total of 2, 4, 6, 8 bands that have fallen in that bin in a sample of 2, 4, 6, 8, 11 bands, so that means that the fraction is

eight out of eleven. It comes out to be a frequency of 72.72%, I get. If you want to express that in probability terms you take the inverse and that means that - I just made some mistake here on my calculator. It's all right. It was eight divided by eleven and you get 72%, so that in fact that's - if you wanted to express that as one over a number you get one over 1.37.

Q. I'm not sure I follow you.

A. That is 72%. If you wanted to know how frequent that was in terms of one over a number, it's one in every 1.37 individuals, or every 3.7 bands.

Q. O.K., now, what's the frequency for the R.C.M.P. data base?

A. The frequency in the R.C.M.P. data base is 844 bands out of 1662. That comes out to be 50.8%, so we have in contrast here a 72% vs. a 50%. That's what I would conclude there.

Q. And again if that was to hold true for, say, a population data base for New Brunswick, would that be a significant difference?

A. If it were to hold true in much larger size samples that would be a statistically significant difference.

MR. FURLOTTE: Well, if you want to break for lunch now, My Lord.

THE COURT: Well, do we want to break for lunch? Why do we want to break for lunch?

MR. FURLOTTE: Oh, because I thought the Crown suggested it.

THE COURT: No, the suggestion was that this computation might have been done over the lunch hour, but it doesn't have to be done now and I think you've finished this aspect of the cross-examining so why can't - can we go on for another 20 minutes here?

MR. FURLOTTE: Sure.

THE COURT: Just to sort of bring this to a conclusion, I presume - the witness wasn't asked this question and I don't suppose it will come around to re-examination but I suppose the witness would perhaps make the same comment as he did earlier that it was a pathetically too small sample?

A. Yes, it's not only too small a sample but in fact it contains two individuals who are known to be sisters, so it invalidates any statistical implications one can make from that sample entirely, because it is not by any stretch of the imagination a randomly derived sample, even though it is so small, or in spite of the fact of it being so small, so in my opinion and judgment in my statistical experience it would have absolutely no relevance or bearing whatsoever in any implications or inferences that one wants to make in this case.

Q. Again, Dr. Carmody, you will not find me disagreeing with you on that. O.K., for the other basic purpose that I have you here, to get back to the calculation of frequencies that somebody out there might match the same bands as Mr. Legere, he's picking specific bands, we'll start off with probe D2S44, which the sizings are on Exhibit VD67. What would the frequency be from the R.C.M.P. data base that somebody out there might share that band with Mr. Legere?

A. The larger of the two bands, I presume you mean?

Q. Yes, the 2918.

A. 2918, that is .09696 or 9.69%.

Q. O.K., if you would maybe mark that down on your paper because I'm going to ask you to multiply these

together for a specific band pattern.

A. All right. All right, I've recorded .09696, which is 9.6%.

Q. And this experiment, Dr. Carmody, I will tell you now that we want to see what the frequency would be that Mr. Legere shares specific band patterns with Donna Daughney, who happens to be in lane 4.

A. All right, she has one band that matches that in terms of its same bin. 2965 - let me just corroborate that - 2965 is also bin 13, so yes, she has her band 2965 would fall into the same bin as Mr. Legere's band 2918.

Q. Yes, O.K. Now again we'll go to probe D1S7, which is Exhibit VD66, and if we look at Mr. Legere's molecular weight band of 7301 -

A. O.K., 7301, and this is probe D1S - it falls in bin 22 which has a frequency of .083 - actually, I can get it more precise than that. Which one was that again?

Q. 7301.

A. 7301, falls in bin 22 and that's 8.345%.

Q. I believe you already calculated that out to come out to one in eleven, is it?

A. One in eleven in rounded numbers, yes.

Q. And the other band in Mr. Legere's lane for the D1S7 probe is 4550?

A. 4550, and I've already done that in previous calculations, that is 7.62%.

Q. One in 13?

A. One in 13 rounded off, yes.

Q. Now, in lane 4 for Donna Daughney, she has a band of 7386?

A. That's correct.

Q. Which would fall in the first band, the largest band, of Mr. Legere's also?

A. That's correct.

Q. 7301?

A. That's correct.

Q. And her second band is 4688?

A. 4688, and that falls in bin 17 which has a frequency of .0 - well, I believe it's the same band as we had before.

Q. The same band as we had before, yes, so in this probe DlS7 Mr. Legere's both bands match both bands of Donna Daughney, is that correct?

A. That's correct.

MR. WALSH: My Lord, again I want to go on the record to make it clear what we're dealing with here so we're comparing apples and apples. I hope Mr. Furlotte is not suggesting that Dr. Carmody is - made a visual match of these bands. My understanding is that what we're matching here is bands that fit in one bin as opposed to bands that actually match with each other.

MR. FURLOTTE: O.K., I think for clarity's sake for Mr. Walsh, would it matter for on a statistical basis whether or not the bands match but for statistical purposes building up the product rule, it's just that they have to land in the same bin?

A. They have to be in the same bin. On the other hand, you can clearly have bands that fall in the same bin but that can be discriminated from one another when you are making the visual match.

Q. Yes, if you want to draw exclusions from it?

A. That's right.

Q. But whether or not they match or not you can still

use this process to see not necessarily if it's an identical match but just for statistical purposes whether or not the frequency out there of people falling in the same bins?

A. Right.

Q. And that's all that we're -

MR. WALSH: Well, no, no, that's fine. I just got the impression that Mr. Furlotte was asking the doctor to determine how many bands match Mr. Legere's when in fact what he's asking the doctor is how many bands fit in that bin.

THE COURT: Yes, well, I can understand that.

MR. WALSH: O.K., I was getting lost on that one, My Lord.

MR. FURLOTTE: O.K., the next probe I'm going to, D17S79, which is Exhibit VD71.

A. O.K., I have my notes on that and the relevant data base table available now, yes.

Q. O.K., I am concerned about the band in lane 3 on this one. Mr. Legere has the smallest one.

A. 1309, that places him in what is bin 3 which has a frequency of 29.1%, O.K.?

Q. O.K., and if we go to lane 4, Donna Daughney?

A. She has a band that indeed on this autorad has the identical molecular weight, 1309, so she will also have one that was 29.1% in frequency in the R.C.M.P. data base, Caucasian data base.

Q. O.K., so I guess the next question in probe D16S85, which is Exhibit VD70, I realize the probabilities are small but would it be proper also to compare Mr. Legere with Donna Daughney in this probe?

A. In this probe he has one band that falls in that first bin. He has one band that falls in that same bin and that frequency of that is slightly over half

the population would have a band like that. 50.8% of the population has a band like that, or at least one band like that.

Q. Now, could you calculate the frequencies of probability that somebody else out there might share these same bands as Mr. Legere?

A. Yes, I could. I'd have to go back. Now, let me just make sure what the calculations are deriving from. We're looking at the D1S7 locus where he had a band that had a frequency of 8.3% and another band that had a frequency of 7.6%, that's the first one, so you take 2PQ there, you multiply those two together, and since I already have that calculation I'll just refer back to it. The frequency of that comes out to be one in 78, and then at the D17 locus we have -

Q. Is this on your 99% confidence level now that you're doing this or -

A. I'm doing this to generate the probabilities that you've asked me to calculate. I can also derive from these - I can put confidence intervals on them if you wish.

Q. But I understood when the product rule was being formulated that you would measure - multiply the frequency of the first band by the frequency of the second band and then multiply by two.

A. That's right.

Q. I'm just wondering, if you have one in eleven, is this the one in eleven and one in 13 one?

A. This using the more accurate number, the one in 11 and one in 13 are just rounded numbers. They are the numbers to the closest ineteger when you divide

8.345% into one, so I'm using this fractional number here when I do my multiplications. I don't multiply this times this. If you did that strictly that, what, it comes out to be one in 143, if you just multiplied this times that and then two over that -

Q. And then if you multiplied by two it would be one in 280 or something like that?

A. Well, actually it's two in the numerator, it's two over 143, so it's about one in 72, roughly, but that's different from the one in 78 because the one in 78 is using the more accurate and the greater precision that is in the number of the frequency itself and not in just the one in eleven or one in 13 which is a rounded number from that, so that when you divide 8.345% into one you get not precisely one in eleven, but you get one in - I can just do it here for you - .08345, and we take - the reciprocal is 11.98322, so it's one in 11.98322 that actually is used in the calculation, and in the same way here the one in 13, that is rounded to the nearest integer that would really in fact be .0762, that's 7.62%, and if you divide that into one you get one in 13.123, and that's the number that would be used. If you multiplied those two together, the 11.98 and the 13.123, and rounded that to the next lowest integer you would get one in 78 - and multiplied that by two, sorry, you would get that number of one in 78 which is actually a rounded version of the .01272 that is multiplying that times that times two.

Q. O.K., then, if I was to say the frequency was one in a thousand for one event and one in a thousand

for the other incident, if you calculate on this formula you don't end up with one in a million, do you?

A. It would be in fact probably slightly higher than one in a million. I mean if they were precisely one in a thousand and you multiplied that by one thousand and then you multiplied that by two, you're first of all going to get two over a thousand times a thousand, which is a million, so you're going to get two over a million so you'd get one in 500,000, if that one in a thousand was the unrounded number. I mean, if it was the complete number with all the decimal places on it, whatever, so you would get one in 500,000 if you multiplied one in a thousand by one in a thousand times two.

Q. So actually there's no need to go around to divide it by two and then multiply it by two because, you know, if you divide a million by two, which you get 500,000 and then multiply it by two, you still end up with - back with the million, so it's -

A. No, I don't understand, because to calculate the frequency of those two bands, each of which had a probability of one in a thousand, you multiply one in a thousand times one in a thousand which gives you one in a million, O.K., but then because each of those two bands could have derived one from the mother and one from the father or vice-versa, you'd have to multiply that one in a million by two, and that's where that two times -

Q. So then you get one in two million?

A. You get one in 500,000 because -

Q. Well, you divide by two, you don't -

A. No, you put it in the numerator. You see, you

multiply two fractions, one over a thousand times one over a thousand, and multiplying the product of that by two which is in the numerator part for that, and so you get two over a million then, and which if you expressed that in terms of its least common denominator, it's one over 500,000.

Q. O.K., I understand now how you're getting the one in 78.

A. Yes, and that number, I think you'll appreciate, is not precisely one in 78, it's actually 78-point something, but it's not 79.

Q. Hopefully I'm better in logic than I am in math, so I'll let you continue with your figures, Doctor.

A. Yes, so for that particular locus the frequency of finding another individual in the Caucasian - R.C.M.P. Caucasian data base, is one in 78, O.K., we'll use that, but now, if I do any further calculations I can do it on one in 78, but further calculations as they're done are actually done with greater precision and you actually are using a number that has four decimal places to it so that if you want me to I can express that in refined detail but -

Q. No, I think that's sufficient.

A. I think perhaps where we're leading is just that these one in 78 times whatever the frequency at another locus is, whatever - now, at the D17 locus, I think that was the next one that you wanted me to do?

Q. Well, I know we have a D2S44, but whichever one you have -

A. O.K., I have the D17 here and I have - just making some notes that I have to confess I'm not sure what

they refer back to, but there was a band that had a 29.167% frequency in the R.C.M.P. data base so now the question is what's the probability of having that particular genotype at that locus times the probability of having that particular band at that locus, O.K., so we're going to be multiplying ultimately by that. Do you want me to just do that right now?

Q. O.K.

A. So one in 78 expressed in decimal terms is .01272. I'm going to multiply that now by .29167, and when I multiply those two I get .0371. If I express that in terms of a fraction I get that that is one in 269.54, or one in 269, I would say.

Q. O.K., so we'll have to put that down to keep the multiplication -

A. O.K., so we've taken care of D1 and D7. Now, we had another one, D16, and D16 there was a band that had - it was one of the bands that was very frequent in the R.C.M.P. data base, in fact had a per cent frequency of 50.8%, and now you'd like me to multiply that number times that?

Q. Yes, please.

A. So we're going to multiply .00371 by .508, and that comes out to be .00188. If I expressed that as a decimal fraction, it's one in 530. Now, my notes do not allow me to backtrack to what the next locus was.

Q. I think it's D2S44, which was a band of 2918.

A. O.K., and that had a frequency of 9.696%, I think that was the one. At least that's why I probably had that down here, so you'd like me to multiply the one in 530 by the .09696.

MR. WALSH: My Lord, if I could understand, what formula is the doctor using? Is it T or 2P?

A. I'm just multiplying the probabilitis that Mr. Furlotte is asking me to multiply, so I have one in 530 which was .00188. I'm multiplying that by .0969, and I get that that comes out to be .00018 and expressing that as a fraction it's one in 5,475.62.

Q. Now, so that's one chance in 5,475 - we'll leave off the .62 - that somebody out there has that same profile as Mr. Legere?

A. That has that exact same profile, that has those exact bins that would fall into those - bands that would fall into those bins, yes.

Q. Now, we know that there is another person out there with that same thing, and as we went through the exercise and the procedure yesterday as you told to the judge and myself, to find the probability that two people matching that same pattern are going to be in the same place at the same time, let's do it.

A. O.K., now, I might point out that this in fact is not the exact probability of what you are saying and thinking that I've calculated, and let me point out the reason for this, that we are picking at those loci where we pick one of two bands. We have a choice, and either of those two bands could have matched. In fact, only one did, so that means we have to in those cases multiply this number by two; that is, that if you have two opportunities to see a band that could match, O.K., and you find one that does match, well, in fact both could have matched or the one that you found that did match

could have not matched and the other one could have matched. It's a somewhat subtle point but the point is is that you had in fact at least two opportunities when you observed these other bands of at least one of those two matching a previous band that you wanted to see the match on, so in fact in those cases where you looked at a particular two-band pattern and found one out of those two that matched one out of the two other samples you you wanted me to compare, in fact the probability is not just one over the frequency of that at this locus times one over the frequency of that locus, because you have to allow for the fact that there were in fact a number of other opportunities where the bands could have matched exactly, O.K., and so you have to multiply that in those cases where you've looked at a single locus and found only one match, you have to multiply that in each one of those cases by two, all right, so in the case of D16 there was only one band that matched so in that case we have to multiply this by two, and in the case of the D1 locus where we only had one band that matched we had to multiply that by two. That means that you multiply one over 5,475 by two for the D1 locus and you then multiply it by two again for the D16 locus, O.K., so you multiply it by four, so that number becomes four over 5,475, which becomes one in - I get one in 1,368, slight bit more frequent, not that I think this is going to change where we're going, but now you want to ask me what's the probability of finding two random individuals based on what we know from this Caucasian data base that would have this particular match like this?

Q. Yes.

A. And in that case you multiply the one over 1,368 by the one over 1,368 and you get one in a million, whatever it comes out to, to higher than one in a million, I suppose. We'll just square that, and it becomes one in 1.8 million.

Q. So it's almost one in two million?

A. Right.

Q. Now, the point I was asking you yesterday was where you see on the probes that were run in this case - where you see kind of a matching pattern over five probes, again I suspected yesterday and I believe you said I was wrong, that there is a chance, or a good chance, that if you use another five probes you're going to get more of a matching pattern between these two individuals.

A. Possibly.

Q. And again if you kept multiplying those bands with what you already had, in the end if you went to 300 polymorphic sites which are available you're going to come up with phenomenal numbers of rarity that Mr. Legere and Donna Daughney could share these number of bands, but yet the facts are there, it's true.

A. What I've calculated for you is not the probability that there were matches in bands of any particular bands of Mr. Legere and one of the alleged victims but that in fact the match was for these specific bands.

Q. I agree.

A. These very specific bands, they weren't any bands, and it's like asking what's the probability that two people - the illustration I gave yesterday, of having

the same birthday. The probability of that is not one over 365 times one over 365, because when you calculate the probability, what you're calculating when you calculate a probability of one over 365 times one over 365 is that two people not only have the same birthday, but they have the prior designated birthday, whether that be the 13th of April or the 14th of September or whatever, that's the probability, so there are 365 ways that two people can have the same birthday. In the same way here there are a very large number of ways that two people could match. It's not just that they matched on these particular bands, there are a very large number of days, so in the case to go back to go back, that I think is the closest analogy and reasonable analogy to understand, the probability if you ask the question, what is the probability that two people that you have at hand have and share the same birthday is going to be one over 365, not on over 365 times one over 365. The only time you would multiply one over 365 by one over 365 is if you asked a different question, is if you asked a question, what is the probability that these two people had a birthday on the 29th of March, and that would be one over 365 times one over 365, discounting leap years and so forth, O.K.? It turns out in that case just as a curiosity that that 29th of March that I've just thought about in fact is the birthday that both Richard Lewontin and myself share, and there's a probability of that of one over 365 times one over 365, and that is quite a curious phenomenon.

Q. Quite a curious coincidence, eh?

A. Yes.

Q. Maybe it's something like the Loto 6/49, I'm sure as a statistician you calculate the odds on a person picking out the right number?

A. I in fact don't but -

Q. Have you ever considered it?

A. Well, I have considered it and in fact it turns out that the probability of your winning the lottery is less than the probability of your dying in the next 24 hours. It's a gruesome figure, but in fact it turns out to be the case. But it turns out to be the case if you look at mortality tables, you have a greater risk of not being alive tomorrow than you do of winning the lottery.

Q. I could believe that one, but yet, as great as the odds are in winning the lottery -

A. Somebody wins.

Q. It's not the fact that just somebody wins, but there's lots of times there are six and seven winning tickets, and what are the odds of that?

A. It's very low.

Q. The numbers would blow your mind. Yes, Doctor?

A. Yes, they would.

Q. When you're dealing with the product rule and you're supposed to be within Hardy-Weinberg equilibrium and you're supposed to be in linkage equilibrium, they say the product rule, as I understand it, is valid so long as you have random mating, i.e., meaning there is no blood relatives either within the data bank or with who you're testing?

A. Strictly that's true.

Q. Strictly that's true. Now, if that's true, everything is by pure chance, right?

A. Yes.

Q. Much like the flipping of a coin?

A. That's the analogy, right.

Q. But when people are related, brothers and sisters, I believe you said there's a quarter per cent chance of the band matching?

A. There's a 25% chance of them sharing - having the same genotype for both bands and for any probe.

Q. So no matter how many times you flip the coin, if they are related you're bound - the coin is going to show them that they are matching somewhere whether in fact they match or not? If you flip the coin and you want to - I don't know how you calculate, maybe if the coin had four sides rather than two sides?

A. O.K.

Q. Say a die or something like that?

A. Right, so it had four sides, right.

Q. If you went to the data base or the DNA profile you could probably flip that four-sided whatever and come out with as many matches as if you went through their whole DNA system?

A. Well, you'd expect that if you looked at as many probes, many more than we have, that in fact for siblings, people that have the same biological parents and were not identical twins, that one-quarter of the times when you looked at a certain region they would share the identical genotype for both homologous chromosomes.

Q. And every time you flipped a coin to see if you're

going to get a match, which you have a quarter per cent chance or 25% chance, because you don't get a match at that time does it mean the probabilities that you're going to get a match the next time you flip a coin are any greater?

A. They're completely independent, except if you're looking at another locus on the same chromosome very closely linked to it, but we're assuming here the simplest model as the case in these probes, they're on separate chromosomes, they're inherited independently, and so there's a -

Q. No, if we're flipping the coin we cannot use the product rule, is that right?

A. No, we can't. We can't.

Q. Any more than we can use the product rule in analyzing the DNA structure of the probabilities of their matching because they're related?

A. I don't follow that last one, if you could repeat it for me?

Q. O.K., you could not use the product rule to determine the probabilities as to how many bands are going to match in theirs because they are related, they are not randomly selected?

A. They are not randomly selected and I would not use that in a data base, no.

Q. Right, so you couldn't use the data base of the R.C.M.P. to show the improbability that two siblings are going to share these exact bands like we did between Mr. Legere and Miss Daughney?

A. If they were brother-sister?

Q. If they were brothers and sisters, this would all be for naught, these calculations?

A. That's correct, because if you knew what the parents' genotypes were there is going to be a one-quarter chance that any children of theirs would share the same genotype for any particular unlinked locus.

Q. And that invalidates the product rule because they are related?

A. Well, no, in that case if you had all five probes on those two brothers or whatever, you could calculate the probability that they would have the identical genotype concurrently and simultaneously for all five probes by in fact using the equivalent of the product rule by multiplying one-quarter times one-quarter times one-quarter times one-quarter times one-quarter, and that would give you the probability that they had the identical genotype for all four or five of these probes, depending on how many times you multiplied one-quarter times one-quarter, and basically there you're using the same probablistic idea that what's happening at one locus is completely independent and unlinked with what's happening at another locus, so whatever the probability is here you're multiplying it by the next probability, multiplying it by the next probability, and so on, and that's what we call the application of the chain rule of independent events, that if at each probe position that you're able to examine you have a probability that these two are going to match of one-quarter, then since we know that they're independent, they're inherited independently, you apply this chain rule and get the probability that two brothers would match or any

two siblings would match on all five loci, you'd multiply those together. What is done in a data base where you don't have any information about two people being related, in fact, is to say well, what's the frequency of these various genotypes at loci and multiply the probabilities together where you know that the one-quarter doesn't come in, in fact the number is a lot smaller than one-quarter.

Q. The fact that we've went through this exercise to show the improbability of Mr. Legere matching with Donna Daughney, who - they are not related, or not supposed to be, anyway, for argument's sake - the improbability of that happening with, you know, somebody who lives in a community or something like that, and the fact that it does happen, does that ring any bells that maybe this community is inbred and they are not randomly selected?

MR. WALSH: Objection. Again he's asking the doctor to make a - to assume that the band of Mr. Legere matched the band of the Daughneys according to the matching rules under the RFLP technique. The point I made earlier, My Lord, was that the comparison that Mr. Furlotte is making is into the frequency in the actual bins. The fact that a band of Mr. Legere's -

MR. FURLOTTE: If you'd just allow the expert witness to answer the question -

MR. WALSH: The fact that Mr. Legere's band may fit into a bin that someone else matches is a completely different question, or at least a conceptually different question, than having two bands that actually visually match.

THE COURT: Well, Mr. Walsh, you've answered the question. Now let's see how the witness answers it.

A. Well, I would first of all go back to the fact that the probability that you had me calculate is the probability of having the exact and precise matches that were found here. They're not the probability that there would be any kind of match for bands of other sizes, O.K.? That is, that there are a lot of ways that people can match. If you know that they have specific bands, then there's only one way that they could match, but I think you're asking me to answer a question that is really using as its premise the notion of the probability of having any kind of match of this number of bands, and that is not what I've calculated. The number that I've calculated is the probability of having a match of these exact size bands, and if I might go back to that analogy that I've been using, you're asking me a question about what's the probability that these two people had the birthday on the 13th of August, and you're not asking me the probability of these two people having the same birthday any day of the year. That's the difference and that's the distinction. You're asking me about a probability that relates to that second question, the probability that they had a birthday that they shared regardless of which day of the year it was, and that is one over 365. The probability that they had the birthday of the 13th of August is one over 365 times one over 365, a much lower probability, so you're asking me a question about a probability that in fact I haven't calculated here.

Q. Well, I understood you were, Doctor, and I thought when we first started this it was the probabilities

that people were going to fall into the same bin and whether they matched or not was totally irrelevant because the frequencies that you rely on is the people who fall in a wide bin size and those calculations, those frequencies, apply whether you're a definite match or you're not a definite match, as long as you fall in the same bin, and that's what I understood you to say when you started these figures.

A. Yes, and I'm not questioning that part. I'm saying that indeed - and maybe I misused the term match and I didn't mean that. What I mean is that in fact what you just said, that they fall in these bins, but the probability that you had me calculate is the probability not that in fact they fell into the same bin for any of the bins, but in fact that they fell into these specific bins, O.K., these and only these specific bins. I'd point out that they could have shared other bins, O.K., and there would be a probability that they could have shared other bins, and that probability and all those other probabilities have to be taken into account if you're asking me the question of well, what is the chance that they fell into any bins that would be called the same, of the same numbers that you asked me here. I'm just point out that - and what I'm trying to distinguish here is the fact that the probability that I calculated for you is the probability that in fact these two individuals fell into the specific bins that were ascertained by these probings. That's not the same as the probability that they had bands that fell into bins that matched for other bins, and what I'm saying is - and maybe

I shouldn't use -

Q. I'm not concerned about that because we know they didn't have bands that fell into other bins that matched.

A. Right, but if they had I could have calculated that as well, you see, and if they had that could have been drawn to my attention, and so what I'm saying is that when you look back it's like the analogy you were using with the lottery, there are times when six people win the lottery. Before that happened that is very improbable. After that happened, that happened, and it's a probability of one, so to speak.

Q. So we're looking at appearance and reality?

A. Well, we're looking, and there are some subtle distinctions -

Q. Appearance says it can't happen but reality says it does?

A. Well, but there is a logical mistake that's made here is that the probability of anything, if you chain altogether all the likelihood, probabilities of any event happening, is very, very small, but yet some events happen, always.

THE COURT: Now, perhaps we could finish off on a new topic after lunch? I think this has been pretty well punished to death, hasn't it?

MR. FURLOTTE: Punished to death?

THE COURT: I think this -

MR. FURLOTTE: You can never punish logic to death, My Lord, it goes on forever.

MR. WALSH: My Lord, if I could impose on Mr. Furlotte to have some general indication of when he might be finished with Dr. Carmody, Dr. Carmody has plane

reservations that he may or may not have to change and hotel reservations he may or may not have to change. Yesterday we were led to believe that he perhaps would be done by the end of today and I was wondering if those projections still hold.

THE COURT: Your plane would leave - I don't know where you're going but -

A. Back to Ottawa.

THE COURT: Back to Ottawa. Your plane leaves at -

A. It's completely open, it's just that I would like to know, I mean, and I'm not worried that if you can't be that definite, I'll definitely stay over, there's no problem.

MR. FURLOTTE: I would have a better idea after lunch than I can put forward right now. Would that be sufficient?

MR. WALSH: That's fine. Thank you.

THE COURT: O.K., but you know, having regard to the fact that the doctor has been now cross-examined for two half-days, surely another half-day like this afternoon would finish it up - surely?

MR. FURLOTTE: I don't want to be in this court any longer than I have to, My Lord, and I'm sure the record will show that I'm not -

THE COURT: I don't want to repeat again the general principles governing cross-examination, I've gone over those a couple of times. Well, anyway, we'll know after lunch, have some indication, so we'll adjourn till - can we say two o'clock?

MR. WALSH: Fine, My Lord.

(LUNCH RECESS - RESUMED AT 2:00 p.m.)

(ACCUSED IN DOCK.)

CROSS-EXAMINATION BY MR. FURLOTTE CONTINUES:

Q. O.K., Dr. Carmody, where we left off before lunch I believe we did the calculation figures as to the probabilities that Mr. Legere might meet up with somebody in this community for five particular bands, band pattern.

A. For these particular bands, yes.

Q. And if Mr. Legere was compared to, say, ten or twenty people in the community and that same frequency kept occurring, would that kind of evidence suggest that we might be dealing with a substructuring?

A. If the people that you were comparing were all from the same family or were brothers and sisters it wouldn't necessarily mean that, but if they were randomly drawn from the community it would make me wonder about it, yes.

Q. Now, Doctor, I'm going to go through some of my notes that I have taken and condensed material that I've set aside which deals on the issue of population genetics, and if I seem to be taking a time before I get from one question to another it's because I'm not properly prepared for cross-examination at this time so you'll appreciate it's going to take a little bit longer than what would normally be necessary, O.K.?

A. I'll be forbearing, yes.

Q. I think it's been found before that the - and I'll just make a statement that in population genetics

this multiplication procedure for determining the combined power of identify or series of individual powers of identity is valid only if two conditions substantially exist, and it says, "Four adjustments are made for deviations from these conditions", O.K., and these conditions are known as, "(1), Hardy-Weinberg equilibrium, and (2), linkage equilibrium. These conditions assure that pure chance will govern observed gene frequency, not other factors so that the laws of probability will be obtained". Would that be a correct statement?

A. That's correct, I would agree with that statement.

Q. Now, if there are deviations from either the Hardy-Weinberg equilibrium or deviations from linkage equilibrium how do you make adjustments for that if you don't know the degree of variations that's involved?

A. Well, as I said earlier, I have done some statistical tests that would show if there was any significant amount of deviation from those assumptions, and the statistical tests that I did indicated that there was no strong evidence to support either deviations from the Hardy-Weinberg law or from the linkage disequilibrium criteria, or from linkage equilibrium, whatever, and so therefore I concluded it was valid to do the calculations because I could show that there were not any strong deviations from those assumptions for the Caucasian populations that I've been analyzing in the R.C.M.P. data base.

Q. O.K., that's when you check for different data bases?

A. No, that's - well, the one thing, yes, I looked at the bin frequencies in Vancouver, Ottawa, Kingston. I didn't see any statistical differences in the bin frequencies. I then, however, in that new amalgamated data base that was put together, I then could check to see whether there was in fact any correlation at each locus of having one band occur significantly more or less frequently than you would expect by random chance for each of the loci. I did a weak test that wouldn't because you can't test every single possible category, you don't have a large enough data base to do that, so you have to, as I was describing yesterday, break that down into four categories at each locus and see whether in fact the bands that are appearing in the first category have any correlation with bands in the other categories, second category with any of the other categories, third with any of the other four, fourth with any of the other four, and I've done that running within a locus for each probe, but I've done that between loci in an equivalent way to see whether the patterns of having particular two bands at this first probe position show any strong correlation with the co-occurrence of a particular double-banded pattern at another probe position, and I've done some tests of that nature. I would be the first to admit that these are not going to pick up perhaps low levels of disequilibrium, but nevertheless, it did not find any and so it was on that basis that I conclude that it's proper to do the product multiplication.

Q. O.K., but I think we established yesterday also that these different areas of Canada where these population was tested, they cover a pretty broad area and where there is a lot of not only random mating but a lot of people from outside coming into these areas?

A. That's right.

Q. Now, in establishing a data base or for checking on the Canadian natives, I don't know but I suspect the testing went into a small community, maybe from one Indian Reserve and checked another Indian Reserve. Would that be a safe assumption?

A. From my knowledge of how those Indian data bases were collected they were not from one single reserve. The case of the West Coast aboriginals that were looked at, I believe they were taken from a relatively large geographic area, but I'm not sure exactly how large, and I know in the case of the - what's called the Winnipeg sample or Northern Ontario sample, they drew from a number of separate reserves and it wasn't just from a single reserve.

Q. O.K., so even though that these small population people, although they were far apart and yet the sampling was taken over a broad area, the different Indian groups in the different areas, they still come up with a significant difference?

A. They come up with significant differences in terms of the bin frequencies, yes. I haven't in those cases done any of these tests to look for Hardy-Weinberg equilibrium or the linkage disequilibrium. We've been spending our time up to now with the Caucasian data base, particularly because it's so large.

Q. Now, if the sampling was taken from just one small Indian Reserve out on the West Coast and one small Indian Reserve in Northern Ontario you could possibly get even a greater significant difference?

A. You could possibly, yes.

Q. And it would be improper to use the data base for one group when maybe the suspect comes from the other reserve?

A. That's right, and certainly as I expressed yesterday, if you had a suspect coming from still a third population that hadn't been sampled but you knew it was an aboriginal population I'd be very worried about which data base to use because I would not think it would be proper to even take an average of those two.

Q. Now, in the Caucasian population in Canada, because of those test results amongst Indians, wouldn't it be feasible and scientifically acceptable and necessary in order to show that we don't have a problem in the Caucasian data base or amongst Caucasians like we do amongst the Indians that maybe a sampling should be taken from some small isolated community amongst the Caucasians?

A. I would say that yes, I would support the idea that it would be good to have that information.

Q. And it's quite possible that if you conducted that test that you would find that if you did a small community say in Eastern Canada and a small community in Western Canada like you did with the Indians - or not yourself personally but like was done with the Indians, that it's quite possible that we may end up with the same results as we had with the Indians?

A. I would say from just what I've seen so far with the Caucasian data base that is very unlikely. I can't completely rule that out but I would say it's unlikely from virtue of the fact that not only do I now have information on the Canadian populations but I've seen some U.S. populations where there are some significant differences, statistically significant differences, at some of these probe loci between some populations at the bin level, the bin frequency level, but yet when you do the forensically relevant calculations they don't make any difference.

Q. Yes, but let's try to stay out of the forensic field again.

A. All right.

Q. Because the forensic field as I understand is borrowing their theory and the product rule from the general scientific community?

A. That's correct.

Q. So I think we should stick with their criteria, would that be proper, for validating or invalidating the Hardy-Weinberg?

A. Fine.

Q. That would be a proper assessment?

A. Yes.

Q. Do you have any idea how long it would take to - as I suggested, to form a data base on a small scientific community - or not a scientific community but a small community in Eastern Canada and a small community in Western Canada amongst the Caucasians?

A. I would guess that that could be done given the money and manpower in three months, four months,

something of that order of time.

Q. Would this possibly dispel a lot of concerns by some scientists?

A. It would dispel some. The problem with it, though, to just go back to the fact, what can really be rigorously tested statistically is the bin frequencies. Right now it still is difficult to test for real Hardy-Weinberg equilibrium at each locus and for linkage equilibrium between loci and it's virtually impossible to do that with small samples, and so one of the problems in sampling small communities is that you're limited in the size sample you could take because even if you exhaustively took every individual in that community the size would still - I mean when we're talking about a community that I'm think about of several thousand people, you know, say two thousand people, having sampled exhaustively every single individual in that small community you wouldn't still have a large enough data base from that community to be able to do these tests for Hardy-Weinberg equilibrium and linkage equilibrium in a rigorous statistical way that could allow you to exclude any reasonable level of deviation from these principles.

Q. No, but we could do a test analogous and on proportion-wise as we did with the Canadian Indians?

A. Well, all that's been done with the Canadians is a look at the bin frequency, and that can be done on virtually any sample size, including the samples of four, five that we had earlier this morning. That can be done regardless of the size,

and you can do statistical tests on that regardless of the size, but the problem with doing rigorous tests for deviations from Hardy-Weinberg equilibrium or deviations from linkage equilibrium are requiring large sample sizes, larger than the typical sort of small communities that we're thinking of and sort of sampling, so it becomes a practical problem then and I would say yes, it would be - and I think it would be for population genetics purposes interesting to sample some small Caucasian communities like that to see how much the bin frequencies vary. I expect that they will not vary very significantly from one another, but to really test the questions that I think population geneticists are worried about mostly are these equilibrium criteria. To do that you need quite considerably larger samples than we have now, and that could not be done in three months. I think we're talking about a research program that is probably going to continue and be ongoing for the next five or ten years to amass enough samples like that, and indeed, to really answer those questions I think what would probably be a better experimental design would be to go back to European populations and take samples of a reasonable enough size from the main ethnic groups that have founded Canada and that are present in the current genetic composition in Canada, so to take reasonable samples from England, from Scotland, from Ireland, from France, and other countries that have a considerable proportion - have contributed a considerable proportion to our population.

Q. I realize it would take a considerable time to prove that there is no linkage disequilibrium but nevertheless, if we did something along the same lines as we did with the Canadian Indians it would be a start?

A. Yes.

Q. And as you said, it would improper to use either data base or, in the Indian population, nor could you average them out, so does that mean it's impossible to do forensic testing on an Indian suspect?

A. No, if you had some idea that they were from that general area, and I think what's going to proceed is to sample still further Indian communities, and what happens is that when you have just a sample of two and they're very different it's the problem of having - if I could make an analogy of sort of two points on a graph. You can always draw a straight line between them but until you've sampled ten or fifteen or twenty you can begin to see some larger pattern emerging, and you can be more confident that if you sample twenty communities and the twenty-first and the twenty-second and the twenty-third all fall within some of the clusters that you've previously seen, you feel more secure as a statistician and a population geneticist saying well, what we've sampled here spans all the reasonable probabilities that we're going to turn up in the future, and so we can then start talking about doing some averaging amongst those, but when you have just two points like that and they're very different you really don't have a sense of what the pattern might be when you took further samples,

and that's really the problem right now with having two, and to a certain extent that would apply even in a case of Caucasian communities. If you're, say, taking a sample of a small one in Kamloops area or something and another one in Newfoundland, it would give you two points and you can relate the other Caucasian larger samples that you had, but then the Caucasian larger samples have been drawn, as you've pointed out, from wide geographic areas and areas where there's a lot of transient influx and immigration from. When you have to isolate communities you'd really want to sample more than that. I would feel more secure if I were going to draw some general inferences from that to really have sampled, let's say, ten or two dozen or something like that, to get a sense that, you know, if there was a geographic patterning, if there was some kind of larger picture that would emerge when you had greater samples, it's all the same question of trying to make inferences on very small samples. It's difficult.

Q. Yes, I understand, and it's like you use Kamloops and some small community in Newfoundland, but if we use Kamloops - say the suspect was from Kamloops and the crime was committed in Newcastle and you had the population data base from each area and they were significantly different like the Indians, there's no way you could draw any conclusion as to what probability factor you could put on it, could you?

A. Not unless you had the data base from each of those communities that were relevant, that's right.

Q. And would you agree that equilibrium is a condition that exists when you find gene frequency to be what you would expect by chance alone if everything were independent and unrelated?

A. That's right.

Q. Would that be a correct statement?

A. That's right.

Q. And a population is in equilibrium when there is no correlation between the allele contributed by the mother and the allele contributed by the father at a particular locus; that is, the alleles are independent of each other?

A. That's correct.

Q. Would you agree that with deviations from Hardy-Weinberg equilibrium the frequency of the allele in the population and thus the uniqueness of the fingerprint can be in question but this is not necessarily related to the validity of the match?

A. Could you state the first part of the question again?

MR. WALSH: Well, if he would tell me where it comes from as well I could double-check it.

MR. FURLOTTE: It comes from the Cashel case at Page 993.

MR. WALSH: So you're quoting from a judge?

MR. FURLOTTE: I would assume. I believe the judge was quoting from Dr. Green in the Wesley case. It says, "Conservative or reduced calculations may also correct the Hardy-Weinberg deviation problems and in bracket, "Dr. Green, Wesley", and it goes on to state, "With deviations from Hardy-Weinberg equilibrium the frequency of the allele in the population and thus the uniqueness of the fingerprint can be in question when there are deviations"

A. When there are deviations it can be in question, yes.

Q. And, "For the tests to be reliable two basic conditions must be met; one, the alleles that are tested for must not be the result of linkage disequilibrium". Is that correct?

A. Correct.

Q. And, "The data base population must be in or approach Hardy-Weinberg equilibrium".

A. I agree.

Q. And, "Hardy-Weinberg equilibrium assumes that allele frequencies in the population will remain constant from generation to generation so long as there is random mating in the population"?

A. That's correct.

Q. And that would go for small communities also?

A. That's correct.

Q. And especially for small communities?

A. That's correct. What can happen in small communities is that there is another phenomenon that we call genetic drift that can happen. That is that it's another level of sampling that complicates our analysis in population genetics, and that is, if I can make some analogy here, it's as though from going from each generation you are taking a genetic sample of what variants are present in the previous generation to represent in the next generation, and if there is a small population you have only a small possible number of alleles to choose from to found the next generation unlike if you had a very large population. That is a very large population can have very, very many

variants present. When you have a small population and if I could exaggerate perhaps and say if you had a population of only ten individuals it's not possible in those ten individuals to have all of the possible variants present that we know can occur. We know, for example, that at the D1 locus there are something like 27 different possible bands that could be present there. Well, if you have a sample of ten individuals it is just impossible to have a representation of 27 bands. At most you could have a representation of 20 different bands, O.K., at the best, so it means that in a small population you necessarily are restricting the possible number of variants that you could have there, and when these individuals leave descendants in the next generation there's a likelihood that not every one of those variants that were present in the previous generation, particularly those that were present in only one copy in those individuals, would get represented in the next generation, so in the next generation there can be a slight shift in the bin frequency patterns, and if that goes on for a number of generations where you keep taking and the population stayed as a sample of ten, you could have changes in the bin frequency patterns happening that were not the result of any selection or mutation or anything else but that what we call as genetic drift. It's kind of like a sampling, it's as though in every generation you're taking a sample and then that becomes the population from which you take another sample and that becomes the population - and so

what can happen is that any point in that process if you lose one of the variants or more than one of the variants that were previously present it will no longer be represented in that population, it will be lost, and you'll gradually in the course of time be continuing to lose some of the variation, so that what happens in a very small population like that, you get what's called genetic drift where the frequencies change just by this accidental sampling that goes on from generation to generation. The smaller the population the more exaggerated that effect is, and in fact you can express mathematicall that exact effect on the variances and changes and the mean time to fixation for alleles and so forth, as a function strictly of the population size. As that population size becomes larger the sampling process is such that you include most of the variation every time you form a new generation like that, and it's not much of a problem, but in small populations, even though they meet random Hardy-Weinberg criteria and linkage equilibrium criteria, whatever, you can still get this effect of sampling from one generation that can make the bin frequency change, so I'm just qualifying my answer to the question of whether if you have Hardy-Weinberg equilibrium and linkage equilibrium the frequencies have to stay the same. I'm saying in small populations they don't have to stay the same.

Q. I'll finish the statement. It says, "Linkage equilibrium is met by seeking alleles from different chromosomes. This increases the probability that the segments measured occurred

randomly rather than being the product of one parent's genetic contribution". Now, that would be correct?

A. That would be correct.

Q. Now, some scientists seem to be concerned about the frequency that would occur in a small isolated community where, you know, people are not moving away from it, you know, they don't have to be isolated by a fence, just the fact that they continue to live in that small community, and a lot of them mention about the small inbred communities. Now, is it safe to assume that they don't only mean by inbred that there is incest but also that there is a lot of extra-marital affairs going on within the small community?

A. No, it doesn't mean that. What we mean by inbred, actually, is a statistical term that means that there is a correlation between the occurrence of alleles at a genetic locus, and that can happen - well, to take the extreme case, all of us at one point can trace our ancestry back to a few common ancestors at some point. We actually can't in practice do that but we just know that the human species derived at one point from a small number of individuals, of some primate, whatever, something like this, so we all have a genetic ancestry that we can trace our lineages back to in that sense, so what we're talking about is the fact that if you find statistical correlations of a particular band co-occurring with that same band, that is, you get an excess percentage of homozygotes, that means that there is indication of inbreeding. It doesn't mean necessarily incest, but it means that a small

community, if you trace - and if that's remained closed to immigration, then it means that after a number of generations if you traced back all the pedigrees and so forth you would find common ancestors to virtually everyone in that pedigree, in that community, and that means that they have a greater probability of sharing the variants that were present in those common ancestors, and we call that the inbreeding effect, so you get an increased homozygosity as a result of getting inbreeding.

Q. An increased rate of homozygosity or a high degree of band sharing or even double band sharing, it would have the same effect, would it not?

A. It means that in fact you get non-randomness is really what it amounts to is that you get a non-randomness in it because the model that generates the random distribution assumes that everybody is not related.

Q. So a high degree of band sharing within a community shows that there is non-randomness?

A. Not just the sharing but in fact, I would say the homozygosity, because if the homozygosity is larger than you expect, that's the indication of inbreeding, and that would lead to a conclusion that there was more band sharing but strictly it's not the band sharing itself, it's the increased homozygosity that is really the measure of that.

Q. Well, the double band sharing, then, for a certain locus, would be just as effective as proving randomness as homozygosity, would it?

A. No, I mean strictly homozygosity, having individuals that had a single band pattern that were a true

single band pattern and not the result of having a double band pattern where the one band had been lost because it was too small and gone off the gel, but a real homozygote where in fact that single band that you observed really reflected the fact that on both chromosomes, the chromosome inherited from the mother and the chromosome inherited from the father, there was the same band present on both of those chromosomes.

Q. Now, again I'll make a statement that, "The Hardy-Weinberg equilibrium assumes that allele frequencies in the population remain constant from generation to generation so long as there is random mating in the population". It goes on to state, "Of course, small deviation from Hardy-Weinberg equilibrium exists in communities for a number of reasons, including the fact that human mating is not in the truest sense random".

A. That's correct.

Q. And what other reasons would there be?

A. Well, as I mentioned, the fact that even if you had random mating, completely random mating, but you have a finite size isolated population, that can lead to deviations from Hardy-Weinberg equilibrium, even though you have completely random mating, because of the fact that you're getting a gradual loss of genetic variation simply by the sampling process and that is in fact a result - a consequence that we call genetic drift.

Q. Did you have occasion to read the Branbury Report by Dr. Lander?

A. I actually haven't read it, I haven't received a copy of it, no.

Q. So there's no way you can comment on it, then, I assume?

A. Not at this point on that particular report. I've read many of the other reports and I've read an article by Dr. Lander that appeared in the journal called "Nature", but I haven't read his remarks in the Branbury Report, no.

Q. The one in Nature, was that what, "DNA Fingerprinting on Trial", or -

A. That's right, that's correct.

Q. Would it be your opinion that Dr. Landers has legitimate concerns?

MR. WALSH: Objection. I'd like to know first of all what document he's going to put to him, I'd like to know what statement Dr. Lander has made that he wants him to comment on. I think that is the least we could expect, My Lord, under the circumstances.

THE COURT: That's fair enough, Mr. Furlotte. I mean the witness must know what you're asking him to comment on. Are you looking for a copy of that?

MR. FURLOTTE: Yes, I am, My Lord.

MR. WALSH: Of the Branbury Report or Nature?

MR. FURLOTTE: The article in Nature, "DNA Fingerprinting on Trial".

MR. WALSH: My position is, My Lord, that if he wants to put a provision in that commentary to Dr. Carmody I have no problem. My understanding of the law, if Dr. Carmody doesn't accept the statement, then I don't think that there's any further that can be made use of it on cross-examination.

THE COURT: I think the only use that's going to be made of it is you're going to read off some proposition

from that that you just recited earlier, in true fashion or otherwise, and you're going to ask his opinion as to whether he agrees with it or -

MR. FURLOTTE: Yes, My Lord.

THE COURT: Go ahead, but we don't need that in evidence.

MR. FURLOTTE: I don't see why it should not be in evidence, My Lord. It's an article that's coming from a professional of high standards in his scientific discipline.

THE COURT: If you want to ask the witness to read it and ask if he approves of the whole thing perhaps it could be put in, but it seems to me what you're trying to do, Mr. Furlotte, is get opinions put in evidence or get a paper put in evidence which isn't supported by anybody. It may be, if the witness says yes, I agree with that, it's supported.

MR. FURLOTTE: My Lord, we're dealing here in this case with opinion evidence which -

THE COURT: Later when it comes to argument, if you want to say, look, Dr. Lander wrote an article called "DNA Fingerprinting", and question and you want me to refer to that, I'll read it. I have already read it. As a matter of fact, it's right in the corner of my desk out there right now, but that's argument, that's not evidence. That's not the way you put evidence in. Go ahead and read your proposition from Lander's article.

MR. FURLOTTE: Well, My Lord, for the record, I would hardly think it would be proper for you to be going out and doing your own research into the reliability of DNA evidence.

THE COURT: I read that article before I was even associated with this case. I didn't read it for the purpose

of the case. Some other judge circulated it among all the judges in the province before I was ever assigned to this case, and quite apart from that, what's wrong with a judge or a court or anybody else reading material on DNA? You know, you and Mr. Walsh have kept me supplied with dozens of American cases and Canadian cases as well, or at least - on this subject, which I have followed, I haven't read them all thoroughly, but there's nothing wrong with my familiarizing myself with the principles.

MR. FURLOTTE: That's right, and I think that's fine because both Mr. Walsh and myself know what you're being supplied with and therefore we know what arguments we have to put forward.

THE COURT: As a matter of fact, that article you're talking about, I think I -- at one of the pre-trial hearings, if my memory is correct, I was the first one to mention that article and I asked both counsel or all counsel present if you were aware of the existence of that article, and that was on December 5, 1990, in Newcastle. It was I who brought it to the attention of you both.

MR. FURLOTTE: That could be. My memory is no doubt not as great as yours.

THE COURT: Oh, I think I'm correct in that because - as a matter of fact, I'm not sure I didn't make reference to it in the - no, perhaps I didn't - in the minutes of that pre-trial hearing.

MR. FURLOTTE: Well, maybe, Dr. Lander (sic), I'll just provide you with a copy just to - and I can refer you to certain points of it so we don't take anything out of context here, and then I'll ask if

you agree with it or not. In the first page of tht article in the third column, the second paragraph, Dr. Lander states: "It is my belief that we, the scientific community, have failed to set rigorous standards to which courts, attorneys, and forensic testing laboratories can look for guidance, with the result that some of the conclusions presented to courts are quite unreliable". Would you agree with that statement, Dr. Lander (sic)

A. I perhaps would have agreed with it in June of 1989 but as of today I would disagree. I think that the scientific community has become much more actively involved and has in fact been setting a number of standards, particularly in the areas of quality assurance, and people have been arguing and debating and proposing ways of testing the data that at that time, which is almost two years ago now, hadn't been considered, so I would say that that statement now, I would not agree with.

Q. O.K., because they are being implemented today?

A. That's right, and have been over the past two years.

Q. O.K., now, what if those quality control standards and other standards that Dr. Landers refers to were not in effect at the time that these results were obtained?

A. That the results in this particular forensic case?

Q. Yes.

A. Well, I -

Q. Would then you have to say that probably the results would be quite unreliable, or there's a good chance?

A. No, because I would say that his statement here is

referring to the fact that because we didn't have those testing standards some of the conclusions are quite unreliable. I think that it's not necessarily the case that they are unreliable, even if those standards were not met. I think that by having the standards we're assured that they're reliable, but that by not having the standards doesn't in and of itself necessarily mean that they are unreliable.

Q. But it would be much more difficult to tell if they were reliable without those standards?

A. Yes.

Q. And about the middle of that third column Dr. Lander states: "It is my contention that DNA forensics sorely lacks adequate guidelines for the interpretation of results both in molecular biology and in population genetics".

A. Again I would answer similar to my first answer about this paper, namely that I think there have been dramatic evolution standards and changes and reconsiderations and further debate about techniques and procedures in the two years since this article appeared that I would not agree with that statement as of this May, 1991.

Q. What improvements have we seen in the debate or the issue of population genetics in the past two years?

A. I think that we have much larger data bases coming from many more populations. We have a lot more data in hand now than was present at that time. We have much more assurance about the way that that data had been collected. We have much more quality control about the fact that perhaps in those early data bases there may have been related people

contributing to it, that the early data bases were based on taking samples from Caucasians in one laboratory in one part of the FBI or something like that, so that those standards have certainly been improved and people are much more aware how not having so-called random sample and not having samples that represent different geographic regions could bias the data which at that time, I would say some of the original data bases suffered from that fault.

Q. At the bottom of - lefthand corner you'll see 504 -

A. Yes.

Q. Do you have that?

A. Yes.

Q. It would be at the bottom of the middle column, right at the last paragraph starting it states: "At the meeting held on the 11th of May the experts agreed upon a consensus statement declaring that the DNA data in this case are not scientificall reliable enough to support the assertion that the samples do or do not match. If these data were submitted to peer review journals in support of a conclusion they would not be accepted. Further, experimentation would be required", and it states, "In particular, the statement cited and the inappropriateness of discounting the extra bands at DXYS14, declaring a match between bands at D2S44 and D17S79 was issues differed by more than Lifecodes' announced threshold of three standard deviations."

MR. WALSH: My Lord, I'm going to object. He's now - I have not objected to what he's obviously doing before

this in terms of I've allowed him to go along, but now what he's actually doing, he's reading from the conclusions that were drawn in the Castro case as if there was some kind of generalized statement with respect to everything. I don't understand the relevance of actually making a statement that if you flip open to the Castro case you'll find the conclusions that were drawn.

MR. FURLOTTE: If Mr. Walsh would have a little more patience so I can explain what I want - I feel I have to read all this so the Court is not taking something out of context, nor will Mr. Walsh jump up and shout with glee, "You're taking something out of context". I'm reading the paragraph to him, then if there's a particular part of that paragraph I want to address. The rest of it is irrelevant for the purpose of my question to Dr. Carmody, but I don't want to be accused of taking something out of context.

MR. WALSH: My Lord, if I may just again so I won't jump up too much here, but if I could just clearly for the record state the Crown's position. Yesterday or the day before or last week, I'm not sure, I referred the Court to The Queen vs. Anderson, a decision that I know this Court is aware of in the Alberta Court of Appeal in which it clearly said the use to be made of authorities in cross-examination, and my understanding, My Lord, is if you take an authority like Mr. Furlotte has and read a section of it to a witness, which he's entitled to do, who denies the authority, then my understanding is no further use can be made of it because in essence what is happening is that Dr. Landers is

testifying and although I may or may not make any inroads on him, I don't have the opportunity of cross-examining Dr. Landers on his opinions, but I have not objected in the last two questions he's asked. Now he's gone even farther than that and he's now going into the actual results of the Castro case which I don't - I think he's taking liberties that shouldn't be - he shouldn't be taking.

THE COURT: I must confess here that I wasn't able to - I haven't got this in front of me and I wasn't able to follow from your reading, Mr. Furlotte, of this whether - just the significance of this. There is an opinion expressed there, is there?

MR. FURLOTTE: There was an agreement, here there was an agreement amongst the defence lawyers and the lawyers for the prosecutors - I'm sorry, not the lawyers - there was an agreement between the defence expert witnesses and the expert witnesses for the people in the Castro case who come to an agreement about certain particular standards that must be met and would have to be met within the scientific community, and I want to point out one of them to Dr. Carmody to see if he agrees with those experts' agreement.

MR. WALSH: That's not correct. What the agreement was in the Castro case is there was an agreement between the prosecution scientist and the defence scientist with respect to the actual inclusions, the matches that were found in that particular case. I don't think that there was any generalized agreement with respect to the standards for the scientific

community as a whole.

THE COURT: Have you another copy of that?

MR. FURLOTTE: O.K., I'll have to have it back.

THE COURT: Can I borrow one just temporarily? At the meeting held on 11 May - and you went right down to the word engagement, prior engagement?

MR. FURLOTTE: I went down to about "three standard deviations", I guess.

THE COURT: Down to what words, prior engagement?

MR. FURLOTTE: Down to the "announced threshold of three SDS".

THE COURT: Yes, but my word, what a terrible question to put to anybody.

MR. FURLOTTE: It's not a question, I was just reading it to him, so now I will put the question to him.

THE COURT: You've already put the question, do you agree with that, but how can anyone agree or not agree with it? As Mr. Walsh says, this is dealing with evidence in some case, what is it, the Castro case?

MR. WALSH: Yes, the Castro case.

THE COURT: The Castro case, and what does the witness know about it? Well, what is your question here?

MR. FURLOTTE: Well, finally we can get to it. Dr. Carmody, would you agree or disagree that the discounting of extra bands in the running of a particular probe, if you were going to interpret band matching and you have more bands than what you expected, would you agree that it's proper to interpret that band, or that probe, if you just discount the extra ones?

MR. WALSH: But this is a population genetics question or is he just -

A. I would say in answer to the best of my ability, and I have to confess that my ability is limited in this area, that I haven't seen these autorads and I'm not sure just from the context here exactly what they're talking about but I'm reasonably convinced knowing that the experts on both sides agreed in their non-acceptance of this data that I would also agree in the non-acceptance of this data in that particular case, were it asked of me, and I think as I interpret this statement in here about the extra bands at the DXYS14, these are bands that are X and Y chromosome bands, I would guess, that I have no expertise in dealing with, and I don't know how often one gets extra bands or gets the right number of bands, or if you have a vaginal swab you may have mixed DNA from both the semen and the vaginal cells so that I don't know what those extra bands mean, actually.

THE COURT: Well, doesn't that mean, Mr. Furlotte, that you should move on to another field here of questioning? The witness says he isn't competent to answer that within his expertise.

MR. FURLOTTE: Do you know what extra bands might mean on a pristine sample?

MR. WALSH: My Lord, again, I'm objecting. If he finds out what the population genetics issue is -

MR. FURLOTTE: My Lord, this is the only witness that the Crown has out of the five that they're presenting that I feel is unbiased, and I feel I should be able to - that there's built-in biases on all the other Crown witnesses. I may be wrong, I may be right, that's for you to determine.

MR. WALSH: I've just heard a statement in a court room, My Lord, that Dr. Kenneth Kidd is biased, and I think I'll just end it there, I'll sit down, because there's no sense trying to talk reason to Mr. Furlotte.

THE COURT: Well, I'm the person who decides bias or not. I want to give you freedom here, Mr. Furlotte, in asking questions, but let's keep it within the expertise of this witness, and mind you, again I'll remind the witness that if he feels unqualified to comment on some of this thing he can -

MR. FURLOTTE: Dr. Carmody, I feel, is being very honest to both the Crown and myself. He qualified his last answer that his knowledge was limited on that because it deals with forensic samples, but I am now asking him about extra bands showing up on a pristine sample.

THE COURT: Well, we'll let him decide whether he's qualified to answer that.

A. I can make some comments about having extra bands on a lane in a pristine sample. I would say that you - as I indicated earlier, where we had a sample that had three bands in the lane, that we're really not sure of the molecular causation of that. We have some ideas about it but they have not been absolutely incontrovertibly tracked down to know why that occurs. It occurs very infrequently in Caucasian populations. One of the interesting things is that when we look in the Canadian aboriginal populations they can be much higher in frequency. You can get as many as four bands in a

lane. We're not exactly sure what that means. There are a number of possible alternative explanations. I can run through some of them but I'm not sure that they're going to lead - well, I don't want to go any further, I guess.

Q. What if even four or five bands, what might that indicate?

MR. WALSH: My Lord, again the Crown objects.

THE COURT: On the ground that -

MR. WALSH: That it's completely outside the - I haven't had the opportunity to direct the man on the area - Mr. Furlotte is now into cross-examination on an area that I haven't had the chance to direct on and I haven't even asked the Court to have him declared an expert in. I know Dr. Carmody is trying to be helpful but Dr. Carmody has not been brought here and has not been offered to the Court as an expert in that field, we have other people for that. Now, it's different if I had actually had him declared an expert, had him directed on those issues, and then he was cross-examined, but I mean, Dr. Carmody is being helpful and I understand that, but I think Mr. Furlotte is going to get into cross-examinations of all kinds of fields and he -

MR. FURLOTTE: I'm just looking for the truth, My Lord.

MR. WALSH: Oh, and the Crown's not? That's an interesting statement. Thank you, Mr. Furlotte.

THE COURT: Well, we're all looking for the truth, aren't we? Go ahead, Mr. Furlotte, and the witness or I will intervene if necessary.

MR. FURLOTTE: If we run a probe, one of the forensic probes that the - and not the sex probe or the

individuals, and this is known to be the case, part of a region of a chromosome can become duplicated and attached to still another chromosome so that in us, and that's what happens in some cases of Down's Syndrome, for example, that there is an extra piece of the 21st chromosome, this chromosome right here, that becomes attached to the 14th chromosome, so for that particular region there are not only the two copies that are on the 21st chromosome but there is a copy on the 14th as well, and so individuals that have that particular composition would show three bands even though there was an internal site. Now, you could get four bands if both of the two chromosomes had an internal cut site. In the same way one could imagine more than one internal cut site that would result if you had two cut sites within the region that normally is not cut you would generate three bands from that one VNTR. The other VNTR if it was not cut would give a single band so you could get four bands in that way, so those are some of the most biologically plausible explanations for what is going on.

One can also get problems in the procedure of just producing these results where, for example, you can - it has happened sometimes that you don't completely digest the DNA; that is that all of the outside sites don't get attacked. If that were to happen, then sometimes if this site were not cut you could get a piece of DNA that would extend all the way to the next Hae site which may be further on, and if that didn't happen all of the time you

would get both some of the copies that had resulted from the two sites being cut and sometimes you would get another band because that site hadn't been cut but there had been a cut down here, so it would give a much bigger piece, so there are some biological explanations in terms of plausible ways that biologically what you're seeing is real, there are also ways that you can get that that are the result of improperly digesting the DNA or potential contaminating the DNA or some laboratory artifact, so to speak, and so I would say that there are two main classes of explanations on how you can get multiple bands. The one category of them are that they are strictly laboratory and procedure and methodological artifacts where something has gone wrong, and the second class of explanations is that there's some biological phenomenon of what we call trans-locations onto other chromosomes or having internal sites that are very, very rare and that don't typically get picked up.

Q. If this was common in a small community what would that indicate?

MR. WALSH: Objection, My Lord, I can't help - but I'm sorry, My Lord, again -

MR. FURLOTTE: Well, we're getting back into population genetics now, My Lord, I don't know how he can object to this one.

MR. WALSH: No, we're not. Mr. Furlotte is aware of the fact that we have probes in this particular case from the case specific evidence that Dr. Carmody has not familiarized himself. Mr. Furlotte is aware of the fact that there are extra bands on some of those as a result of incomplete stripping

of the autorad in which another probe is laid to eliminate them, but what he's doing is he's asking Dr. Carmody to testify in a field he has not been declared in and he's asking Dr. Carmody - he's directing this particular testimony to case specifi evidence that Dr. Carmody has not reviewed before he took the stand, and I find -

THE COURT: Well, really, you're trying to tell Dr. Carmody, Mr. Walsh, that he should not answer the question, that he isn't prepared, but let's let Dr. Carmody decide that. If he isn't I'm sure he'll say so. Go ahead, Mr. Furlotte.

MR. FURLOTTE: My Lord, I could ask for a mistrial in this case because if the Crown is trying to influence Dr. Carmody into not answering the questions, which is what -

THE COURT: Oh, you could ask for a mistrial but you wouldn't be granted a mistrial, so go ahead and ask the question.

MR. FURLOTTE: Well, I know that, My Lord, but that doesn't mean I shouldn't ask for it.

THE COURT: Go ahead and ask the question here.

MR. FURLOTTE: Dr. Carmody, you feel your expertise is sufficient that you can answer these questions that I'm proposing?

A. I feel I can give an answer but to be honest I don't know and I can't say that I've considered all of the possible - particularly the methodologic problems that could arise that would give extra bands, so with that limitation - I mean, I've mentioned some of them. I'm sure there are others that I haven't thought about or that I haven't

considered. I'm more interested in the sort of biological potential causality in this case. I mean I find that a fascinating thing and I think that there are people who are trying to work out whether in fact you do sometimes get these internal cut sites or not.

Q. If these internal cut sites were common in a small population - I'll try again - in a small community, what would that do for the Hardy-Weinberg formula or the product rule, or would it show that maybe there is a substructure here or -

A. If you found an abnormally high incidence of these in a small community that was not similar to the frequency that they occur in larger samples it would indicate that there are some genetic variants possibly there that are in higher frequency than in the larger population. It could indicate that.

Q. Would it be true, Dr. Carmody, that the mis-identification of a small number of allele lengths could substantially alter the frequency calculated from the data base?

A. This is a case of the punitive excess homozygotes that are not really homozygotes because you're seeing a single band where there is actually a heterozygous state because one is moving off the gel. Since you can't see that other band it could have a slight influence if you called all those single bands homozygotes and used those as a double in your frequency calculations for the bins. It could have an effect on increasing the frequency of those particular bins. On the other hand, one would expect under Hardy-Weinberg and linkage

equilibrium conditions that the occurrence of those missed bands, those bands that were not seen for methodological reasons, would occur randomly with all of the other bands on that gel, and so it would not lead to a very great difference, I wouldn't think. I'd have to do the calculations but it could lead to some slight difference in the bin frequencies, yes.

Q. You would still probably end up with big numbers after you used the product rule?

A. Probably.

Q. Do you know whether or not Dr. Lewontin is of the opinion that, "Individuals may form endogamous groups based on religion, ethnicity, and geography" and that if, "genetic substructures exist between these group with respect to VNTR's then mating is not truly random"?

A. I know he has written that, yes.

Q. And I understand one thing to invalidate the Hardy-Weinberg and product rule would be that if mating is not random?

A. That's right.

Q. That would invalidate the ability to use the product rule?

A. Depending on the degree of that, yes. I mean, it's a question of degree. You know, there are degrees of non-randomness, and if there were slight amounts of non-randomness and if you averaged it out, if it was a slight amount of non-randomness it may not be serious enough, it would -

Q. How do you know when you exceed that degree?

A. Well, you have to look at the genotype frequencies

and do statistical tests, actually, as the only way to know. There isn't any way just by telling me that the degree of non-randomness, whether it would have a significant effect or not. To give you an example of why just knowing the degree of non-random mating wouldn't help you, it would make absolutely no difference, for example, if in the different non-random mating subgroups, be they religious, ethnic, cultural, geographical, whatever, if there were really no differences in the frequencies of the various bins. If there were no differences in the frequencies of the various bins, then if there was non-random mating it wouldn't have any effect. The effect of the non-random mating only becomes significant and becomes greater and is a degree important if the amount of bin frequency difference is great between the different non-random mating groups.

Q. Yes.

A. So that if you had, I don't know, a significant religious subgrouping, that would only have an effect genetically if there were a significant difference of the bin frequencies in, let's say, the Roman Catholic subgroup and the Protestant subgroup.

Q. And the Canadian Indians are a good example of that?

A. Yes. Yes.

Q. Now, since you studied under Dr. Lewontin I'm sure you followed a lot of his opinions on this matter of substructure?

A. I'm familiar with his opinions, yes.

Q. And that he feels that, "It's necessary to assume that substructure exists rather than doesn't exist

because analogous studies involve blood type, non-VNTR genes show there is substantial substructure within European Caucasians"?

A. Yes, I know he's written that.

Q. And do you agree or disagree with that?

A. I would disagree in applying that to the Canadian Caucasian population data base that I've been involved with because I've been very much aware of that and the motivation for my doing the tests that I have done on it are strictly to try and corroborate or show that that is incorrect, and I would say that the tests that I have done have shown for the Canadian Caucasian data base, given the admitted limitations on that, though it's 750 individuals, still not as great as one would like ideally, and the fact that we don't have samples from every geographic region in Canada, nevertheless, I find no evidence in the tests that I've done to support what he is saying there.

Q. But you would admit your tests are very limited?

A. Yes, and the tests would not pick up slight differences.

THE COURT: Is that Dr. Lewontin quoted in the - are we talking about the -

MR. FURLOTTE: In Jacobetz. I'm reading Dr. Lewontin's testimony from the Jacobetz case.

THE COURT: Oh, yes.

Q. How important is it for scientific reliability in the general community to be able to duplicate the results of higher tests? If you're going to run a test twice, you know, to show that your results are reliable, how important is it that they are duplicated?

A. Well, you always try to duplicate it as closely as you possibly can because if you don't and you find differences, then you're not sure what to attribute the differences to, so that one tries to control, and if you're trying to replicate a previous test, previous experiment in science, you typically try to duplicate the conditions as closely as you can in order to eliminate any possible problem of not knowing what the real explanation is.

Q. O.K., if you run two tests and the results are, we'll say, substantially different, is it scientifically accepted and acceptable in the community to pick or choose one of the tests that you say, well, I'm going to rely on this, or is it more appropriate to throw both of them out and do it again?

A. Well, I'd say in a scientific community in general we have the luxury often of not having to make a decision. We can live with that ambiguity until it's resolved, we don't necessarily have to accept both, reject both, or accept one or accept the other. We have the option of saying, well, let's wait and see and do still a better test. Unlike in forensic proceedings where in fact you have to say one or the other, yes, no, as I understand it, and you know, maybe my naive approach to legal matters, so I think that if in that case if you have two results that disagree one first looks to see if there's any difference in the methodology of conducting those two experiments to see whether in fact you can explain the disagreement, first of all. Perhaps it was done in a different temperature,

perhaps it was done on a different population, perhaps the analyses was done improperly or whatever, so ruling those types of explanations out one is left with perhaps a contradiction, a paradox or whatever. One then sits down and one of the most exciting parts of science is to then say, well, how can we understand this, how can we design an experiment that will critically decide what the explanation is, and you then try and design or people try to design still another experiment that would attempt to resolve what the differences are in those first two that didn't jibe.

Q. But if you took these tests through, say, for peer review, the scientific community is probably going to tell you, well, look, Doctor Carmody, you go back to your laboratory and do it again a couple more times and bring us something that is not contradictory?

A. Yes, that's right, that's right, that if you find two results in your own work like that that are contradictory the tendency would be to say, well, look, try and resolve it and then come back to us.

Q. Right, because it wouldn't be reasonably reliable to depend on either one since they contradict each other?

A. That's right, because there's either some variable that you're not taking into account or some phenomena happening there biologically or chemically, whatever, that we don't understand yet, and so let's get better results before we put it in the published literature.

Q. And they're also liable to tell you that, well, look,

Dr. Carmody, you know, your opinion might very well be right but since you've conducted the test there might be a built-in bias in your opinion that you wanted the result to turn out a certain way so maybe your opinion is directed towards that result?

A. That can happen but that's one of the reasons that we use statistics, because I know there is that common impression that you can say anything with statistics but that's not true. One is very limited and one resorts to statistics because they have an objectivity to them that is very difficult to prejudice in the direction that you're trying to hope the results will come out in. There are subtle ways that you can deceive yourself into getting results that you would like to get but that one of the reasons that we use statistics, because it's very difficult to do that if you have statistically valid procedures and are doing things statistically appropriately.

Q. And procedures that have standards that are set by the scientific community?

A. That's correct.

Q. So that if you're going to interpret the results of some testing, then you're interpreting according to those standards?

A. That's correct.

THE COURT: I wonder if that wouldn't be a good place to stop for ten or fifteen minutes and then perhaps you were going to, Mr. Furlotte, indicate perhaps whether this witness would be free this afternoon, freed up by the end of the afternoon?

MR. FURLOTTE: I spoke to Mr. Walsh and to Dr. Carmody and

I figured that maybe at four-thirty I might be able to give a better indication.

THE COURT: You don't want to keep going till four-thirty now before the break?

MR. FURLOTTE: No, I think a break would be appropriate at this time.

THE COURT: Let's take the break and if you can do anything to finish - I don't know how much you've got left but if you can finish -

MR. FURLOTTE: I stated, My Lord, to Mr. Walsh and Dr. Carmody that if at four-thirty I thought I could finish up by six o'clock I would ask the Court to continue until six o'clock.

THE COURT: Well, even five o'clock. O.K.

(RECESS - RESUMED AT 4:00 p.m.)

(ACCUSED IN DOCK.)

THE COURT: Just before you start, Mr. Furlotte, I just wanted to correct a statement I made earlier which was incorrect. I suggest that I had read the article, "DNA Fingerprinting on Trial", and I think I suggested that I may have brought it to the attention of counsel. I was confusing that with another article, "When Science Takes the Witness Stand", which was published in the Scientific American back in May, 1990, and that was the article. I don't think I've ever read "DNA Fingerprinting". It was this article that I was thinking about. Now, both counsel, I'm sure, have copies of that because I think I did mention this at the pre-trial hearing.

MR. FURLOTTE: I believe you gave us a copy of that. I believe you did.

MR. WALSH: Yes, I understand that's a popular magazine article and I've had it sent to me by probably half of the population that read that. I've had it sent to me in one form or another, My Lord, yes. It's widely circulated.

THE COURT: It was circulated before this Court ever originated - one of the judges on the Court, I think picked it up and thought it would be of interest and circulated it to us. Now, go ahead. You were going to indicate that you would be through by five o'clock.

MR. FURLOTTE: I did? I know I've got a short memory but it's not that short.

THE COURT: But you were going to try to be, I guess that was what you said.

MR. FURLOTTE: I'll try my best, but not to the prejudice of Mr. Legere.

THE COURT: Well, let's start anyway.

MR. FURLOTTE: Dr. Carmody, did you study all the autorads that were collected in compiling the R.C.M.P. data base?

A. No, I did not.

Q. Did you study any of them?

A. I've gone through the procedure on a sample of one to see how they actually do it. They have a computerized system that reads them and so forth but I've only done that as an exercise of how one goes about doing it. I did not see more than that one and I did not see the procedure implemented on all of them.

Q. So what did you rely on, just the computer sizings

or -

A. I relied on the computer sizings and the summary that comes out of the data base program that they have at the forensic labs, yes.

Q. So you don't know the quality of the autorads that compiled the data base?

A. I cannot say that I can comment on that yes or no. I do not know the quality of them, no.

Q. Whether those autorads had multiple bands? No?

A. I don't know.

Q. Or faint bands?

A. I don't know.

Q. Now, when the data base is compiled and using the autorads testing they basically just run the one gel once, is that correct?

A. That's right.

Q. And then they'll take the computer sizings and bin them?

A. Yes.

Q. Now, do they also run a monomorphic probe to see if there's band shifting when they're running these gels?

A. They run standards, of course, molecular weight ladders on the gel in a number of lanes to get calibrations for that gel. They also run a gel and from the blots that are produced they probe that with more than one probe. I'm not sure if on those data base blots that they actually do the monomorphic probe as well. I don't know whether they do or not.

Q. So if - we'll say for instance if they don't do the monomorphic probe with their data base to show whether or not there is band shifting it would then

be possible that the actual sizings of the data base could be out by as much as their band shifting in that system, would that be right?

A. Well, I would expect it to fall within the quality assurance limits that I know in other work they have done where they've run the same specimens on different gels and compared the sizings that they read off of those different gels. That is, if there's a set of experiments where you calibrate your system, so to speak, to see how often on pristine samples like this you do get any band shifting or what the variability and uncontrolled variation in the system is. Once you've established that and you follow the same procedures, one would expect that in fact all of the future uses of that same procedure would give you results that were within that quality assurance criteria, and so that you wouldn't expect that there would be changes.

The other control that is run that I know on each gel, they do run what's called a cell line, that is that it's not probing for a monomorphic probe in each lane but you know that on that gel there is run a standard that is run on every gel, and you know what those band sizes are so that's in a sense a control between gels, and if there were band shifting one would see it as well in that cell line, one would expect, as well as in the samples that - the unknowns in the data base sample.

Q. Well, the cell line, that would only tell you whether or not there was band shifting because you got something other than what you were expecting within that lane?

A. Yes.

Q. But if the gel had, say, 20 lanes, then there is band shifting from lane to lane and they are not the same, is that right? That does occur?

A. It could, but in these systems it's been shown that in fact you always fall within this - in fact, much less than the 5.2% window, so that one wouldn't expect that if you had band shifting in general it would leave the band as an estimate of molecular weight remaining in the same bin.

Q. Yes, but even though the band shifting would be much less than the 5.2% window the R.C.M.P. like to say for the monomorphic probe, that doesn't mean that the other probes run, that they could shift greater than the band window, 5.2%, couldn't they, depending on the molecular size?

A. No, the 5.2% would apply to any size band on the gel. It's a percentage, and so for larger size bands you can allow for a greater absolute difference because it's a percentage of that size.

Q. In band size?

A. The band size, so that at the top of the gel where you have larger band estimates you can tolerate a greater shift than you can at the lower end, so to speak, where you have a percentage again and the sizes are smaller.

Q. You're talking about base pairs, number of base pairs?

A. That's right, the percentage of base pairs.

Q. The percentage would be the percentage of, say, a 5,000 base pair or the percentage of a 2,000 base pair, you're going to -

A. That's right.

Q. But the percentage you're saying would be about the same?

A. Well, that's what's found.

Q. You might get a 50 base pair differential in a 5,000 band fragment or in a 20 base pair in difference in the -

A. That's typically what's found, yes, that it seems consistent in terms of looking at different sizes across the gel.

Q. What would happen if you didn't have that consistency Would that tell you there was something wrong with your system or would that be called an anomaly that -

A. It would suggest there's something wrong with your system that there should be some higher quality control implemented on your system, there's something that you're not controlling for, either the batch of agarose that was used or, I mean, there's dozens of reasons why technically one could get a change like that.

Q. If there was something wrong with your system as such where maybe you were getting this kind of phenomenon or anomaly or whatever we want to term it, what could that do to the validity of your data base if that happened with all the autorads through your data base?

A. Well, if every single rad in the auto base had band shifting and they were in the same direction for all the lanes except your control lanes and your standards lanes that could possibly move the bin frequencies up a bit and shift them in the direction that you were getting the band shift. One expects, though, what would happen is that if you had some

problem with your quality control that in some gels the band shifts might be making the bands faster or therefore called smaller in size, and in some gels you might have a retardation in the band and it would be sizing it as larger, so that if it were a quality control problem where from one gel to the other you were getting band shifting sometimes up, sometimes down, sometimes greater or less, that on average in fact that should balance. Now, if you had a type of band shifting where consistently on every gel that you ran, and only on the samples that are the unknowns do you get the band shifts and that the cell control lines and the standards ladder calibrations are not band shifting, then in fact you could get a change in the bin frequencies in your data base where they would possibly all be shifted down by an amount that the band shifting would indicate.

Q. O.K., I believe Dr. Waye had testified that when you get the phenomena that you've mentioned that one band was running fast and the other one was retarded, called something like reverse band shifting, I believe he stated that in those conditions then the test is inconclusive because a phenomena has occurred that is unexplainable. If this happens in the formation of the data base should that sample be used to put into a data base?

A. If you have some anomalous phenomenon like that and you're aware of it, that should not be put in the data base.

Q. The samples that are done for the data base, do you know if there was any controls within the gel to check to see if there was reverse band shifting?

A. I don't know if there were any controls like that done. The only controls that I can imagine, and again it's not in the same lane but would be the cell lines that are run on that gel.

Q. But would you agree that you can only check for reverse band shifting by running the same sample twice? Do you know of any other way to check for it?

A. I don't know of any other way to check that, no.

Q. Now, some scientists hold, and I believe in the Yee case which, for the benefit of yourself, Dr. Lewontin and Dr. Lander and Dr. Hartl testified, I believe they believe that there's no scientifically acceptable compensation factor has been or could be built into the FBI's Caucasian data base that could adequately respond to ameliorate the potential effects of possible substructuring. Would you agree with that or would you have a different opinion?

A. They don't use any correction factors for either an imagined deviation from Hardy-Weinberg equilibrium or linkage equilibrium because it's - the assumption there is is that it has not been observed and it is more likely to not be there than to assume that it is there and to use some correction, because if you're going to use some correction you have to know how much exactly is there to know how you're going to correct it. If you don't have any evidence of it being there the conclusion has been that you assume that Hardy-Weinberg equilibrium is met and that has been tested in the Devlin-Risch publication that was submitted in evidence on direct examination, and so there is no strong and good evidence to

indicate that there is real deviation in any of these data bases from Hardy-Weinberg equilibrium and there is no evidence at the present time that there is linkage disequilibrium or deviation from linkage equilibrium so that there are no corrections applied.

Q. But in science when a scientist is attempting to promote a theory and test results and validity of such, isn't the onus on that scientist to prove to the scientific community that his calculations and his theory is proper, valid, and highly reliable?

A. Well, it gets a little bit into a philosophical issue. In science you never prove anything. In science you're only able to disprove things, that any scientific evidence can only disprove a hypothesis, and so what you're constantly doing in science is testing a hypothesis, and if you are able to disprove that, then you're able to accept an alternative hypothesis, so by finding results that are consistent with a certain hypothesis doesn't mean that you've ever proven it, so to speak. You've been able to disprove alternate hypotheses.

Q. So the best a scientist can hope for, then, is to either form a working model and a hypothesis and prove to the scientific community not that it's absolute but that it's workable?

A. Yes.

Q. And if you - basically if you can convince the general scientific community that it is workable and it's probably reliable for the purposes that you want to use it for, then that is sufficient and

then generally accepted in the scientific community, is that right?

A. That would be, I think, a fair statement of how science proceeds, yes.

Q. So it's basically the scientific community says, yeah, it's probably a good working model?

A. Yes.

Q. And once you've reached that stage, then it's up, I suppose, to other scientists, what, to come to their peers and review committees to prove that it's not workable?

A. To prove by evidence, by objectively obtained and objectively supported evidence, that in fact disproves that generally acceptable conclusion.

Q. So what I understand to be happening in the field of forensic evidence here in relation to DNA analysi is that the forensic scientists are going to the general community and they're saying, look, we have a system here that's probably tenable and it's workable for our purpose and it suits our purpose for what we want to establish in court; now you prove we're wrong. Is that basically what's going on?

A. Well, I think there is evidence in support of the position of the forensic community, and they're saying that, show us evidence that we are wrong, so I guess I would agree with your conclusion.

Q. So in here basically what the scientific community does, they've put a reverse onus on the general community or the general scientific community?

A. Well, I'd say I'd characterize the state at present in the scientific community is that there are differences of opinion.

Q. And basically what it's boiled down to at this point - I guess I won't walk into that one - at this point is that the forensic field is stating to the general scientific community that, look, we have a working model and our product, the end result, our figures, tells us that it's reliable, now you prove that our theory is wrong; is that what they're doing?

A. I'd say that might be a slight caricature of it but I think basically that's the situation.

Q. And the general scientific - well, at least a good many people in the general scientific community who are not into the forensic field are telling the forensic field that, look, guys, you're putting the cart before the horse - not in those words but to that effect?

A. Well, I would characterize it by saying that there are some people in population genetics and in the scientific community outside of population genetics who are expressing cautions about the use of data like this and that are saying there is great potential in it but perhaps we should delay a bit till we have more samples and have looked further and have been able to do better statistical tests on larger data sets. On the other hand, there is a significant component in the population genetics community who are proceeding to do tests, design tests, look at the data as it is to try and show and corroborate what the procedures are that are being applied by the people in the forensic area.

Q. I believe also in the Yee case Dr. Caskey - you kow who Dr. Caskey is?

A. Yes, I know who Dr. Caskey is.

Q. And I believe he - in past experience he usually is called as an expert witness by the proponents of this in the forensic field?

A. Yes, he is, and he chairs a committee of the National Academy of Sciences that is in the process of deliberating and coming up with a report.

Q. And his position was that the population genetics have had considerable controversy in the calculation area, is that right?

A. I don't recall that specifically. I'd have to say that I would have to look back at that.

Q. But basically the debate is still open?

A. I'd say the debate is still open, yes.

Q. And the scientific community in general, not just the forensic field, are in the process of trying to decide whether or not the forensic field, that it is proper for them to use the Hardy-Weinberg formula and the product rule?

A. I'd say that there is at the present time testing going on and people writing things on both sides of the issue, yes.

Q. But I assume it's your position that it's still safe to use the product rule even though the scientific community cannot decide on the issue yet?

A. I feel that it's safe to use it because I feel that there is enough justification and the people whose opinion I regard with equal value with Doctors Lewontin, Hartle and Lander indicate that there really isn't any significant deviations that we're going to ever find and that if there were some slight deviations the effect on these calculations

is going to be very minor. That would be my position.

Q. Yes, and rightfully so, you're entitled to your opinion in your expertise, but looking at it - when you look at what the stakes may be if your opinion is wrong, and especially in the States where they still have the death penalty, is it really safe to attempt to - or is it good science to try and force your opinion in instances like this that are under great dispute and seriously deserve examination by the scientific community before any result is made? Is this good science?

A. I think it is. I think that the weight is so - I mean, I would say that even if we were to find ultimately in five, ten years from now that there were some small amounts of deviation from Hardy-Weinberg equilibrium and some small amounts of deviation from linkage equilibrium that the effects I think we already know are going to be in the - some effect on the third or fourth decimal place in these calculations that are not going to have any significance in terms of the forensic implications. That would be my - and so I think that in fact the technology and the statistical techniques are mature enough to actually apply at this time, and I don't have a concern that these rather, to my mind, esoteric refinements are really going to make any difference, ever, in these calculations. That would be my position.

Q. Would you admit, Dr. Carmody, that if it is improper to use the Hardy-Weinberg formula and the product rule, you know, there's no logical validity for the basis of using those formulas, that the mere fact

because you end up with big numbers, that that is also invalid?

A. Well, I think it's not an either/or situation where if you find some slight deviations from one or both of those laws that it means you're never going to use them. I think that you'll see that in population genetics where in fact we use these formulas in situations of analyzing populations where we know and can measure the amount of deviation from these laws, we can apply correction factors, and we use the principle with a little correction factor and there is a mathematical technique for doing that. Those correction factors in the cases of human populations and in my studies of the data base so far are going to be of a very small size and are going to have, in my judgment, very little impact or minor impact on the ultimate calculations.

Q. But in Dr. Lewontin's studies of the European Caucasian he found there was significant difference and he's of the opinion that there's no formula that you can make a correction factor for the variants in that I believe you've admitted that the difference within the Canadian Indians, that you don't know how to resolve the problem, that you could not use one or the other or you couldn't average them out, and it just seems that with that kind of evidence out there that there is substructure which is substantial which would invalidate the use of the Hardy-Weinberg formula and the product rule, and without studies of those situations being in the Canadian Caucasians does that not cause you some concern that just maybe,

maybe your opinion is wrong?

A. It doesn't cause me concern because I've been involved with the studies on the Caucasian data base and I see nothing like the evidence that Dr. Lewontin has shown for ABO blood group frequency differences in European populations. We don't see that in Canadian Caucasian populations, serological studies. We certainly don't see it for studies on the VNTR loci. I would have concerns, and I have voiced them to both Crown attorneys and at the R.C.M.P. forensic labs, about the difficulties of using these calculations on native aboriginal data bases where you don't know which is the relevant data base in particular. I don't see a problem with Caucasian populations in North America. I think the studies have been done and the studies are continuing to be done to an extent that we can rule out quite surely in my mind slight deviations that may in future ever be found.

Q. Dr. Carmody, if in the Canadian Indians data bases you said that, you know, it's improper to use one or the other, but if you did use one rather than the other could you possibly convict an innocent person? Could that kind of information to a jury or a judge - could it possibly convict an innocent person?

A. Well, I think that the calculations that I've seen, even when you use in that extreme case of the native Indian populations, that could possibly change your net frequency of perhaps one in 50,000 to perhaps one in a million. If that degree of difference were going to make a difference of a conviction or non-conviction, then I would have a

worry. I'm not - I don't really feel that it would. I mean my feeling is that even if you can show something - I'm expressing my opinion now - I think if you can show some forensic evidence that the probability of this match, getting a random match like this, is less than one in 10,000, to my mind that's low enough for me to call it beyond all reasonable doubt. Once you get up into the astronomical figures much greater than that it doesn't carry any more weight to me personally, and so my feeling is that once you've been able to establish that it's at least one in 10,000 -

Q. So you state that one in 10,000 would be beyond a reasonable doubt for yourself?

A. For myself. I mean, I would like to look - and the other thing about this is that I'm not aware of cases - there may well be them and I'm sure there have been some - where in fact it's only solely and exclusively the DNA evidence that is convicting somebody. It may carry a lot of weight in a particular case but I haven't seen instances where that is the only evidence that we have. I think it has to be corroborated by other evidence.

Q. O.K. For instance, you were involved in this study of the hair analysis which come out to, say, the number one in 4,500?

A. Right.

Q. Would that be enough for your personal opinion to create a reasonable doubt or would that be proof beyond a reasonable doubt?

A. I would want to have other evidence if it was just based on the hair matching alone in isolation and there was no other evidence. I would have some

concern about convicting somebody for a serious crime where they were going to be kept incarcerated, I would have doubts in that case whether I would consider that only alone.

Q. But the one in 10,000 you would consider that alone as sufficient?

A. Probably, I think, but I would also - and again I haven't heard of cases where that's the only evidence, and I would even in that case, I guess, if there was no other evidence, I would be a little bit leery of just taking that alone. I would -

THE COURT: One in 20,000?

A. I know there has to be some magic boundary, My Lord, I'm not sure I know what that is, I have to confess, and I don't know. I mean, on the other hand, one of the things we get hung up here on is the fact that if you have three eyewitnesses or something, what number can we put on that? We just do that by our seat of the pants feelings and I think in any case that I were having to make a judgment on I would never want to do it on something as simple as just numbers. I would want to use some kind of intuitive feeling about other testimony and other evidence and credibility of eyewitnesses and whatever was involved in the case.

Q. But I'm sure you probably realize, just the numbers would be sufficient enough for some of the general public to accept it beyond a reasonable doubt like yourself?

A. Possibly.

Q. And maybe the one in 10,000 is sufficient for you, maybe one in 4,500 is sufficient for somebody else?

A. That's correct. I think the other aspect of this is what we're talking about is a probability of an individual matching a certain forensic specimen. It gets into the whole area then that even if that specimen was contributed by that individual does that mean that that individual is guilty of that crime that he's charged with. I mean, there's always that problem. If the hair that was found at the scene of the crime indeed, we could have a hundred per cent assurance that it came from that individual, does that necessarily mean that that individual committed the crime? You see, I'm not sure that the probabilities we're giving say that that's the probability that that person committed the crime.

Q. That would depend on the evidence?

A. That's right. That's right exactly.

Q. Now, you mentioned - I guess I'll go back to the Canadian Indians, the difference in the population data bases that with the low figure of one in 10,000 that you would convict on, or a good chance you'd convict on anyway, considering that type of a low figure, again, if you were to use the improper data base as with the Indians when you realize that they're not valid and you yourself wouldn't use them, but if you were to use them there would be a good chance that you could convict an innocent person.

A. Well, you could get a number -

Q. If one showed one in 10,000 and the other one showed one in 2,000?

A. It's possible that you could get differences of that magnitude.

Q. So -

MR. WALSH: My Lord, again, I swore at the break that I would try and limit the amount of objections but I'm forced to my feet. I object; Mr. Furlotte is asking the doctor, in my humble opinion, to talk about his opinions with respect to the probability of the guilt or innocence of an individual as opposed to what we're dealing here, the probability of whether or not two particular forensic specimens match, and I don't see the relevance of that particular line of question.

THE COURT: Well, I wonder if we haven't canvassed the witness's opinions with regard to the Indian population statistics quite sufficiently, Mr. Furlotte. We've touched upon it numerous times in the course of the examination. I think the witness has probably said everything he need say about that.

Q. Do you know a Dr. - what is it, Ron Acton?

A. Ron Acton? Yes, in fact, I've spoken with him and I was at a meeting that he was at about three weeks ago, yes, from the University of Georgia, I believe, or Alabama - I've forgotten, he's from the South, anyway.

Q. And how would you rate his expertise?

A. I would rate it quite high. I'm not familiar with all of his work. I know he has done some studies on black populations in the South and I believe some Caucasian populations, but I'm not actually familiar with his results.

Q. And what field does he in particular deal with, the population genetics?

A. Population genetics from what I know of him. I don't know that much of his previous publication history. I think it's very much human population genetics but I'm not certain.

Q. You say that he did a study between the blacks in the United States?

A. Between different populations of blacks, as best as I recall, and found that there were differences in bin frequencies in different populations.

Q. Amongst blacks?

A. Amongst blacks.

Q. Similar to the Canadian Indians?

A. Similar to the Canadians. I don't know the magnitude of the differences. I can only attest to the magnitude of the differences, really, in the Canadian Indian populations, and I don't know how much the differences he found compare to the differences I found for the Indian population.

Q. And were his findings found to be generally accepted in the scientific community?

A. I don't know because I actually haven't seen the publications, to be honest, and I would be leery of commenting upon them. I haven't seen them cited yet in any other publications that I have read.

Q. But as a population geneticist or whatever, a publication as such that would normally take your interest?

A. Yes, it would. If in fact that you brought it up here I'm going to make an attempt to look into it more deeply in future, but that's not relevant to what I can comment upon here.

Q. Now, the fact that the forensic field uses what I

suppose some scientists call a continuous allele system rather than a discrete system like when you're analyzing blood groupings, the Hardy-Weinberg formula and the product rule, is it the same or is it harder to apply to the forensic field than it is to categorize the frequencies of blood groupings?

A. It is more difficult to apply because you have to in fact create these bins in order to generate frequencies, and there are different ways of creating bins, a number of different approaches on doing that, and it's not as clear-cut and necessarily have a single way of analyzing it as you would with a discrete allele system where you have as the case of ABO blood groups or whatever, discrete frequencies of alleles. Here we are defining artificially what we call an allele by setting up a certain bin boundary and by saying that - and if I could make an analogy again, perhaps, looking back at the distribution of something we might be more familiar with, let's say we had a spectrum of distribution of annual incomes, that if we wanted to do statistics on that what is typically done is you make bin boundaries and you divide all of that continuous distribution up into categories of let's say $1,000.00 ranges, something like that. If you want to then do some statistics and compare the distribution of income in one part of Canada to another part of Canada you break it up artificially into some bins and you compare the frequencies in these two areas. If you wanted to know if the distribution of annual incomes in British Columbia were different from the distribution of income in New Brunswick

you may not just want to know whether in fact the mean incomes were different but in fact if there was a different profile on those two. There are tests that allow you to handle those continuous distributions without breaking them up into some categories and then doing some tests, so in the same way with the continuous system like that it's necessary to break up what is otherwise a continuous distribution of size fragments to be able to do any statistical tests or to treat that in any genetic way.

Q. But when you're using the product rule in relation to the blood grouping there is no problem there because you're very limited with your bin sizes, if you want to call it a bin, and there is no possibility of making a mistake in identifying the allele, is there?

A. Well, it's not strictly true, because I can give you examples in the case of what I've just described as the ABO blood group that we say there's an A allele, a B allele, and an O allele. It's known in fact that serologically what are called the A allele can be further subdivided if you want to use more refined serological techniques into an A1 and A2 and so forth. The fact that they were agglomerated or conglomerated or consolidated into what you just call A doesn't really affect the fact that you can use still the product rule and the Hardy-Weinberg equation to calculate frequencies even though we know that really there are some sub-alleles within those categories of what we call A and indeed there are sub-categories within B, so far as I understand.

so what I'm saying is the fact that you just have to consolidate things into a class doesn't in and of itself necessarily invalidate the use of these mathematical tools.

Q. But in forensics if you're going to do your blood typing between known and unknown sample you're going to get your blood typing right, are you not?

A. Yes, if you're calling it right in terms of - but again there I could say that let's say you said that a person had a Type A and it was a match because the forensic specimen was a match in Type A. I could say, well, you know, it could be a Type A but perhaps this was an A1 and that was an A2, and indeed that's the case. Now, I don't know the relative frequencies of those, I'm not an expert in serology and I'm not going to go any further there, but the point is is that there can be some sub-groups there and you could be making a mistake by saying, well, this is just A, when in fact if you had more refined methodology you could say, well, no, it's not just A but it's actually A1, and this is not an A1, this is an A2, and you could have called it a match when in fact it wasn't.

Q. But whether it's A1 or A2 they call it just A?

A. In general that's my understanding. I don't know, I can't comment on serology, I have no expertise in that area.

Q. O.K. For compiling a data base would it be more difficult to do it handling forensic evidence rather than pristine samples?

A. Yes, it would.

Q. So that would make it more difficult to interpret

an autorad where you're analyzing forensic samples than pristine samples also?

A. In general I think that's the case. I'm not familiar with all of the problems that can happen to a forensic specimen but one can imagine that if a blood stain were subjected to bacterial action and having been frozen and thawed several times, whatever that the DNA could change in some ways that I couldn't predict, so it's less reliable than a freshly drawn blood sample that you know has been kept at minus 70 until you use it and so forth.

THE COURT: Would you like to take a few minutes recess, Mr. Furlotte, while perhaps you decide whether you do have any other questions and if you didn't -

MR. FURLOTTE: My Lord, it's a matter of going through this volume and this volume and identifying the areas that deal with population genetics. I have the areas dealing with microbiology highlighted in yellow and the population genetics in orange, so it's a matter of leafing through to see which ones are in fluorescent orange, read it, and see if I haven't already covered the topic.

THE COURT: Well, how long would it take you to do that?

MR. FURLOTTE: I think I've covered most of the topics already but I have to go through to make sure and -

THE COURT: Would five minutes sort of give you an opportunity to - five or ten minutes?

MR. FURLOTTE: O.K., if you want to take a break.

THE COURT: We'll take a break for five or ten minutes. See if you can't sort of - I think you'll probably find that you've covered most - surely to God you've covered most all aspects. I can't imagine -

MR. FURLOTTE: My Lord, if you haven't learned anything in this proceeding yet I probably am wasting my time.

THE COURT: Oh, I'm learning all the time, but I'm having it drilled into me for the tenth time now, some of it.

MR. FURLOTTE: I don't think I'm covering any of the topics twice or I'm -

THE COURT: Well, we'll take a recess. You look through it. If you can finish quickly, or fairly quickly, Mr. Walsh presumably has some re-examination?

MR. WALSH: Yes, My Lord, I hope my re-examination won't be very long.

THE COURT: Let's go from there - ten minutes.

(BRIEF RECESS - RESUMED AT 5:10 p.m.)

(ACCUSED IN DOCK.)

THE COURT: Now, Mr. Furlotte?

MR. FURLOTTE: My Lord, I've been going through the booklet here and I find that there are just too many issues left that I haven't touched on yet and there's no possible way I could finish with this witness this evening.

THE COURT: Well, do counsel have any suggestions as to do you want to adjourn now for the night or -

MR. FURLOTTE: Yes.

THE COURT: How do Crown Counsel feel?

MR. WALSH: Mr. Furlotte has indicated that there's no reasonable expectation of finishing this evening, I see no choice but to set it over till the morning.

THE COURT: Can you give any indication, Mr. Furlotte, how much longer you might be with this gentleman? You

know, do you have ten questions or -

MR. FURLOTTE: Oh, no, I have more than ten or twelve. I expect I will be at least all morning.

THE COURT: Well, surely you can sort of set noon-hour as a deadline on yourself, couldn't you?

MR. FURLOTTE: My Lord, I have no intentions of setting any deadline for cross-examination of this witness.

THE COURT: You're the first defence counsel in the world who I know who hasn't set a deadline on himself when it comes to cross-examining witnesses on the opposite side, and I stated the reasons for it earlier. However, that's your problem and I'm not going to tell you how to run the defence, but self-discipline, you know, is required of counsel in deciding what questions they're going to ask and what they're not. Beyond that I won't say anything. What time do you want to start in the morning, nine-thirty?

MR. FURLOTTE: Nine-thirty.

THE COURT: Dr. Carmody, you would fly out, then, tomorrow afternoon, presumably?

MR. WALSH: Tomorrow afternoon.

THE COURT: I can see that he wants to know when to give up his room, I suppose, at the hotel.

A. In fact, I've given it up but I'm sure I can -

MR. WALSH: We'll make arrangements, believe me, My Lord. Dr. Carmody will be -

THE COURT: Provide him with a tent overnight?

MR. WALSH: He has given up his room and changed that but we'll fix it for the morning, My Lord.

(ADJOURNED TO 9:30 a.m., MAY 8, 1991.)

(RESUMED AT 9:30 a.m., MAY 8, 1991.)

(ACCUSED IN DOCK.)

CROSS-EXAMINATION OF DR. CARMODY CONTINUES:

Q. Dr. Carmody, are you familiar at all with the multi-locus probes that they used in England?

A. Yes, I am somewhat.

Q. And how do they establish their data base or how do they determine their degrees of frequency?

A. I think in a somewhat similar way as we do with the single locus probes in that you take a sample from a population and you look at the various patterns that you get and tally up frequencies of the different types of patterns.

Q. And how many bands do they use for that in the multi-locus probe?

A. Well, the multi-locus situation is very difficult to interpret and I would say that I wouldn't want to get into the details of it here because it gets very complex, and I think part of that complexity is one of the reasons that in North America and now even in the U.K. they are starting to use the single locus probes.

Q. Do you know whether or not they feel that band sharing between unrelated individuals is at approximately 25%?

A. I don't know that. To be honest, my feeling about the multi-locus probe system is that it is very much poorer than the single probe system, and my great prejudice against the multi-probe system is the fact that when you look at the profiles of two parents and you look at the profile of a child there

can be bands present in the child that are present in neither of the two parents, and biologically we don't understand what is causing that, and so because of that I have great reservations about the multi-locus system and I would feel I'd like to exclude myself as being an expert from that area.

Q. Basically because it has an anomaly that is unexplainable?

A. It's unexplainable biologically at this point in time and I think that the multi-locus probes are used very much in the same way as the traditional fingerprint from a finger is used where you just look at the number of matches and you don't understand the actual biology or the molecular biology of what is causing a certain pattern on a fingerprint and it's like scoring almost any anthropological trait where you don't fully understand the molecular details of it. The great virtue with the single locus probe system is that in almost all aspects of it we understand fully and at the level of resolution of DNA exactly what's going on.

Q. But unlike the fingerprint analogy that you're using, you need so many matching points. I believe at law you need for fingerprints something like ten matching points but for DNA you will admit that you're asking - well, at least you're asking the courts to accept much less than ten matching points in DNA structure?

A. In this in fact there are ten matching points when you use five probes.

Q. When you use five probes, yes, you would.

A. Yes.

against the system in terms of what it means biologically was so great that I haven't spent any time really studying it in detail.

Q. I believe that you stated that the probability of siblings sharing bands was what percent?

A. The probability of two siblings having the same genotype at a probe locus is one-quarter.

Q. Do you know whether or not in England they feel that it's roughly 57%?

A. Of them having the same genotype at a probe locus? No, I don't know that.

Q. Are you familiar with the works of Z. Wong, Wilson, Patel, Povey, and A. J. Jeffreys, titled, "Characterization of a panel of highly ariable minisatellites cloned for human DNA"?

A. That was an early publication of theirs and I read it a few years ago but I don't remember the details of it. I would like to just say again that in using those multi-locus probes bands don't mean the same thing as the bands that we're looking at here because in fact with that multi-locus probe you're probing in fact an unknown number of sites on all of these chromosomes and you never know when you're probing sites that are closely linked on the same chromosome whether there are different chromosomes, when two bands match whether it's the result of a locus down on chromosome 18 and a match with chromosome 5, you have absolutely no knowledge of that, and so any figures or any numbers that are generated from multi-locus probes have absolutely no relevance to the single probe locus system.

Q. Now, my understanding is that not all forensic

laboratories in North America use the flowing bin approach.

A. Well, what we use is called the fixed bin approach. Some places use what is called the floating bin approach. The places that use the floating bin approach, my understanding is that these are mostly paternity testing laboratories in the United States. I believe to my knowledge the forensic laboratories are pretty much agreed upon using the fixed bin approach that the R.C.M.P. uses but there are some laboratories that do use the floating bin approach.

Q. And do you know how many laboratories use the fixed bin approach? Is it just the FBI and the R.C.M.P.?

A. No, I'm quite sure that the data that was given to me from Dade County, Florida, State of Minnesota, Texas, and I believe that the forensic groups that are active in a technical working group on DNA analysis all use the fixed bin approach, and I think that - I'm guessing here but I think most of the jurisdictions, the state jurisdictions in the United States, use the fixed bin approach, but I could be wrong there. I think most of them do, I mean, that's my feeling from what I've seen.

Q. Would you agree that ultimately it would be desirable to define alleles discretely?

A. Yes, I would. Yes, I would agree fully, and I would say at the present time that is a methodologica limitation in the system.

Q. And you're hoping that can be done with PCR?

A. Ultimately, yes. There are at the present time some other difficulties with PCR. Ironically, it's so sensitive that sometimes with PCR as it can be

done now you can get DNA being looked at that is not really the DNA that you thought you were looking at, and that's the technical limitation now but there is a lot of active work going into trying to make that better.

Q. And would it also be advantageous to reduce measurement imprecision?

A. Oh, yes, certainly. Both of those things, if one can look at discrete alleles, it without question would be better than having that limitation as of the technique that we have today.

Q. Now, if you were to reduce measurement imprecision would that also reduce the size of the windows that the different laboratories use?

A. Well, they might still agree to go with the fixed bin approach and keeping the bins the same size, but you could argue if the resolution became such that you had discrete alleles that you would only then use the frequency of that particular allele that you were able to determine from the methodology and so in that sense you would be using a bin that was of a discrete known single allele. There might then be in the case of some of the probes that we use today where we have broken things up into perhaps 27 or 30 bins in case of extreme - some alleles, it may be that there really are only 18 or 21 discrete actual alleles in there, and so in fact you might then - it would be the equivalent of saying, well, where we have 30 bins today we're really looking at something where there really are only 23 or 18 discrete categories, and so we then only have 18 bins, but we'd know precisely and

exactly the biological foundation for classifying individual bands into a particular bin then, so the bins then might in some sense become wider because you have fewer bins spanning the same data, so to speak, but I think in most cases the bin boundaries as such would be narrower because the resolution had increased so much.

Q. But if the system we have today is reliable enough to, you know, sentence people to death, why should we bother trying to make it better?

THE COURT: I'm not going to allow that question. You'll have to express it in some other way.

MR. FURLOTTE: What's the necessity, then, of trying to find discrete alleles and to perfect the system?

A. Well, because regardless of how low with the present system the chance of an incorrect match is, if you have a still greater resolution and have a discrete allele system you could make that probability even lower, and so it seems to me that we want as perfect a system as we can reasonably get, plus there's an interest in knowing exactly what the genotype of an individual is without any equivocation at all.

Q. So by having the more discrete allele system it would give us a more powerful tool to exclude individuals who we may be calling matches on now?

A. That's correct. That's correct.

Q. Would you agree that although efforts have been made to be conservative by the R.C.M.P. that there may be rare cases where the frequency of a given allele could have been greatly underestimated because - you know, for any given population, and particularly in an inbred one?

A. I don't feel there is a likelihood that it would be grossly underestimated. I wouldn't exclude the possibility that the estimates that we're using might be a couple of percent higher than in fact it should be if we have more data and a more refined system, but I don't significantly think it would change, and I particularly don't think it has great forensic consequence because where in some cases we are presently perhaps overestimating the frequency of one bin we have to necessarily if we're over-estimating some bin frequencies, we must be under-estimating other bin frequencies, so I think that at the present time there's imprecision in the system. I'm not sure that that imprecision always or necessarily most of the time leads to an under-estimate of the frequencies. I think they could easily be overestimating the frequencies.

Q. Would you say it's more difficult to distinguish between alleles where the alleles are large, or the fragment length is large, and the repeat sequence is short?

MR. WALSH: My Lord, the Crown would continue its objection from yesterday. Hopefully I'll make it one objection and it will apply throughout. The Crown's position was that -

MR. FURLOTTE: My Lord, I think we know the Crown's position, he's been stating it all day.

THE COURT: Well, let Mr. Walsh finish his -

MR. WALSH: Dr. Carmody was declared an expert by this Court in the field of population genetics, and Mr. Furlotte has saw fit to go into another field that he has not been declared to give opinions on in

this court. The Crown objects to that and we would make it a continuing objection for every question that he puts to Dr. Carmody that is not within the field of population genetics.

MR. FURLOTTE: I think you already ruled on that yesterday, My Lord, after about five objections by the Crown and -

THE COURT: The objection is noted. Go ahead.

MR. FURLOTTE: Pardon?

THE COURT: I say the objection is noted.

MR. FURLOTTE: Would you say it would be more difficult to establish the size of alleles, the fragment sizes, when the fragment sizes are large and the repeat sequences are short?

A. With larger fragments, again as part of the limitation of the technique, it is more difficult to estimate the absolute size, that is, the number of base pairs. In terms of the percentage error that you have, the percentage is not an absolute measure on base pairs. The percentage takes into account that if you have a larger sized piece you have a wider window that takes into account and corrects for the fact that in the larger pieces you're going to have a wider window. That is, a 5% window of, let's say, a 20,000 base pair piece is going to be wider than - in absolute base pair terms, than a 5% window of a 1,000 base pair piece, so percentage-wise in the experimentation that has been done, whether you use a 5% window for very large pieces, absolutely large pieces, or very small pieces, it seems to be the case in empirical data that the 5% window holds quite well throughout

the range of size bands that people are estimating from these gels, but in terms of the precision in absolute base pairs, that is, that a 20,000 base pair piece, 5% is what, a thousand base pairs, I guess, you have a thousand base pair window. In a 1,000 base pair piece you have a 5% window and that 50 bases, so that the percentage error is the same or the percentage window or error margin is the same but in absolute terms you have greater imprecision in absolute base pair terms for larger pieces than for small pieces.

Q. O.K., but to get back to my question, would it be easier to make a mistake in the measuring of the fragments you're comparing if your repeat sequences is short on the probes you're using or your restriction enzyme? If your restriction enzyme is making short sequence pairs or long sequence pairs which would be harder to - or easier to resolve?

A. I'd have to say in this case that it's getting out of my area of expertise and I don't know the consequence of the size repeat unit making it more or less easy to distinguish in terms of size. It's getting out of my area of expertise, I haven't considered the problem.

Q. That's quite fair, Doctor, I would appreciate you saying so whenever it does. You mentioned about using a 99% upper confidence level; if you were going to use a 99% upper confidence level or you were going to use a 95% upper confidence level, would that change the requirements of the number of sampling units that you would need to form your data base?

A. I don't think there is necessarily a connection

between the size confidence interval that you would use and the size of your data base because it would depend on how precise you wanted to make - with what precision you wanted to have on your results, and I don't know as there's any objective set standard precision that is agreed upon or people have thought about. It's still very much people using a kind of reasonableness argument about it rather than having a completely objective scientific boundary as to what is too wide a confidence interval or what is not wide enough.

Q. Do you recall ever reading an article or paper by S. J. Oldeberg, the title is "Characterization of Eight VNTR Loci by Agarose Gel Electrophoresis"?

A. I don't think I've ever read that. I think I've seen the reference to it but I don't recall seeing it. Is that a multiple author, does he have -

Q. It's multiple, yes. I'll show you the title.

A. O.K., it sort of rings a bell and I think it was the American Journal of Human Genetics. Ray White, yes, O.K. Well, I'm vaguely familiar with that and I can try and answer some details but I don't remember the details of it.

Q. O.K., maybe you could give me an explanation as to what they mean by it.

A. O.K.

Q. It's on Page 13 of that report. It states, "Using this approach for locus D2S44 with the desired precision of D equals 0.01 and a confidence of 95% yields a required sample size of 907 individuals. All other characterized loci require a sample size between 1,768 and 4,669 individuals".

A. I'm not sure I understand the context that that comes from. I know that this - and that is the lab, Ray White's lab in Utah that has been developing these probes but I'm not sure of the context in which those numbers are being used. Whether that means to discriminate two different racial groups or what it means, I don't know what the context of that is.

Q. The only purpose I ask that is he seems to be using a 95% upper confidence level but he's saying that he needs a much larger sampling up to, you know, 4,6 and I'm just wondering if you're going to use the different upper confidence levels do you need different bin sizes, or sample sizes?

A. Well, as I say, I don't understand the context of that because, I mean, I don't know what the purpose of generating those confidence limits are in that context. You know, it could be that he's said previously there that if you want to know the size of the band to within three base pairs or ten base pairs or 100 base pairs that you would have to have that size sample, I don't know the context there so I have to confess I'm ignorant on that point.

Q. The discussion is under statistical considerations and maybe - it's only a page and a half so maybe if you read that you would be able to get a fuller context?

A. O.K.

Q. It starts here and this is where I've picked up this, so maybe you could start from the first.

A. Would it be useful for me to read this to the -

Q. Just read it to yourself, I think would be appropriate.

A. Or -

THE COURT: Well, perhaps you better read it out loud if you're going to comment on it.

A. O.K. This is under a discussion section called "Statistical Considerations". It says: "A 95% simultaneous confidence interval was estimated separately for each allelic frequency, using the confidence coefficient" - there is an equation $c = 1 - alpha/2n$ where n is the number of alleles. I could just comment at this point that this is a technique where you are calculating the confidence of the bin frequencies using the information in your total sample concurrently, it's called a simultaneous estimate of confidence intervals, so the formula there gets a little more complicated than the ones I've used, but that's just my own comment at this point.

To continue: "This method of estimating confidence intervals is the correct approach because it takes into consideration the multinomial distribution of allelic frequencies. These confidence intervals are approximations and therefore require sufficiently large sample sizes. The sample sizes in this study do not meet this requirement; however, calculating confidence intervals based on these small sample sizes illustrate the approach and allow us to obtain some idea of the accuracy of the estimate. Characterization of loci with many alleles requires a large sample size for obtaining good estimates of allelic frequencies and their confidence intervals. Often the binomial distribution is used when estimating

sample sizes; for example, see Elandt-Johnson, 1971", which again in aside is a textbook, a statistical textbook in this area that was written by a population geneticist at North Carolina State University, and then there is a formula that n should be greater than or equal to - and a rather complicated multinomial expression here which is called equation 5, I don't think I have to go into that for purpose of the court.

"where n is the estimated number of chromosomes in the population." Some other formula about the looking at the upper hundredth percentile of the standard normal distribution. "d is the acceptable deviation of the point estimate from the true parameter (which has a probability of 1-alpha). 1-alpha, by the way, is typically what we're talking about, being 95% or 99% and so forth, "and p_i is the expected allelic frequency of allele i. A possible approach for esimating the sample size is to determine n for the largest, observed allelic frequency by using the above equation. This approach provides us with a safe estimate, because it always determines the maximum value when calculating n separately for all allelic frequencies (assuming the same d).

Now, d is going to be your pre-established - again this is an aside and is not what I'm reading here - what they mean by d is the amount that you would pre-decide has to be the smallest imprecision that you would allow, O.K., so that d is the number that you would decide, as we say in statistics, prior or a prioi to having looked at the data, and

you make a decision ahead of time and say, well, look, I want that frequency to be less than one per cent, 10%, 2%, 1.2%, 5.2 - whatever your feeling is, and that doesn't come out of any numbers that you've ever seen, but just from your knowledge of the whole context of this what the precision is that you want to have on that estimate, so you would decide ahead of time whatever that d is, and then what they're going to say here is what the sample sizes would have to be in order to be sure that with 95% confidence you would be getting a number that was going to be within that limit.

To continue: "Besides, when using this approach, one takes into consideration that power of exclusion and probability of matching is highly influenced by the frequency of the most common allele observed". Again as an aside, what they're saying here is that what you need to look at is the most common bins because they're going to be determining this precision more than in fact the very infrequent bins. Now, getting to the point of the context of this, "Using this approach for locus D2S44 with a desired precision of d = 0.01" - what they're saying there, they're saying that they've made a decision a priori, ahead of time, that their precision has to be within one per cent of the real frequency in the population, so they're saying that they're going to use as their criteria that they never want any of their estimates to be off by more than one per cent. More than one per cent, and it's going to be dominated by the precision of the largest frequency bin, so that's the thing

that in fact I didn't catch in what you had to say and that's the important point in this, that they've made a prior decision that their frequency estimate has to be within one per cent. They want to know how big a sample would you need to be 95% certain that the frequency that you've estimated for the most frequent bin is never more than one per cent away from the real frequency which, alas, we can never know in the population without looking at the entire population, so now I say - I'll just read that sentence starting at the beginning again.

"Using this approach for locus D2S44 with a desired precision of d = 0.01 and a confidence of 95% yields a required sample size of 907 individuals (all other characterized loci require a sample size between 1768 and 4669 individuals). Sample sizes used in the study reported here ranged from 78 to 151 individuals. Assuming a desired precision of d = .05" - so now they say - well, they just stated the numbers and how large a sample would have to be in order to give a one per cent precision and to just reiterate those, it was for this locus a sample size of 907 individuals, which they didn't meet in this study. Now they say well, suppose we had a pre-established precision of d = .05. What they're saying now, we did the calculations on how big the sample sizes have to be to have a one per cent precision, how big would the sample sizes have to be to have a 5% precision, and to continue: "Assuming a desired precision of d = .05, the analyzed sample size for these three loci (D2S44, 151 individuals; D14S13, 82 individuals; and D1S74, 78 individuals)

is larger than the estimate (37, 75 and 71 individuals, respectively)", which they had in their sample, so what they're pointing out here is that indeed, to have a precision in your bin frequency estimates where you need to have a precision pre-assigned and predetermined of one per cent, you would need these very large samples of 907, at least. If you were willing to accept a 5% error margin in the frequency of the most frequent bin the prediction is that you would need 151 individuals, so in that context I think - I hope I haven't been too didactic here or whatever, but in this context it doesn't necessarily mean that if you had a sample as we had of 750 individuals that we couldn't make precise estimates. Our estimates are likely not to be within the one per cent range in each frequency but they're certainly within a 5% range of each frequency from this context.

Q. O.K., thank you, Doctor, and I believe you already stated you were not familiar with Dr. Lander's article, "The Population Genetic Considerations of Forensic Use of DNA Typing", known basically as the Branbury Report?

A. I'm not familiar with that particular publication of his. I have read the Nature article which we were referring to yesterday, and in fact, he has - I've seen a recent commentary that he had in the American Journal of Human Genetics which I think is quite up to date, in fact.

Q. Did you say you were or were not familiar with Ronald T. Acton's paper on "The Comparison of VNTR Allele Frequencies in White and Black Populations"?

A. I'm not familiar with the actual publication, I have not read it. I am familiar with the general conclusions that he's arriving at and I've just seen it commented upon in some other publications that he has found significantly significant - well, significantly - significant statistical differences between black populations and I think it's either Alabama or Georgia, I've forgotten which of the southern states he works in, but I know it's - and I would say what he has found is comparable to the findings that we have with the R.C.M.P. data base with the Canadian aboriginal populations, and I'd say it does show that -

THE COURT: I think you covered this yesterday, Mr. Furlotte.

MR. FURLOTTE: Pardon?

THE COURT: You asked this question, you covered this area yesterday.

MR. FURLOTTE: Yes, I covered the area, but again, I thought he said yesterday that he wasn't familiar and I just wanted to make sure.

THE COURT: You said, "I know Dr. Acton, he comes from either the University of Georgia or the University of Alabama", and he would rate his expertise quite high, and then went on.

Q. Would you agree, Dr. Carmody, that the Hardy-Weinberg equilibrium is not a law of physics but that it - which must apply to a population and that it is a testable description of whether the population is genetically well-mixed? Would that be appropriate?

A. Yes, I would agree. I agree it's not a law of physics, it's a law of statistical prediction of how mating occurs in a population. If the criteria and

assumptions of that law are met it should be an appropriate description of a population and one can use it, as we call in sciences, as a null hypothesis that you can try to refute, and if there is a deviation from the assumptions and if you have a large enough sample, one should be able to statistically show that that law is being violated, but it is not a law of physics, I would agree.

Q. Could there be measurement imprecision caused by loading variations in the analytical gels?

A. That's known to be the case. That is, if you load too much DNA, in great excess, you can affect the migration rate through a gel. Beyond that it's getting into an area of expertise that has to do with physical biochemistry here that I don't feel I'm qualified to say much further, but I do know that you can get, I guess I would call them artifacts, because of the amount of DNA that's loaded on the gel. I have some ideas of why and how that could occur on a biophysical level, but I'm not an expert in that area.

Q. And if you had that consistent through, say, when you're forming your data base, then you could have an unreliable data base?

A. That could be, but when you're generating the data base, because that's generated from pristine samples that have been handled and treated in exactly the way that you understand they should be, part of that proper handling is a very accurate knowledge of the exact amount of DNA that you're loading on those gels for those samples. The cases where you get problems with overloading is when you're

extracting DNA from a forensic specimen, and some forensic specimens, as you know, could have become degraded or could have been contaminated with various things, and there sometimes, I understand, with forensic specimens the amount of DNA that you're loading is known very much more poorly than you would with the standards that are loaded on to create a data base, so I think the loading, an excess or underloading in the specimens that are used to create the data base, I don't see any problem with those. I think it's the forensic specimens that there can be a problem with.

Q. O.K., so there's no need for overloading with, as you say, pristine samples?

A. No, because in fact you have a very good idea and a very precise idea of how much DNA you actually have because you've used known volumes of blood or known volumes of whatever and it's just very precisely known.

Q. And your protocol ought to tell you how much you need?

A. Exactly.

Q. To run this test?

A. Exactly, whereas you extract some DNA from a blood specimen or some kind of contaminated vaginal swab, it's very difficult to know ahead of time how much DNA is going to come out of that.

Q. Would it be safe to say that some scientists dealing with population genetics feels that there has to be - you know, you have to be faced by incorporating some reasonable estimate of operator and measurement error in the final probability? As

I understand it from your testimony yesterday, when you're calculating your final probabilities there's nothing in the end product that calculates for operator error during the process of running your probes?

A. That's right, that's correct, and I think that comes under quality assurance again and custody of samples and so forth where as one can imagine in a laboratory it in fact is - there's always the probability that one could have mixed up two samples or that a sample had become contaminated or something like that. I think to address those issues, from what I've seen and from what I've seen of the protocols followed in the forensic labs that I have any knowledge of in Ottawa and the FBI laboratories in Quantico, Virginia, there I think they take the utmost precautions to avoid any possibility of that, and I'm convinced that the chance of operator error in the labs that I see in Ottawa and when I've seen them do these procedures is very low. Unfortunately it's one of those things that is virtually impossible to quantify, to my knowledge, and you know, there's always a possibility even in these procedures of loading a gel that you load something in the wrong lane or whatever. I think the chance of that happening is very, very small but I can't put a number on it and I wouldn't know how to factor it into the equations.

Q. Is that some reason why some scientists feel there should be an upper confidence level of maybe 95%?

A. Well, I have seen some people - and there was a letter to the editor in the American Journal of

Human Genetics earlier this year, in January-February where they tried to use some data from the FBI laboratories in Quantico where there was in 500 runs in their data base one mistake or something like this, and saying well, if that's the probability of operator error of one in 500 we should factor that somehow into the equation. That's the only thing I've seen actually written on that of a quantitative form. I haven't seen, actually, somebody write and say that's the reason for putting a confidence interval on it, but I would say in this particular case that applies to any laboratory procedure of any sort. One can imagine operator error in standard blood grouping. There's always a probability that somebody has called something an A blood group when in fact they used the wrong reagent and it actually was a B or O or whatever.

Q. But if there are never any proficiency tests or blind trials, then operators may have a tendency to get sloppy if they know they're never being checked out?

A. If there are never any proficiency tests and quality assurance and so forth and re-running and standards, then there is a problem. I know that that's not the case in the R.C.M.P. laboratory. They have proficiency standards, they have quality assurance standards, they have measures of replicability and reproduceability, reliability, that meet the highest quality control that I'm aware of. I guess if I could just continue, and I don't mean to belabor my answer to the question, but in virtually all these cases where you're involved with forensic work, when

you're trying to see whether two specimens match, what is going to happen if there is operator error and if there's some problem in the procedure is that you will get a false exclusion much more likely than you would get a false inclusion. I mean, it's just overwhelmingly the case that if you're going to make a mistake it's going to give you the wrong answer and it's more likely to be in the direction of giving you an exclusion. I use the analogy to if you were to drop your wristwatch there's a probability that it might keep better time after you dropped it, but more likely it would keep poorer time, and that's the same analogy here. When you make a mistake it's going to lead to results that would exclude, you know, they would be wrong and they would exclude more likely than they would have given you a false inclusion.

THE COURT: Does your objection, Mr. Walsh, extend to these answers that have just been given?

MR. WALSH: No, My Lord, but as much as those answers are helpful to the Crown to no end, to the nth degree, to use a statistical term, I still maintain my objection that Dr. Carmody has not been declared an expert for the purposes of this particular proceeding and I'm not going to -

MR. FURLOTTE: My Lord, we could have him declared an expert for the purpose of this proceedings if that's Mr. Walsh's desire.

THE COURT: No, carry on. Sorry I started up.

MR. FURLOTTE: Now, you were given a copy of Dr. Shields's report in a case in the States that the FBI were

involved in?

A. Yes.

Q. Were you also given a copy of Dr. Hartl's report from the Yee case?

A. Yes, I have read Dr. Hartl's report in the Yee case, yes.

Q. The problem that Dr. Hartl found with the rebinning of the FBI's data base, could that occur in the R.C.M.P. data base? Is it possible the same thing could happen -

MR. WALSH: My Lord, I would like Mr. Furlotte, please, if he would, to actually read the particular provision and the context in which it was made. I make an objection to that particular question as he's phrased it.

Q. O.K., I'll read from Dr. Hartl's report at Page 5: "The results of the analysis were quite astonishing. Unless I had been told that these bands were from the same individuals I would have been forced to conclude that the sampled individuals were different. In fact, if the laboratory protocols and scoring were reliable the probability that the samples are actually from the same population is so small that it is off the published charts, and when I tried to calculate it by hand I found that my calculator balked because the number was too small for it to handle, so very conservatively let us say that the probability of the tests and retests matching so poorly even if they were different samples from the same population is considerably less than one in one million per locus", and you're aware that Dr. Hartl in that case, the FBI had rebinned and they

had rerun the same DNA from the same individuals and come out with astonishingly different results?

A. That's right, that was in an early test where I believe it involved 50 specimens that were run once and then run again, and indeed, that was quite worrisome at the time, that that would happen in that laboratory. Since then they have run any number of new ones and I think levels of quality assurance and proficiency testing and so forth have gone up markedly since that time.

Q. So it's amazing what quality assurance can do?

A. That's right. That's right, and again I know it seems perhaps to - the legal process that a period of two years or 18 months is miniscule in the time that things go on. In science, and in this particular area of science, things are happening weekly and we are working on a different time scale, and so the fact that that was the case two years ago and in some tests done two years ago is, I guess, to the legal system like something that happened in maybe 1850, I don't know. That's a sort of comparable scale, that things are happening very quickly here and these procedures are evolving at a very high rate.

Q. O.K., I'll go on to read from Dr. Hartl. He says: "On the other hand, these data are known to come from the same group of individuals. What is one to make of this? In essence the discrepancies mean that the FBI is unable to identify its own agents as being themselves".

A. That's correct, in that test of two years ago, yes. It's a nice irony to that sentence, yes.

Q. And, "The only plausible explanation that I can fathom for discrepancies is that the electrophoresis protocols are completely unreliable". Would that have been a fair analysis?

A. I don't think a fair analysis at the time, I think he's being a bit exaggerating there and sarcastic and so forth but -

Q. O.K., "or the scoring so sloppy and subjective that little or no confidence can be place on the statement that two genotypes match". It says, "For unknown but very serious reasons identical bands are being classified into very different bins on different runs and this invalidates the entire binning procedure". Would you agree with that?

A. He said that at the time and I would agree that he said that at the time, and that I've since in fact seen a letter that he has sent to a justice in - not a justice but district attorney in the United States where he is quite concerned about the fact that his submission in this particular case, I think this is the Yee case, has been widely cited and used in other cases where he feels it is quite inappropriate and he is quite concerned that it is being used in this way, because in my opinion I think it pertains specifically to that particular that was done once in the FBI laboratory.

Q. Well, on the FBI's data base?

A. Data base in the FBI's laboratories on a particular set of standards some two years ago, and I think to keep dragging that up today is not relevant, but that's my opinion.

Q. But it may be that some other forensic laboratory is

actually doing it right?

A. It may be that some of them are doing it right, it may be that none of them are doing it right.

Q. Have you checked the R.C.M.P. data base like Dr. Hartl checked the FBI data base?

A. I know that I've done tests where if you take half the data base and compare it against the other half of the data base, you take the data base from Vancouver and compare it to Ottawa, or you take Kingston versus Ottawa or versus Vancouver or whatever, that there's complete consistency, and there's never any difficulty -

Q. But you haven't run the gels over or anything like that?

A. I haven't run the gels over, no, but there has been proficiency testing done and quality control, and there have been many tests of the same sub-set of samples run again and again.

Q. As a result of Dr. Hartl's discovery with the FBI data base and the binning do you know whether or not the R.C.M.P. decided to run a second check on theirs?

A. I don't know whether they did. However, I also know that in the Yee case the Court decided to use the data.

Q. Courts do wonderful things.

A. Because they had expert witnesses that said that it was O.K. to use the data, perhaps.

Q. So if a person's DNA was run twice and it was out by as much as, say, 5% or - it could fall in different bins when you would rebin it, could it?

A. It would if it was out by greater than 5%. It could fall in different bins. In many cases it would fall

in the same bin because the bin widths are roughly on the order of nine, ten per cent, but there are some bins, particularly some that are 6% or whatever, where if you were off by 5% you could be in another bin.

Q. I believe Dr. Hartl referred in that context in his report, he referred to the works done by Dr. Acton, and Dr. Hartl, I believe, stated that: "The most detailed evidence for population subdivision in Caucasians in respect to VNTR's is given by R. T. Acton, L. Harmon, R. C. P. Geo and B. Budowle" - so it's not that one - "entitled Comparison of VNTR Allele Frequencies in White and Black Populations". I guess even Bodowle was a co-author of the Acton paper?

A. I'm not sure of that. I know there was a case where some of Bruce Budowle's data was used by some people, in fact without his consent, and his name was put on the publication without him ever having seen the publication, and perhaps it's considered hearsay but I understand he was quite disturbed by that, and I don't know whether that was the publication or not. I confess I'm not familiar with that publication.

Q. And Mr. Budowle works for the FBI?

A. He works for the FBI, he's the very strongest proponent of the fixed binning system and has been, I'd say, one of the leaders in the forensic use of DNA in the United States, yes.

Q. Now, Dr. Hartl states in his report that - he says, "Burden of proof in claiming that a sample is representative lies with the claimant and not the doubter". Does that usually apply in science?

A. I don't know. I think that that varies. Science proceeds - when you have a sort of generally accepted theory in law I think the burden of proof lies with the doubter, but when a law is not that securely accepted or a theory is not that securely accepted, the burden lies with the people who are proposing that rule, so I think it would vary with the particular scientific question at issue. I'm trying to make the point that if somebody were questioning gravity or something like that I think the burden of proof would be with the doubter and skeptic, whereas if somebody were doubting some theory of how the immune system worked the burden of proof might well be with the person who was supporting this new theory.

Q. Dr. Hartl, when using the Hardy-Weinberg frequencies, he stated that: "Several witnesses in the instant case seemed to assume a priori that alleles in a population must be statistically independent of one another when they become combined into genotypes. However, this is an unwarranted assumption and it is generally unjustified unless appropriate preliminary studies are carried out to verify it", and Dr. Hartl claims that those studies have not been done.

A. Well, again that is a report that's a bit old by the standards of progress in this field. I have given in earlier testimony in this hearing evidence that I have done tests. Tests have been done by Devlin and Risch to see if there's any excess homozygosity, almost a year ago now they did that test. All of these things I think supersede the

testimony and the contentions that Dr. Hartl was making in the Yee case. If I could reiterate again, I think the burden of proof in that particular case that was accepted by the court was that in fact the use of DNA was appropriate, reliable, and accurate enough to be used in that particular proceeding.

Q. That was the test the courts used, but what test is generally used in science?

A. The test that's generally used in science is to, if you have a question like this, you get empirical data to test it, and I feel that I've presented results of what I've done with the Caucasian data base here in Canada that indicate clearly statistically that there are no strong deviations evident in that data base that -

Q. I think we went over that yesterday.

A. Yes.

Q. And I told you why that maybe because your study was extremely limited that to large - or wide bands of population contributing just because you took it from a small area, the Kingston Base, but those people come from everywhere and we know it, that's not -

MR. WALSH: Is this a question or again are we testifying here?

THE COURT: No, this is evidence that Mr. Furlotte is giving. Are you giving evidence, Mr. Furlotte?

MR. FURLOTTE: No, My Lord, I'm just -

THE COURT: Good.

MR. FURLOTTE: Nobody would listen to me anyway. However, Dr. Hartl states, he says, "In terms of general acceptance it is my opinion that a qualified

reviewer of a journal article submitted for review would not allow a gratuitous assumption of Hardy-Weinberg forensics to go unchallenged", and aside from Dr. Hartl challenging the reliability of the data bases being compiled by the FBI and supposedly by the R.C.M.P. in view of this evidence that there was likely substructure out there, and I believe you stated that it is now before a scientific panel?

A. There is a National Academy of Sciences in the United States that has struck a committee that is coming up with recommendations in this area.

Q. When can we expect a report from them?

A. You'd have to really ask them. My understanding is that they felt that the report was going to be out several months ago, and I am not familiar with what their new projected timetable is or whatever.

Q. And how many scientists are on that panel, do you know offhand?

A. I don't know offhand. I know that Dr. Lander is a member of that panel. I know Dr. Caskey is a member of that panel. I think Dr. Kidd is but I'm not sure, I don't know the entire composition of that panel, but it certainly is of pre-eminent composition and I would guess it's on the order of a dozen or more people with the various researchers that work for that. It's something like the equivalent of what we might here in Canada call a Royal Commission, if you will.

Q. So it must be a very major and legitimate concern?

A. It certainly is. On the other hand, I could say in terms of a statement that you read just a moment ago that Dr. Hartl felt that no peer review journal

would accept a publication - and I forgot the exact words there, but I can cite publications that have appeared in peer review journals since that time which I think answer his questions that again I would say reflect the state of the art two years ago, and I think they have been superseded by later empirical data, later studies, later publications in peer review journals.

Q. Well, he just says it wouldn't allow a gratuitous assumption of Hardy-Weinberg frequencies to go unchallenged, and the fact that the panel has been set up is evidence that it's not going unchallenged.

A. Well, that panel is not looking solely and strictly and in isolation at the question of Hardy-Weinberg equilibrium. They're looking at the whole issue of the DNA and the use of DNA evidence for forensic purposes.

Q. Dr. Hartl also states -

MR. WALSH: My Lord -

THE COURT: Don't you think, Mr. Furlotte, really, that we've beat poor old Dr. Hartl to death, and you're sort of fighting a losing battle with him, too, aren't you?

MR. FURLOTTE: O.K. Is it possible, then, Dr. Carmody, that the theoretical foundation of probabilities lies in Mendel's laws and not in Hardy-Weinberg, that the validity of Mendel's laws for nuclear genes in humans is not in dispute and that whereas use of the Hardy-Weinberg principle requires a multitude of questions and often invalid assumptions that it would be better to use the Mendel's laws and not Hardy-Weinberg?

A. Unfortunately that's not the case and that's not the situation. Alas, it would be great if we could just rely on Mendel's laws where it's so simple to calculate the probability that two siblings are identical in genotype. In actual real populations the world is more complex than just analyzing what happens within a family. As you can see, there are influences of population size, there are influences of historical origins of populations, there are different ethnic groups and so forth that have to be addressed in real populations and that Mendel's laws are insufficient to draw the conclusions that we need to extract from real populations. I think that was a difficulty when this area was first started to be used in forensic applications in that molecular biologists felt very strongly that, well, we know Mendel's laws, everything that happens genetically is predictable from Mendel's laws, and they didn't appreciate the fact that indeed there are complexities when one looks at populations that are not derivable from Mendel's laws, and so one needs to resort to these other statistical tests, namely the Hardy-Weinberg equation, linkage disequilibrium, and one of the reasons that people like myself have been, I must say, dragged into this area, if you will, is that in fact the molecular biologists and Mendelian geneticists didn't have the sensitivity to realize that in fact you can't just use Mendel's laws to analyze these data, and so I would strongly disagree that Mendel's laws are all we need. It would be marvelous if that was the case but the real world, alas, is too complicated for that.

Q. I believe, then, from reading Dr. Hartl's report that he is in agreement with you that an upper confidence level should be used also?

A. Well, he believes, I guess, in terms of making any estimates, that when you say it's a probability of one in five million that the precision of that really has to be conveyed by giving some kind of confidence interval or some kind of measure of how accurately we really mean that figure, and if we say one in five million we don't mean that it's not one in four million or one in six million or, in fact, whatever the confidence interval you can put on that, and that confidence interval is determined by the sample size that you had to base that estimate on, and sometimes when we quote these estimates of one in five million it conveys this precision to it that is, I would call it spurious, and I think that has to be conveyed by saying that well, we know with 99% confidence it falls in this range, and we can't really be any more precise than that, and so I would agree with him, yes, to answer your question, that we need to use some - and to convey some indication of the softness of this estimate, if you will, if I wanted to call it that.

Q. I think one other concern of different scientists is that in using the product rule that if you're making errors along the way, and they can be little errors, that you keep multiplying error upon error upon error, and we come out with a ridiculous error.

A. Well, that's why as you see in the submission I made in writing that in fact, indeed, you can start out with an individual imprecision of when you say at a locus it's one in 78, that could range really from

worry of the false exclusions. I think properly our justice system is more worried about false inclusions than they are false exclusions, but one always has to worry about that side, too, that you don't want to exonerate guilty people.

Q. But the R.C.M.P. assumes without taking in the probability of possible false positives - the R.C.M.P. assumes that there are no false positives when they do their calculations?

A. No, in fact, this calculation that we come up with that's saying one in five million or whatever, that essentially is the probability of a false positive, that it could be somebody else and not the accused.

Q. In the final analysis of Dr. Hartl in the FBI data base of the rebinning he found that according to the FBI test and retest data the probability that the same FBI agent was assigned different genotypes in the two tests was 84%.

A. That's what he wrote two years ago, yes.

Q. And therefore that brought it down to a probability that the FBI was only right 16% of the time?

A. Again I would -

Q. That was his calculation?

A. That was his calculation. I think his calculation is right. I would say again I don't feel it has relevance two years later today, and Hartl himself has written that he is quite concerned as to the way this report that was written for the Yee case has been used, in his words, I think he used the term abused, in using it in other cases, because I don't think it's relevant any more.

Q. Because as far as you know the FBI has done a third rebinning and remeasuring?

MR. FURLOTTE: My Lord, I think that's a very unfair comment, and undeserving.

THE COURT: All right, we'll take a 15-minute recess.

(BRIEF RECESS - RESUMED AT 11:35 a.m.)

(ACCUSED IN DOCK.)

THE COURT: All right, Mr. Furlotte.

MR. FURLOTTE: Dr. Carmody, are you familiar with the article by Dr. Lewontin entitled, "Population Genetic Problems in the Forensic Use of DNA Profiles"?

A. Is that the submission at the Yee or Jakobetz? I'm not familiar with a publication with that title, I mean a publication in a peer review journal of that title. I have read a submission that he made, I think it was to the same proceedings that Hartl's -

Q. Same proceeding as Hartl.

A. Yes, but that's what I would be familiar with.

Q. Are you familiar with that report?

A. Yes.

Q. I attempted in the past to just get you to comment on the basic assumptions of these experts but Mr. Walsh continues to object to that pattern so he wants me to refer it to you, so maybe I'll give you a copy of it. I'll refer you to certain page numbers, Dr. Carmody. On Page 3 in that report -

A. Yes.

Q. Entitled, "Under the Genetic Substructure in Actual Populations".

A. Yes.

Q. The last sentence of the first paragraph states: "In the end, however, as I discuss below, what needs

to be done if DNA profiles are to be used for making probability statements in a forensic context is to go out and get the data on VNTR's directly". He states, "There will be significant genetic substructure among biological sub-populations in a conglomerate population like the Caucasians of North America if the following things are true: (1) there was genetic differentiation among the ancestral populations that contributed the immigrants to the population in question; (2) only a few generations have passed since the mixing and/or, (3) there is pronounced endogamy such as that descendants of the original immigrants tend to marry each other rather than forming a large panmictic biological melting pot", and then on Page 4 he states: "In fact, all three of these conditions are true within the North American Caucasians, black and Hispanic census populations. Thus these census populations are not internally panmictic but consist of genetically differentiated subgroups that must be separately specified when a probability calculation is to be made in a particular case". Now, does Dr. Lewontin suggest that if a crime was committed in a particular area, then we should submit to a population data base for that particular area?

A. That's what he is saying here, yes.

Q. And I believe on Page 6 he was using an example between the Poles and the Italians?

A. Yes.

Q. And where frequency might be one in 540 for the Poles it could differentiate by as much as 162,700 for Italians?

A. That's a calculation, yes, based on these three genetic loci, not VNTR's. This is some blood grouping data that he has, yes.

Q. And a concern amongst many scientists in the general community is that these differences may also apply within the Caucasians in North America?

A. That's correct.

Q. And if that difference, one in 540, where you stated yourself that you would probably convict in one in 10,000, but here in the Italians we have one in 62,700 and a different sub-group may have a frequency rate of one in 540 which would hardly bear attention in a court?

A. Yes.

Q. So there could be substantial and crucial mistakes being made if we are not aware of the effects of sub-groups within a population?

A. This is what he's stated in his example here, yes.

Q. And I understand you rated Dr. Lewontin as the best in his field?

A. I would say as a population geneticist he is pre-eminent.

Q. I believe yesterday you ranked him as number one in the world?

A. If I had to do that ranking I guess I would put him there, yes.

THE COURT: But, Mr. Furlotte, you've had the witness read that into the record, but are you going to follow it up with any question or are you just using this witness to get this into the record or are you going to ask him his opinion on that?

MR. FURLOTTE: I intend to follow on that. I have one other

MR. WALSH: My Lord, this is the process that Mr. Furlotte has followed since yesterday. I objected till I was hoarse in terms of I kept referring to the Anderson case and Mr. Furlotte has Dr. Lewontin, he's going to have Dr. Hartl, he's probably got some more there that he wants to testify. I'm going to have a hard time cross-examining, obviously, not that I would make too much inroads, but that's the point, he's misusing this information in the Crown's humble estimation.

MR. FURLOTTE: No, My Lord, the purpose of this is the Crown is trying to prove through these witnesses that the Hardy-Weinberg formula and the product rule is valid in the forensic field and that it is accepted in the general scientific community. This evidence that I am putting in this way is to show the Court and anybody else who's interested that there's a good chance it is not generally accepted in the scientific community and I am testing on cross-examination the validity of the opinions of the Crown's expert witnesses who are coming to court and saying that it is generally accepted in the scientific community.

THE COURT: I've made clear that I'm not accepting these quotations from articles as evidence of the contents of the articles, I've made that abundantly clear. They're being allowed in or -

MR. FURLOTTE: Well, it's a question of weight that you would want to put on it, that's your discretion.

THE COURT: No, they're - well, they're not evidence. They're the basis for asking this witness comment on the thing. Presumably at some later stage of the voir dire you

will have a witness, Mr. Furlotte, who will perhaps suggest these as being valid - this being valid doctrine or whatever and then you will have tested the Crown witnesses against it and so on. If you had a witness who says, look, these are my views, what this gentleman put in that article or in that submission, and if you hadn't tested the Crown witnesses on those things, of course, that would have weakened your own case, so you're quite properly doing this, I see no objection to this whatever, but I was merely pointing out a minute ago that you haven't - you've posed the quotation or the substance of this report to the witness but then you haven't followed it up asking his opinion or doing whatever else you're going to do with it, so -

MR. FURLOTTE: This is the last one that I want to refer to for this particular field.

THE COURT: All right, but you will be asking questions about this, will you?

MR. FURLOTTE: Yes, and which includes Dr. Hartl also. Now, Dr. Carmody, I believe you stated that the product rule and the Hardy-Weinberg formula is - it's proper to calculate frequencies?

A. Yes, from the empirical evidence that I've examined and tested statistically I feel confident that it is the proper approach.

Q. And I believe you also testified that it is generally accepted in the scientific community?

A. I believe that there's a general acceptance in the scientific community of it, yes.

Q. I pointed out to you that - and let's see if you agree with me or not and I'm not misstating something

here - Dr. Lewontin does not agree with that?

A. He gave examples in this report that shows that he does not agree with that until there's more empirical data, yes.

Q. And that it's unreliable?

A. Well, he's saying that one needs more empirical data is my conclusion from reading what he says.

Q. And Dr. Lander does not agree with it?

A. Dr. Lander also is saying that we need more empirical data.

Q. And Dr. Hartl?

A. He's saying that we need more empirical data.

Q. Dr. Ron Acton?

A. I don't know exactly what I said earlier that I haven't actually read things that he has written. I am guessing that he's saying that we need to address the question of population subdivision and get more empirical data but I have not actually read what he's written.

Q. So there are a considerable number of eminent scientists in that field of population genetics that disagrees with those people in the scientific community who accepts it?

A. Yes.

Q. And you don't know the numbers as that maybe there's more that accept it or more that reject it because a poll was never taken?

A. That's correct. In my opinion and in my judgment there are also pre-eminent people who feel as I do that the empirical evidence that we now have is strong enough to support using the Hardy-Weinberg equation and the product rule.

Q. But that's a position the forensic field took from, I suppose, Day 1 when they started bringing this evidence into court. That's not something that they've now formulated, they were of that opinion to begin with, were they not, the proponents of it?

A. I suppose they were. I wasn't involved with it at that point.

Q. Are you aware of any of the proponents for it to begin with who are now opponents? Which ones have switched?

A. I think Dr. Lander is one, in fact. I think that he originally - and he is not a population geneticist In fact, coming from molecular biology he was perhaps typical of molecular biologists who felt that there weren't any problems that had to be addressed in terms of population genetics. In fact, I would say that there were many people from the molecular biology end who weren't sensitive to some of the complexities and difficulties that one can run into in real populations, particularly human populations, and I think Dr. Lander was one who was supportive. He's still supports developing the technology and feels that upon getting further data it can be used, but he is one that is now, I would say, expressing skepticism about the use of the Hardy-Weinberg equilibrium and linkage and the product rule without further empirical data.

Q. And what about Dr. Caskey, has he changed positions?

A. Not that I'm aware of. I believe he also testified, and I haven't seen anything written that he submitted to that same case that both Lewontin and Hartl

testified or submitted documents to. I don't know what his present position is. I believe he is on the panel of the National Academy of Sciences in the U. S., he may indeed be the chairman of it, I don't recall, who is investigating this further. I don't know what his current position is and I haven't seen anything that he's written on it.

Q. What about Professor Weir, do you know him?

A. Yes, I do.

Q. Do you know whether or not he accepts the Hardy-Weinberg equation and the product rule being used?

A. I know that he's been involved in doing statistical tests and I haven't seen anything written by him yet but I believe that he supports it.

Q. You believe he supports it?

A. Yes.

Q. Dr. Carmody, before you came to court this week, and I guess prepared to rebut the evidence that's going to be given by the defence witness, Dr. William Shields, did you consult with Dr. Kidd?

A. No, I did not. I have had no personal communications with Dr. Kidd for two years.

Q. Did you consult with anyone?

A. I have consulted and spoken with some people in the Los Angeles area, Charles Brenner and Jeffrey Morris, I have spoken with a population geneticist at York University, Brian Golding, about these matters. I have spoken with a colleague at the University of Ottawa, Donal Hickey, about them, another colleague, Linda Bonen, about them, but that's the extent of the experts in this area that I have spoken with in population genetics.

Q. That's in particular in preparation for rebuttal of Dr. Shields?

A. No, it wasn't. In fact, in none of those cases was it with respect to any rebuttal of Dr. Shields' evidence. I have not consulted anybody about that.

Q. O.K., so that's strictly your own opinion?

A. That's strictly my own opinion and my own knowledge of our own Caucasian data base.

Q. Do you know Dr. Lawrence Mueller?

A. I know the name and I know of a couple of his publications, yes.

Q. And he is also in the field of population genetics?

A. Yes, he is.

Q. Do you know his position on whether or not the Hardy-Weinberg rule and product rule would be applicable or reliable?

A. I know he has testified that he has reservations about it and I would put him in the area of having the same opinion as Dr. Hartl and Dr. Lewontin and Dr. Lander at this point in time - at this point, My Lord.

THE COURT: Thank you, you're learning.

MR. WALSH: I'm happy to know I'm not the only one.

MR. FURLOTTE: We're not sure what we're learning, but we're learning something. Do you know Dr. Charles Taylor?

A. I know him. I know him from work on drosophila, the same organism I work on. I don't know what his position is and I don't know of any testimony or publications he's made in this area, I'm unaware of them.

Q. He, too, is a specialist in population genetics?

A. Yes.

Q. You don't recall any studies you may have heard of Dr. Taylor's in regard to foxes?

A. Foxes?

Q. Yes, on different islands?

A. That doesn't ring a bell with me, no. I'm more familiar with his work on drosophila, I don't know of his work on foxes on islands, no.

Q. Do you think it would be possible for, say, foxes in one general area to have all the same DNA like identical twins?

A. I would find that surprising. The only case where I know that's been shown for any organism is for some elephant seals, actually, where they seem to be completely uniform and monozygous for all of the loci that have been looked at; none of these that I'm aware of but all the loci that have been looked at. I would be surprised if foxes were uniform through any significant extent of their geographic distribution, I'd be very surprised.

Q. Do you know Professor Seymour Geiser?

A. Yes, he's a statistician at the University of Minnesota, yes, and I've seen some of his - or at least one summary article that he wrote for a journal called "Chance".

Q. And would you agree that he's - what, Dr. Geiser is at the School of Statistics at the University of Minnesota?

A. Yes.

Q. And the School of Statistics which - Geiser heads that school?

A. I don't remember exactly but he is a statistician, he's a recognized known statistician, and he has

been looking at this area of population genetics, yes.

Q. Yes, and do you know what his opinion is on the validity of the FBI using the product rule?

A. My summary of his position would be that he would like to be able to have the data from the FBI to be able to analyze, and in what I've seen written by him is that he has been chiding the FBI for not being forthcoming with their data to allow other people to analyze.

Q. Are you aware of any books that are out in libraries on - you know, you might not know this particular book but I have a book here from my library - it's titled, "How to Lie with Statistics".

A. It's very interesting, by Darrell Huff. I can tell you a long anecdote about that book but in fact it's a book that when I was in high school first turned me on to statistics, actually.

THE COURT: What was the appeal?

A. Well, the appeal was, and in fact I gave - I can remember in Grade 11 or whatever I gave a report on that book in an Economics course that I was giving to show how we can be deceived, particularly in the news media, by charts and graphs that can distort the actual numbers, and I've been very sensitive to these issues ever since. It was in fact - it's curiously enough the book that really got me interested to see how statistics has been misapplied by people who are very naive about numbers, and I feel that it has been a source of motivation for me to try and correct that poor knowledge. I've been very active in my own university to try and construct

a course that we might call colloquially statistics for poets or whatever, but statistics and statistical inference for people who don't feel comfortable using mathematical tools, and I think it's a great deficiency in our society that we don't have a better general understanding. Not only is there a lack of numeracy but particularly in this area of statistical inference there is a great number of misconceptions out there that I think - and a great number of ways that I feel statistics is abused in the media that I think need to be strongly corrected in our educational system.

Q. Sometimes it's very difficult to reveal the fallacious appeal that it does have or to unravel the false appearances that it has?

A. Sometimes, but it's surprisingly easy in most cases, in fact, because people use them so naively, and I would say often in this area of forensics, for example, I feel that my advice has been sought in some cases where people who calculate a probability of one in 78 have the sense that they can really know that that is one in 78 and not one in 79 and not one in 76, and they don't have a sense for the imprecision in that estimate, and I think that that's an area that people have to understand. I've also been involved in a number of cases where at Carleton in our school of journalism we conduct nationwide polls before various national elections and so forth, and I've been involved in advising them on how to design their random samples, and it is surprisingly more complicated than one might imagine when you're doing a telephone polling across the nation.

Q. It's probably something, too, like the example you gave yesterday about the different birthdays.

A. Yes.

Q. Your birthday and Dr. Lewontin's is on the same day and you said you would multiply 365 by 365.

A. That both of us would have a birthday on the 29th of March, yes.

Q. I believe you used that figure, multiply 365 by 365 to get the probability -

A. To get the denominator of the two, yes.

Q. But again that's assuming that there's an equal amount of people born on the same day every 365 days?

A. That's correct, and that is a very naive model, I agree, that in fact -

Q. So that would not be a proper calculation?

A. That's right. That's right, if you wanted to refine that you would have to take into account the distribution of births across the calendar days of the year, and I know that that is not equally distributed across the calendar days of the year. There's some very interesting numbers involved with that, too.

Q. Like when all the fishermen are out to see two months of the year and you can't expect too many children nine months from now?

A. Well, that's in that particular area, but there also are some very interesting aspects of that in terms of different times of the years there are different sex ratios, for example. There are more males born at certain times of the year than at others and there has been some statistical analysis of that and we

don't understand the biology of that, quite, because but I feel we're getting off the -

THE COURT: We're getting rather far afield - or out to sea.

Q. Dealing with genetics, Doctor, I suppose in some sense we're looking at - we want to form some kind of statistical basis as to what would be the frequency of men having blond hair or men having black hair or men having brown hair. Would you be able to do that similar to the way we do it with DNA?

A. No, you wouldn't. There are correlations there, particularly when you start looking at other physical traits for people, that to do things like trying to assume that hair colour is independent of eye colour or skin colour and so forth, they are in fact complex genetically determined traits. In some cases there are genes that have a common effect on skin pigmentation and eye colour and so forth, so you would not be able to simply just do probability calculations as -

Q. It's not just determined on genetic structure, your hair colour?

A. Well, it's determined ultimately genetically. I mean suppose we eliminate bleaches and dyes and so forth, presuming, and it's presuming there is hair available on the individual to determine what the colour is, but you can't do simply kind of probability analysis in those cases as we can with these biologically undisputed genetic loci.

Q. Now, I understand there's a particular - in the gene for hair there is a particular sequence for the different colours as with eyes?

A. Well, there is. It's not known what it is, where it is, at the present time. It's not known if there's only a single location, it's unlikely there's only a single location. Not an awful lot is known about that at a molecular level. I could tell you about eye colour in drosophila but I feel I'm not an expert in that area so I'm limited, but I know that there is not a simple genetic basis for determining hair colour.

Q. Because we notice many times in babies their hair colouring - or in young children their hair colouring will change from black to blond and maybe go back to black as they're growing up.

A. That's correct, and those of us as we get older notice the increasing appearance of grey hair.

Q. Don't tell me about that.

A. Or the increasing disappearance of hair in some phenotypes.

Q. Does that mean there's a genetic structural change when the hair colours change?

A. No, it isn't, because what we're seeing is what we designate in the study of heredity as the phenotype which is the expression of genes, and genes change their expression in some cases at different points in development, and so that it's not that the basic genetic structure is changing but which genes are expressed and in which tissues has a developmental pattern of expression associated with it.

Q. Is it possible - and you're not familiar with the testimony given by Dr. Geiser, but is it possible that if we were going to use a 95% upper confidence level on the FBI data base or, since the R.C.M.P. is

similar to the FBI, that the computations could change as drastically from one in 1,000 - or from one in six million down to one in 1,000, if you used the 95% upper confidence level?

A. I think it would be possible. I'd have to do some detailed calculations and see some actual figures but my reaction would be that yes, I think that would be possible in extreme cases, yes.

Q. That's a big difference.

A. Yes, it is.

Q. So if I was accused of something I didn't do and the basic coming in that - you know, statistical figures coming in at, well, one in six million or rather, one in 1,000, and those figures depend on whether or not an upper confidence level should be used, I - and would you be greatly concerned as a scientist even?

A. Well, I wouldn't because I know the specific case in detail here, and I know that that would not be possible with the frequencies that are used in this particular case. I think in order to generate what we would call a counter-example, one has to hunt through that data base and take the absolute extremes to get that kind of a calculation. I know that in the case - in the details here where these loci are in virtually every probe that has been used, some of the most frequent that are found in the data base, and that frequency and that highness of frequency remains consistent through Caucasian populations that I've had access to, that we're not looking at a case where by just shifting a band by a few base pairs we're going to go from one in three

million to one in a thousand, it's just numerically impossible.

Q. Yes, but this is just whether or not the system, if the system is - you know, there's too much measuremen error within it or to allow for different things, if you're going to use a 95% upper confidence limit on the system because it might not be proven to be absolute, and the difference between using that upper confidence level and not using that upper confidence level, the product rule gives you a difference of one in six million down to one in 1,000, and you know, this basically has got - I don't believe it has anything to do with the individual or the number of probes, it's just that the figures can change that drastically.

A. Well, that's saying - and when I gave those confidence intervals I was not by any means proposing that one uses the extremes at each end of that and taking that for each locus and multiplyin them through and comparing the difference at the two ends that you come out with of the 99% or the 95% or whatever on the two extremes like that. I was proposing, and I'm sure Professor Geiser would propose, that in fact you take the best estimate which is the estimate that is in the middle, and you multiply that through and you look at the width of that confidence interval, and the width of that confidence interval that you generate, you can do that for some extreme cases and that might vary in the extreme of one in 1,000 to what was it, one in six million? I've forgotten what the numbers were. In the same way you'll see in the numbers as I calculated them, they ran in one case from one in

175 million to one in 1.3 billion, and I think the amount of difference that I found there, if you took the extremes, would be, I think, numerically probably as great as he found, but he's not suggesting and I'm not suggesting that you use those extremes in those cases. Those extremes are just to give you a notion of the imprecision in that estimate and they're saying that, well, when you see that estimate, realize that it could be on the one level, in the case that I calculated one in 175 million, or as much as one in 75 billion, and the possibility of it being down at the low end is no more likely than the possibility of it being up at the high end. They're equally likely under this model, and in that case one takes the best estimate which is in the middle but it gives you a sense of the fact that if you were to base this on a different sample where would your new estimate fall, and it gives you, as the name implies, a sense of confidence or a sense of how precise or imprecise that actual measure is.

Q. Is Professor Geiser - or how do you pronounce his name -

A. Well, in fact, it was interesting because the one thing I read of his he claimed that the counsel was mispronouncing his name deliberately. Now, I don't know whether that's paranoia on his part or not but I think it's pronounced geyser, that would be my guess, but I have never heard it pronounced by him so I can't comment. In fact, I've never met him.

Q. How would you term his expertise?

A. I think it's quite good.

Q. No, but he's not a population geneticist?

A. He's not a population geneticist, he's a statistician.

Q. And he's an expert as a statistician?

A. Yes, and I -

Q. And you are not an expert as a statistician, are you?

A. No, I'm not, I'm a population geneticist. I have some expertise in statistics and some in molecular biology but I'm a population geneticist.

Q. So whether the scientific community - I assume if you're going to get together and decide whether or not it is valid to accept the Hardy-Weinberg formula statisticians as Dr. Geiser should be included in the panel?

A. And indeed they have.

Q. And this is an expertise that is being evolved?

A. Yes, it is, and in fact I can mention a number of statisticians around the world who are involved in this area. One of them in England is going to be visiting me in June, his name is Ian Eviett, and he's published extensively in this area and a highly well-regarded statistician.

Q. So you would admit that they would be a valuable asset in determining whether or not the Hardy-Weinberg formula and the product rule is valid in this case?

A. Yes, they are, and we would depend on their expertise quite heavily.

Q. And if a person such as Dr. Geiser was going to conclude that, you know, the computing these statistics the way the R.C.M.P. and the FBI does it is neither valid nor acceptable in the scientific community, then they should be listened to also?

A. Yes.

Q. Do you know a Dr. Randall Libby?

A. Randall Libby? The name doesn't ring a bell, no.

Q. And you've stated you've never yourself worked on forensic samples?

A. No, I have no experience personally on forensic samples.

Q. So you could not form the opinion whether or not the FBI system is reliable dealing with forensic samples?

A. I know of a study that has been published in the peer review journals by people at the FBI and with joint authorship by people at the R.C.M.P. where in fact they have done, in Dr. Lander's view, the best experiment that they could have where they have examined and used specifically forensic specimens and compared them to blood specimens from the same known individual, and it's been shown conclusively that there is no problem with forensic specimens in this extensive study. I would refer you to an article published in the April issue of "American Journal of Human Genetics" -

Q. But that may depend on which system the experiment is being processed through also?

A. And it was done on the system that is run and developed by the FBI in collaboration with the R.C.M.P. and is the same system that's been used for the data that we're present - has been presented here.

Q. Dr. Carmody, would you agree that without the knowledge of the frequencies of certain alleles as represented by DNA fragment sizes in a population it is impossible to calculate the likelihood that a

match could arise simply by chance?

A. Without knowing the frequency in the population, yes.

Q. Without knowing the frequency in a population?

A. Yes. Yes, I would.

Q. And you would not be able to comment on saying well, it's highly unlikely or anything without the numbers showing you that it's highly unlikely?

A. Well, I would say that one can say something is highly unlikely without having to put a precise estimate on it. I think we do it every day colloquially.

Q. But you would have to have some statistical basis to support that conclusion that it's highly unlikely, i.e., knowing what the frequencies are?

A. That's right, so that for example, the monomorphic probe, for example, that is present 100% and if you didn't - hadn't done the study to know that, you wouldn't be able to say, yes, and I know of a case where in fact because it was felt that the statistics were not known carefully enough that there was a feeling in that case that the purpose of the DNA was not of any value.

Q. Are you aware of any panels out there studying the implications of DNA in forensic use that they are recommending the formulation of data bases for specific communities rather than using a general one for the country?

A. I haven't read anything specifically on that. I know there is a report in the United States by the Office of Technology Assessment. The title of the report is "Genetic Witness". I have not read that

entire report and I'm not sure what the precise recommendations were there.

MR. FURLOTTE: My Lord, I assess at this time that I will probably be at the most maybe one more hour with Dr. Carmody, and I'm just wondering what his schedule is for this afternoon, if we want to break for lunch or go through to accommodate him.

THE COURT: Well, I think we better break for lunch, perhaps. You would be going one hour and at the end of one hour I'm going to ring a bell and that is going to be the end, the absolute end, and protest will avail you naught, Mr. Furlotte, unless you're finished in one hour. I give you one hour more, and then, Mr. Walsh, you're going to require some time for re-examination?

MR. WALSH: I would think, My Lord, probably fifteen minutes for redirect.

THE COURT: And that would permit you to get away this afternoon, presumably.

DR. CARMODY: That will be fine, My Lord.

THE COURT: So let's take until quarter to two.

(LUNCH RECESS - RESUMED AT 1:45 p.m.)

(ACCUSED IN DOCK.)

THE COURT: All right, Mr. Furlotte?

Q. All right, Dr. Carmody, I have one last thing to do with you and it's basically the same as what we did with comparing the profiles of Mr. Legere with one of the victims, Donna Daughney.

A. All right.

Q. And there are a few other comparisons I would like to make on those autorads. I'll get the appropriate

sizings. I'll try to put these in order as I have them on my list. Now I would like to compare the two sisters, Donna and Linda, which are in lane, I believe, 3 and 4.

A. All right. No, it couldn't be, lane 3 is -

Q. Oh, lane 3 is Mr. Legere, I'm sorry - lane 4 and 5, it would be.

THE COURT: This is with reference to VD -

A. -67.

Q. VD67 and that's for probe D2S44?

A. That's correct.

Q. And they would share how many bands for that probe?

A. Well, they both have a 2963 - sorry, a 2963 in the case of lane 5 and a 2965 in the case of lane 4. That puts them into bin 13, and bin 13 there is .097 -

Q. That should calculate out the same frequency as we had for Mr. Legere? Mr. Legere fit in that category also.

A. O.K., so they both have that band in common and then you want to know the frequency that they would both have that band?

Q. Yes, do you have your calculation there that you did for Mr. Legere?

A. Yes.

Q. It should be the same as his, would it not, just to save time?

A. Well, it's just that here we have two sisters, and if you want to know the probability that two sisters have the same band it's one-half. That is if you have two children from the same parents they have - they're going to have received one of the two bands

from their father and one of the two bands from their mother, so the probability that two siblings share a band is one-half.

Q. Right, but if we were - let's do it on the assumption that we didn't know they were related, O.K., in order to compare - make the comparison how Legere fits in in comparison as to how the two sisters fit in.

A. O.K.

Q. It might be better to assume that they're not related.

A. O.K., if we made the assumption that we didn't know they were related, then the probability that they both had a band like that would be the .097 or whatever. O.K., I'll - I guess it's .09696 for that. It's rounded to .97 here but I remember pretty accurately that that was the probability that one of them would have a band like that, and then the probability that another would have a band like that, if we didn't know they were related, would be that number times itself, and that comes out to be .00940 when you do that multiplication.

Q. O.K., now, the next - that's the only bands they share on that probe?

A. Yes, one has a 3576 and a 3884 -

Q. They would not fit in the same bin?

A. They would not fit in the same bin, no, they would be in bins 15 and 16 respectively.

Q. Now, for probe D1S7 -

A. Which is Exhibit VD66.

Q. Right.

A. Again they're in lanes 4 and 5?

Q. Again in lane 4 and 5, and I believe they do not share any bands in this one, do they?

A. That's right.

Q. O.K., so now we'll go to probe D4S139.

A. That's Exhibit VD68, lanes 4 and 5. Looks like they don't share any but I'd have to check the sizes there.

Q. And I have that they do not share any here either.

A. O.K., looks to me like they don't, I can just - that's correct, I corroborate they do not share any bands for locus D4.

Q. Now, next probe D17S79?

A. Yes, lanes 4 and 5 - this is Exhibit VD71.

Q. They would share one band in that one?

A. Yes, they have one that was estimated at 1515 base pairs and the other at 1542, so that would fall in the same bin, yes. I get that as a bin 5, which is 13.1%, so it's .131 is the probability of that, and you want me to calculate the probability that they both had that same size so it's going to be 13.1% times 13.1%, and I get that comes out to be .01716 or 1.716%.

Q. Now, our next probe is D16S85.

A. All right, D16S85 -

Q. That is Exhibit VD70.

A. Here lane 4 has two bands in bin 1 and lane 5 has one band in bin 1.

Q. So they would match in one band -

A. In one band they would match, yes.

MR. WALSH: Just to clarify, My Lord, we're talking about matches at bin frequencies?

MR. FURLOTTE: Matches at bin frequencies. I would expect

the band fragment lengths would match, too, because one is 538 and the other is 537.

A. Yes, and that particular bin for D16 occurs in over half the samples so it's a very common bin. I'll multiply that and that comes out to be the chance of a match for that particular bin is 25.806%.

Q. O.K., now, the next probe is D10S28.

A. And this is Exhibit VD69. Looks to me like they share one band, the 3967 and a 3959. That's in bin 16 which has a frequency of 4.6% in the population, and when I multiply that I get .00212 as the frequency of having a match for that band when you look at two bands in two different individuals.

Q. O.K., I believe that's all the bands that they share, so maybe you could do your product rule.

A. O.K., so I'd be multiplying .00212 times .2506 times .01716 times .00940, and that comes out to be - and would you like me to express this as one over a number because -

Q. It may help and then you can -

A. O.K., because the number is, and the way we record this is at 8.55346 times ten to the minus 8th power. The reason I'm saying this is because it's not probably the way that people normally talk about these very low numbers, but if you express that as one in a number, that's the equivalent of saying it's one in 11,691,174. That's what I get as expressing it in that way.

Q. And I believe between Mr. Legere and Donna Daughney it was one in 1.8 million, if I remember correctly?

A. I don't remember the number, to be honest, but I'd be willing to accept that.

Q. So it looks here if there was much less probability, if I'm correct, that there would be much less probability here for the two sisters to match than there was for Allan Legere and Donna Daughney to match?

A. I would say that's an incorrect statistical inference.

Q. Why so?

A. Because in fact the numbers that I'm calculating are in this case taken between known sisters and we are selecting so-called after the fact, after we see these numbers, calculating some probabilities and that they could range from virtually 25% to up to some astronomical number, and I would say that there's no statistical difference that one can infer from the difference that we see in matching one of these sisters with Mr. Legere, matching the other sister with Mr. Legere, or matching the sisters with each other. That kind of little trio of pair-wise combinations is not going to tell us anything of statistical value in this forensic case that I'm aware of.

Q. All right, let me put it this way, if you had the three individuals, Allan Legere, Linda Daughney, and Donna Daughney, and you did not know their names, you did not know their sex, you did not know their relationship, if somebody put these figures to you and they said, Dr. Carmody, two of these three individuals are related, which two would you say was related?

A. I would choose the two that had the more frequent probability.

Q. The one in 1.8 million?

A. If that is the closest of the two, and if I were looking at just these, and if I had just this partial information.

Q. Yes.

A. If I did the calculations based on what other alleles they had and did not have in common, I could make a better inference by not just selectively taking the alleles that they share. I could in fact conclude -

Q. But to do it just on the basis of these alleles it would appear that Mr. Legere is more related to Donna than her own sister?

A. That's correct.

Q. O.K., now let's go on and do another one. Let's do lane 2, Mr. Murphy.

A. We'll start with D2 or -

Q. We'll start with D2 again, start all over again.

A. O.K.

Q. That's the order I have them in so it's easier for us to keep it together. O.K., D2S44 is what we're dealing with?

A. Right, this is Exhibit VD67.

Q. Let's compare him with Donna, I guess, lane 4.

A. Between lane 2 and 4 it looks as though they have one allele in common. Lane 4 has a 2965 and lane 2 has a 2919.

Q. Maybe on your notes we could put the comparison between who we're comparing with on the top, O.K.?

A. O.K., on here, and this was - who were we comparing on this one?

Q. That was Donna and Linda, lanes 4 and 5.

A. O.K., and now who are we comparing?

Q. Now we're comparing Murphy and Donna, lanes 2 and 4.

A. O.K., lanes 2 and 4, and they share - looks to me like one band in common, 2919. You want me to write on the same thing or -

Q. Maybe so. You could write it all - it would be this here same calculation at the top.

A. It will come out the same?

Q. Yes.

A. O.K., well, I think rather than get myself confused I'm going to put D1 over here and I'll take your word that it's the same bin and we get that.

Q. I don't want you taking my word for it. If you have to check, you can check.

A. Well, sure. 2919 is in bin 13 and that's .097, and I did that calculation earlier so yes, that's correct.

Q. O.K., now we'll go to probe D1S7.

A. Which is on Exhibit VD66, and so it's lane 2 with lane 4 again?

Q. Yes.

A. Looks to me like there's no matches there.

Q. There's no matches, correct. Let's go on to the next probe, D4S139.

A. It's Exhibit VD68. I would say there are no matches there either.

Q. No matches there either, correct. Go on to probe D17S79.

A. D17S79, where in lane 2 we have only one band, it's a 1504 but it looks like it would fall in the same bin as 1515 and maybe even 1309. 1504 falls into bin 4, and 1515 actually falls in a different bin

so - and 1309 -

Q. Are they both on the border?

A. They're both very close to the border, and if you'd like me to use the frequency of the higher of those two -

Q. What would be the appropriate thing to do?

A. It would be to use the bin frequency that was the higher of the two adjacent bins in that case, so let's say for 1504 - so you'd use 29.2%, and the 1515 which, though it's officially in another bin, would be so close to the border that you'd use the higher of the two in the adjacent bins, so again you'd use a .292, that is 29.2, and if you multiply those together you get .08526 which is 8.5%.

Q. O.K., so the next probe is D16S85.

A. Which is taken from Exhibit VD40, and here lane 2 has a three-banded pattern and lane 4 has a typical double-banded pattern. As I mentioned yesterday, three-banded patterns are taken as somewhat anomalous because we're not sure of their molecular basis, but I can go through these calculations based on the fact that lane 4 has two bands that would fall in the very first bin and lane 2 has two of the three bands that would fall in the first bin, I would guess. This is what, D16? The first bin boundary is at 1077, so that both of the bands that are in lane 4 are also present in two of the three bands that are present in lane 2, O.K., and would you want me to calculate -

Q. Whatever is appropriate, Doctor.

A. Well, it depends on what the question is here in terms of appropriateness.

Q. Well, we're looking for the frequency that they would share these bands, I guess, so maybe all four bands should be - two from each?

A. If that's the frequency - I'm not sure that's the appropriate question but if that's what you'd like me to do I can calculate that.

Q. Well, I don't want you doing something that would be inappropriate, and I think you understand the technique we've been going through and what I'm trying to accomplish in the end so -

A. Well, no, I'm not. I'm not, I'm just trying to answer your questions.

Q. You're just trying to answer the questions. Well, it appears here they each have two bands which would fit into the same bin, is that a correct assumption?

A. No.

Q. It's not?

A. They both have two bands that fit in bin 1.

Q. They both have two bands that fit in bin 1?

A. That fit in bin 1, right, and we're calculating - if you want me to multiply .508 times .508 times .508 times .508 we're calculating there, and that's an answer to the question what is the probability that they would have two bands each that fell into bin 1. We're not answering the question about what is the probability that they would have two bands each that match.

Q. Oh, no, no, we're not answering that.

A. No, we're not answering that, so this has nothing to do with matching.

Q. No, this has nothing to do with matching.

A. O.K., and I get that multiplying .508 times itself

four times I get as an answer .06660.

Q. O.K., we'll go to the next probe, D10S28.

A. This is Exhibit VD69, and again I'm comparing lane 2 and lane 4.

Q. There are no matches, or nothing that would fit in -

A. That's right, there are no bands that would be placed in the same bins, right.

Q. O.K., will you calculate those figures, please?

A. O.K., so I'm going to multiply .0660 times .08526 times .00940, and I get a number .00005, which expressed in terms of the usual way we're talking about these as one over a number, that's one in 18,735 - is that right? That's what I get. Is that correct?

Q. Well, you got me, Doctor.

A. Well, I'd want to do these a little more carefully. I could have made a mistake by just -

Q. O.K., maybe you could do it over again, then.

A. O.K., .0666 multiplied by .08526 multiplied by .00940, I get again it comes out to the number of decimal places that I have on my calculator here, .00005. If I expressed that the way we're normally talking about these as one over a number it is one in 18,734.

Q. O.K. Now, again, if you were comparing and you knew these individuals, we'll say Murphy, Donna and Linda, and you were asked - and you were told two of these three individuals were related, who would most likely be related to each other?

A. Well, I would answer and say that the calculations that you've asked me to do cannot be used to answer that question.

Q. Because they don't make any sense?

A. That's right.

Q. Right.

A. In terms of the question you've asked. They make sense but they're an answer to a different question.

Q. But we're dealing here with just statistical probabilities as you're dealing with just statistical probabilities when you're faced with the product rule for human identification through DNA analysis? The principle is the same, Doctor.

A. The principle of multiplying numbers, yes. I don't deny that in my calculations I'm using fundamental arithmetic principles. There is a theory that is behind using them to answer certain questions and if you pose certain questions one can use arithmetic calculations to generate an answer to those questions.

Q. But the bottom line, Doctor, isn't it that you're using the statistical basis and the product rule in order to give a good scientific tool to identify people - or even let's leave people out - to identify events and the best possible chance of this particular event happening?

A. Yes, I'm attempting to do that, yes.

Q. And if we were going to use this tool to try and identify related individuals, i.e., Mr. Murphy and the two Daughney sisters, as to what's the best probability that which two are related, we come out with Mr. Murphy and Donna as one in 18,000 and we come out with the actual two sisters as one in 8.8 million. Now, that's an awful variation when we use, I will say, the product rule.

A. These numbers are not an answer to that question and cannot be used to answer that question.

Q. Right, but many scientists think that those numbers and the product rule cannot be used to answer the question of identification on DNA forensic evidence.

MR. WALSH: Is that a question, a statement, or -

A. There are some scientists who feel that we need more empirical data on some populations in order to answer the question of what the probability is of a random match between a forensic specimen that has been found.

Q. And you will agree that in the use of statistical probabilities and such that results can be very misconceiving if they are used wrong?

A. Yes.

Q. As the book, "How to Lie with Statistics"?

A. Yes, I would fully concur with that conclusion, yes, that statistics can be misused.

Q. Do you know that one of the methods of proving that an argument is fallacious is that you use - it's called - I forget now - refutation by analogy?

A. I've heard of that logical term, yes.

Q. Would you agree that this might be refutation by analogy?

A. I don't think so. I think what you had me do was to make a perverse caricature of statistics.

Q. That's the plan, Doctor, that was the exact plan, I suggest that -

A. And I think it's transparently obvious to anybody working in this area and that anybody who thinks that you can just multiply numbers and get a result that has some meaning, I think that there is an

agreed upon objective scientific basis for the calculations that we used in this case and bear absolutely no relation to the perverse caricature that you had me carry out here and to do these meaningless calculations, and this is not reasoning by analogy at all. In fact, it is showing that indeed one has to know what they're doing and the people that are doing this know what they're doing.

Q. So it would be helpful if we had experts in statistics to assist this Court in forming its conclusion?

A. I think that I feel confident that for this type of calculation I - being duly humble, I think I'm an expert enough in statistics to know that the simple proper application to statistics of this data would stand up under scrutiny, as it has, to some of the best statistical minds that have looked at it.

Q. And I would assume, Doctor, that once the panel that's investigating this has investigated the matter sufficiently that time will tell?

A. I wouldn't agree with that statement. I think that time will tell probably in any case. I'm not sure that this panel will have - and I'm sure this panel will not have the ultimate and final glimpse of truth, and there may well be other things that are wrong with it that heretofore have not been elucidated.

Q. Doctor, as I understood when we started this discussion yesterday, that you could calculate the areas of probability that certain people would share distinct bands of their DNA, and you could do that, by using the product rule you could do that,

and that meant if a person who had this band, what were the probabilities that he shared these two bands and maybe this band and that band with anybody else, and you told me you could do that with the product rule and the same scientific principles that you're using for identification in human DNA analysis.

A. I'm using the product rule but I also remember very accurately that in fact I said one had to be very careful about what question the application of that product rule in a particular case where you're picking and choosing specific bands after the fact, after you've looked at a complex number of bands, and you're just picking and choosing, not random bands, you're picking and choosing specific bands - that calculating the probabilities of that answers a different question than the question that I think you were putting to me.

Q. You're not saying I was misleading you?

A. I say you were putting a question that was different than the question I was prepared to answer on the basis of doing those calculations.

Q. Well, I understood you to understand the question perfectly when I put it to you yesterday but now are you saying you're confused now because you don't like the results?

MR. WALSH: Objection, he's being argumentative. He's not asking a proper question, in the Crown's humble opinion, My Lord.

THE COURT: Do you want to answer that?

A. Yes, My Lord. I feel that at this point I'm not confused and I believe that my testimony yesterday, as best I can remember, was saying that when you

had me do the calculations they were answering a different question and they were applicable to a different question than the one you were asking me, and I think I'm consistent in my answer to what you've posed to me.

MR. FURLOTTE: Well, I believe the record will show what particular questions I asked you yesterday, Doctor, and for the purpose, I believe, I will be finished with this witness on cross-examination.

THE COURT: Very well. Thank you. Now, are you ready for your re-examination?

MR. WALSH: Yes, I am, My Lord.

REDIRECT EXAMINATION BY MR. WALSH:

Q. Dr. Carmody, any of the tests that you conducted for Mr. Furlotte's interest yesterday and again today, could you tell the Court what if any scientific value they do in assisting the Court in determining the questions that's now before it?

A. I don't feel they have any relevance and any bearing on any of the conclusions that the statistics that have been calculated and that have been presented by myself to the Court - I don't feel it has any relevance to those calculations or any bearing on it except to show that perhaps one has to have some knowledge of how to go about this procedure in order to carry it out properly.

Q. Thank you, Doctor. Doctor, what if any beliefs do you have as to whether or not a data base from New Brunswick would create a statistically significant or forensically different result than what is present here?

MR. FURLOTTE: I believe he dealt with that on direct examination, My Lord.

MR. WALSH: Not to the extent that Mr. Furlotte has over the last couple of days delved into that issue.

THE COURT: Yes, it was dealt with on direct examination to some extent, as I recall, in a general way, but I think you did get into a more particular consideration of that on cross-examination. I'll permit the question.

A. I don't feel that from my knowledge of the Canadian Caucasian data base and from my comparisons that I've made with a few American Caucasian data bases that there is any reasonable doubt that the New Brunswick Caucasian data base would be any different, that the Caucasian New Brunswick frequencies would be substantively different from the numbers that I have calculated.

Q. And, Doctor, Mr. Furlotte asked you questions related to sampling individual communities, small communities, in the last couple of days. The fact that small communities have not been sampled, for example in New Brunswick or in the Maritimes, what if any opinion do you have as to whether that affects the opinions you have given in direct examination in relation to the reliability of the R.C.M.P. data base or with respect to the reliability of the figures that have been generated in this case?

A. I don't feel again, based on the calculations and the empirical evidence that derive from existing Caucasian populations that I've analyzed, that I have any reasonable doubt that applying these to the New Brunswick Caucasian population causes any concern. I furthermore feel that having sampled isolated

communities while to flesh out this science would be desirable, and I know is going to be continued in future, I don't feel at the present time it has significant bearing or implication in this particular case.

Q. And Doctor, Mr. Furlotte asked you about inbreeding and the effect inbreeding would have with respect to the calculations or the use of data bases. You indicated, Doctor, if I'm correct - to preface my question, you indicated, and correct me if I'm wrong, that increased - true homozygosity, increased homozygosity, is a measure of inbreeding, is that correct?

A. That is correct.

Q. And if, for example, Mr. Legere was to have no homozygotes, no homozygosity, would that indicate - what would that indicate to you?

A. Well, it doesn't necessarily mean that he is not inbred. I mean the fact that an individual is not homozygous does not mean that they themselves, that the indication of homozygosity says about that population - if you have excess true homozygosity that of that population there are likely to be correlations between what band is present for one allele and what band is present for another allele. The fact that two bands are not identical in an individual does not mean that that individual cannot be inbred.

Q. You're referring to excess homozygosity in the data base?

A. In the data base.

Q. And is there any concern of yours with respect to the R.C.M.P. data base in relation to inbreeding or

any evidence of inbreeding?

A. No. No, there isn't.

Q. And do you know of any people or any textbooks in this particular field that have talked about the coefficient of inbreeding with respect to Canadian Caucasian populations?

A. Yes, there have been a number of studies particularly done in the Province of Quebec where there are excellent church records that can be gone back to, and I don't know the figures precisely but I have seen figures on this in the past that the highest level of inbreeding that has ever been found in any Canadian Caucasian populations is on the order of .003 or something of that nature. That is three in the third decimal place as a measure of the amount of deviation from Hardy-Weinberg equilibrium.

Q. And would that have any effect on the forensic purposes these VNTR's are being put?

A. In my judgment they would have no significant impact in changing these frequencies in a statistically significant way.

Q. And with respect to the - you indicated, Doctor, if I'm not mistaken, the confidence interval is a measure of correcting for sampling error, is that right, or am I mistaken?

A. I wouldn't put it in those exact terms. I would say it's a way of indicating the limitations that are being imposed by having a finite sample size of the size that was used.

Q. Does the binning method in any way allow for that kind of - does the binning method do anything similar to what the confidence intervals do?

A. What the binning method does is because it places bands together that if we had a better technique would almost certainly in some cases be separated, means that the frequency of the bins that we calculate is probably in most cases higher than the actual individual genetic variants that we cannot precisely measure would be in if we had an even better and more highly and a technique with a greater resolution. That is to say that the binning method is in general a very conservative way of looking at the frequencies of these actual genetic variants.

Q. Doctor, you had mentioned - Mr. Furlotte had done a demonstration or asked you some questions in relation to the probability of finding one person with one hair in one spot and another hair would be in another - in the same place at the same time, and you had referred to Gaudette and Keeping in a report. Now, would you tell the Court, please, where you came in in relation to that report? Did you actually - were you part of the actual preparation of that report or did you consult in it or what did you actually do?

A. I consulted in that report, as I think my previous testimony might indicate. Barry Gaudette who is now chief scientist at the forensic labs in Ottawa, in the biology division, in any case, conducted this study and there was criticism of the statistical analysis of that study when it was first published. There were some letters to the editor of the Journal of Forensic Sciences which Barry Gaudette was responding to, and he asked me for some statistical help in rebutting the criticisms being levelled at

the original study. I have no co-authored publications with him on that, it was strictly, again, an attempt to be as helpful as I could. There was never any contractual monetary relationship between us. I helped him in that study and I think probably it's one of the reasons why he approached me last August to take a look at their data base.

Q. And, Dr. Carmody, Mr. Furlotte asked you a number of questions with respect to Dr. Hartl, Dr. Lewontin, Dr. Lander, Dr. Mueller, Dr. Geiser. You indicated in answer to his questions that - and correct me if I'm wrong - that these individuals are saying that there's not enough data yet before - there needs to be a collection of more data before we actually go ahead and use these figures; am I correct?

A. That is the way I would characterize their objection to the present use in forensic science.

Q. And do you know Dr. Hartl, Dr. Lewontin, Dr. Lander, Dr. Mueller, Dr. Geiser have done the work that you've done in relation to the R.C.M.P. data base?

A. No, they have not. I think that Dr. Geiser, in fact, in reading the one publication that I mentioned of Dr. Geiser's in a journal called "Chance", he, I think I would say inadvertently, made me think of a way of testing it that hadn't been tested before and is sort of unknownst to him the person who made me think of doing the statistical test that I did, but he has not done that test on his data or any data that he has available or has not published it if he has.

Q. And do you know if those other distinguished gentlemen have done the work you've done with the

R.C.M.P. data base?

A. I know they haven't done it with the R.C.M.P. data base.

Q. And Mr. Furlotte made much of Dr. Hartl in relation to his reports. Are you familiar with the blood grouping system that Dr. Hartl depended on as part of - depended on to give his opinion in Yee? Were you familiar with -

A. I don't remember the blood group system, to be honest. If you could tell me the name I will be probably familiar with it but I -

Q. The M.N. Morant system?

A. The M.N. system?

Q. Yes.

A. I know it as sort of a textbook example that I teach in genetics but I really am not an expert in serology.

Q. O.K., fine, Doctor, and this particular National Academy of Sciences that you say are now looking at certain issues on DNA analysis, are you aware whether or not that includes looking at whether we should be using data bases for sex offenders to collect data over time?

A. It has a very broad umbrella that it is looking at all of the aspects of using DNA -

MR. FURLOTTE: My Lord, I don't see the relevance of this. That wasn't touched on in cross-examination.

THE COURT: Well, there was a suggestion, I think, in the evidence given or the questioning on cross-examination that a lot of things were suspect and because the committee of the Academy of Science was investigating it or was set up to investigate it, and I

don't think there has been any effort made previously to describe the parameters of that investigation. I think it's a fair question, Mr. Furlotte.

MR. WALSH: I'm just concerned, Doctor, I wanted to clarify. Mr. Furlotte asked you questions about the National Academy of Sciences and you answered in relation to that in terms of their looking at DNA questions. The questions that they're looking at, do they include other things other than just simply the technique in bringing it into court?

A. Yes, they are. They're looking at every aspect that seems relevant, including what kind of national data bases, whether there should be an equivalent DNA fingerprint data base kept that is equivalent to the now traditional thumbprint or fingerprint, as we normally think of them, data base that the FBI keeps, responsibility in the United States of state governments versus federal government, all sorts of issues of that nature that are not related to specifically the technique or the analysis per se.

Q. And, Doctor, although Mr. Furlotte asked you a number of questions in the molecular biology end of the technique, I just wanted to delve into one to clarify something. You gave some evidence with respect to extra bands -

A. In a lane, in a lane you might have extra bands.

Q. And why you had some reasons. Have you done any forensic testing of human DNA samples yourself using the RFLP technique for forensics?

A. No, I have not.

Q. Have you given any consideration to the various methodological reasons why there may be extra bands?

A. I haven't given it close looking at. I have done RFLP analysis in non-human - with non-human and non-forensic material, and I know some of the methodological reasons where you can get extra bands that have to do with artifacts but I haven't looked and I wouldn't consider myself to be enough of an expert to say that I fully understand all of the ways that one can get artifactual extra bands.

MR. WALSH: Thank you, Doctor. I have no further questions, My Lord.

THE COURT: Just a couple of questions I have, and I'll give counsel an opportunity to ask further questions on these topics if they want to. One is is the Committee of the Academy of Science concerned only with the forensic use of DNA typing or does it extend beyond that to the diagnostic and -

A. I think it is but they may well be also considering the diagnostic, and particularly in the United States there's quite an industry developing in paternity testing, and I think they're looking at that and the diagnostic aspects as well, and particularly with a lot of issues that have to do with privacy of information. That is that if you have information on individuals who should this information be available to. People are worrying about whether insurance companies could get privy to this information, because as this information grows and becomes more secure in terms of being able to map more and more regions of the human genome there will undoubtedly be shown to be correlations of certain diseases with certain bands, and there is some concern then that whether insurance companies

should be permitted to have this information to make a decision as to whether you are an insurable risk or not, so they're looking at a number of issues that get into, I would call them ethical or bio-ethical issues. Whether in fact when - if this technique were used for amniocentesis, for pre-natal screening, whether that information should be made available to parents if it would allow them to decide whether they were to abort a child strictly on the basis of sex or strictly on the basis of whether there was a 70% chance that they had a certain disease, and try to set up kind of objective policy standards in these areas.

THE COURT: One other question, you testified in the voir dire in the Bourguignon preliminary -

A. That's right, I did not testify at the trial itself.

THE COURT: - and not at the trial, and you're aware of the ruling made there on the voir dire that while evidence could be given of the DNA typing techniques and so on I think it was prescribed that any reference to problematical chance or whatever would be - or to matches or the chance of matches would be that such matches are rare or extremely rare. You weren't required to face up to the conundrum of how you were going to describe rare or extremely rare without using fractions or decimals. Is there any way it can be done? How was it done in that case? It was done through Dr. -

A. Dr. Waye, and I don't know if Dr. Bowen was involved in that case or not. It was done through Dr. Waye and from what I've heard I think it was in fact

quite limiting because defence could not ask anything that had to be answered by using numbers, so if defence were to ask, well, exactly what do you mean by rare or very rare, this is exactly, I think, the question you're asking, how can you answer that question without using numbers, and I don't know what was done. I think it was just - I think Dr. Waye, as I recall, or what I've heard, said that it's astronomically rare, and I think that's in fact what is in the transcript.

THE COURT: Which injected a new level?

A. Yes.

THE COURT: I take it that you would find it very difficult to testify as to the probability of a match without resorting to decimals or figures. It would be almost impossible, I would think.

A. Yes, I would certainly have no hesitation in calling it rare. I personally would say that the probability of a match is very rare, but that's a matter of opinion and is nothing more than that, and whether I'm a statistician or not a statistician, a population geneticist, I can't define rare versus very rare except in the case of when I order my steak.

THE COURT: I was going to suggest that you might be even getting into medium rare. Now, do you have any questions, Mr. Walsh, that you'd like to put on either of these topics?

MR. WALSH: That second topic, My Lord, yes.

THE COURT: I don't think the first topic is particularly relevant.

MR. WALSH: No. The second topic, Doctor, you talked about

confidence intervals. In your opinion, Doctor, could I have your opinion, please, as to whether you think giving a confidence interval is a correct way of describing the phenomena that we're dealing with here, the probabilities of match?

A. I feel it does because I feel that using the probabilities in isolation of saying one in 5.2 million can convey a spurious precision in that estimate that is not warranted on the grounds upon which it's based, and I think that by giving that interval, though it's more complicated and it's a more abstract concept and I'm fully aware of that, conveys to an extent, to the best that I know, the imprecision of the actual number that is often quoted in isolation.

Q. Could I have your opinion, please, as to whether that would be - would that portray an accurate foundation for any qualitative statement to be made by an expert? What I mean by that is the use of the term very rare and then supporting it by reference to a confidence interval, do you think that would be - whether or not you would consider that to be an appropriate way of conveying the rarities of any matches?

A. I'm not sure that the question of how you, if I might put, draw the bin boundary between rare and very rare, is establishable. If there is some legal precedent or some precedent that some judicial committe would like to agree upon as to what the numbers should be to split between those two, it is not a question that I feel a confidence interval or a standard error put on that or any number of other statistical ways that you can

measure that imprecision will help you. I think the problem of whether you call a thing rare, very rare, astronomically rare, is unfortunately in the mind of the beholder, to an extent.

MR. WALSH: I see. Thank you, Doctor.

THE COURT: Mr. Furlotte, do you want any questions to the witness on those two points?

MR. FURLOTTE: Just one, I believe. Dr. Carmody, but in order to be able to say that something is rare, very rare, or astronomically rare, no matter which term you would use, the Hardy-Weinberg formula and the product rule would have to be assumed to be a valid scientific principle to obtain some kind of figure in the first place?

A. At the present time I see no way of making any judgments of that without resorting to some mathematical model or making that inference, and the mathematical model that is appropriate in this case is Hardy-Weinberg equilibrium and the product rule, yes.

Q. But basically if the numbers were not reliable, then there's no way you could say the thing was rare?

A. That's right.

MR. FURLOTTE: No further questions.

THE COURT: One other question I have, and I'm not going to give counsel a chance to examine you further on it, do you undertake to tell your students not to use the expression, at this point in time?

A. I do, My Lord.

THE COURT: You may be excused, then. Thank you very much, Doctor.

(BRIEF RECESS - RESUMED AT 3:15 p.m.)

(ACCUSED IN DOCK.)

THE COURT: Now, we're still in the voir dire and you have another witness you'd like to call?

DR. JOHN BOWEN, called as a witness, being duly sworn, testified as follows:

DIRECT EXAMINATION BY MR. WALSH:

Q. Would you give the Court your name, please?

A. John Hales Bowen.

Q. And your occupation?

A. I am a forensic specialist in the DNA Unit of the Central Forensic Laboratory in Ottawa for the R.C.M.P.

Q. Dr. Bowen, I'm going to show you this document. Would you look at it for me, please, and tell me whether you can identify it?

A. Yes, this is my curriculum vitae.

MR. WALSH: My Lord, may I have this entered, please?

THE COURT: Yes, that will be Exhibit VD-86.

MR. WALSH: With the Court's permission I would like to lead Dr. Bowen through his C.V.?

THE COURT: O.K.

MR. WALSH: Dr. Bowen, you have a Bachelor of Science with Honours in Biochemistry from Carleton University in Ottawa, Ontario?

A. That is correct.

Q. You have a Master of Science in Biochemistry from Queen's University in Kingston, Ontario?

A. Yes.

Q. And you have a Ph.D. in Biochemistry from the

University of Alberta?

A. I do.

Q. You have won a number of awards and scholarships throughout your educational experience?

A. That is correct.

Q. One of the dissertations, I note from your C.V., one of your dissertations was an evaluation of DNA in hair roots.

A. That is correct.

Q. Would you tell us, please, where and when and why you prepared that particular dissertation and for whom?

A. That dissertation was prepared in 1986 while I was doing my in-service training as a hair and fibre specialist in the Edmonton Forensic Laboratory for the R.C.M.P.

Q. I see, and your present role at the R.C.M.P., would you describe it, please, what your role is there and what you actually do in relation to DNA and DNA typing?

A. I am currently in charge of operations for the Molecular Genetics Section in the Ottawa Forensic Laboratory.

Q. I see, and in this particular regard do you do - actually do case work?

A. Yes, I do.

Q. And do you do anything in addition to case work?

A. I am also responsible for training of new individuals into the program.

Q. I see, and is that training - are you actually conducting training at the present time, training other individuals?

A. Yes, I am.

Q. And these individuals will be going where and doing what?

A. These individuals will be working in the Ottawa Laboratory or working in the Regional Laboratories for the forensic lab system in the R.C.M.P.

Q. And regional laboratories, would you give some examples of where, Doctor?

A. Halifax, Sackville, Winnipeg, Edmonton, Regina, and Vancouver.

Q. I see, and who have you worked with at the R.C.M.P. Laboratory in relation to your present role?

A. I have worked with Dr. John Waye and Dr. Ron Fourney.

Q. Dr. Waye having testified last week?

A. That is correct.

Q. You are a member of the Canadian Society of Forensic Science?

A. That is correct.

Q. You're also, I see here, a member of - you are a Canadian representative in the Technical Working Group on DNA Analysis Methods (TWGDAM) sponsored by the F.B.I. Research Laboratory?

A. Yes, I am.

Q. Would you explain to the judge what that is and what your role is there?

A. The Technical Working Group first met, I believe, in 1988. It is a group of individuals that at that time were interested in performing DNA analysis or had already implemented DNA analysis in forensic case work. It is a group sponsored by the FBI and includes members from state labs throughout the United States and one or two laboratories in Canada.

Q. And does that relate to the actual DNA typing technique?

A. Yes, it does.

Q. I see, and what kind of technique would that include?

A. It includes the Restriction Fragment Length Polymorphism technique, RFLP technique, and discussions on the Polymerase Chain Reaction, PCR.

Q. And you are also, I see from your professional associations, a member of a Workshop for Statistical Standards on DNA Analysis sponsored by the F.B.I. Research Laboratory, is that correct?

A. That is correct.

Q. Would you explain that, please?

A. That is a group of individuals also hosted by the FBI Laboratory that includes private laboratories interested or performing DNA - forensic DNA typing, individuals from the academic world, population geneticists, statisticians, and several people from the TWGDAM group, including myself and the FBI.

Q. And what kind of things do you actually discuss there?

A. At those meetings we discuss the interpretation of a match for forensic purposes, the statistical analysis of a match, and the interpretation.

Q. Doctor, could you explain, please, where you or how you began actually doing RFLP typing and what experience you have with RFLP typing?

A. My first experience with RFLP typing was at the University of Alberta during my Ph.D. dissertation work. The actual forensic application of RFLP typing was not something I performed until 1988, and it was done in conjunction with a research project

for the R.C.M.P. at that time.

THE COURT: May I just ask here, Dr. Carmody, can you hear this adequately back there?

DR. CARMODY Yes, I can.

THE COURT: It's coming through the loudspeakers all right?

DR. CARMODY: Yes, I can hear him.

MR. WALSH: You have a low voice, Dr. Bowen, I'll just ask you to speak up, please. You have testified, Doctor, as a molecular genetics specialist, I see from your C.V., in the Provincial Courts of Ontario and Saskatchewan and the General Court of Ontario?

A. That is correct.

Q. And I understand since the typing of this that also in the Supreme Court of British Columbia?

A. That is correct.

Q. And as a molecular genetics specialist, would that be involved in the forensic application of DNA typing and the significance of the results?

A. That is correct.

Q. And were you declared an expert in those cases?

A. Yes, I was.

Q. I see from your C.V. that you were also a defence consultant as a molecular genetics specialist in the Court of Queen's Bench in Alberta, is that correct?

A. That is correct.

Q. Would you describe and explain how you became a defence consultant?

A. I was called by a defence attorney who was handling a case involving DNA typing. In this particular instance it was a case involving the polymerase chain reaction, PCR, that was being used as evidence

against his client. I was consulted over the phone. I actually went out and visited him during the trial and consulted with the Crown witness at that time and we came to an agreement on what could be said about the analysis at that time.

Q. And what could be said, was it less or more than what was going to be said before you became involved?

A. It was much less than what would have been said if I had not been involved.

Q. And were you actually with the R.C.M.P. at that time?

A. Yes, I was.

Q. Dr. Bowen, I see from your C.V. - perhaps I'll ask you this question, in your case work do you actually get involved in doing other things than inclusions? Have you ever been involved in case work where there's been exclusions?

A. Yes, I've been involved in several cases where there have been exclusions.

Q. And what has happened in those particular cases?

A. In one of those cases the DNA evidence was ruled irrelevant. In two other cases the charges were withdrawn.

Q. And, Doctor, I see that you have some abstracts and conference proceedings. I take it those were abstracts that you were involved in the preparation of or proceedings that you actually attended?

A. I was involved in the preparation of those particular abstracts and also I attended some of the conferences.

Q. And those included conferences involving DNA typing?

A. That is correct.

Q. RFLP typing in particular?

A. That is correct.

Q. You have also lectured or given lectures at the Twelfth Annual Conference of the Canadian Identification Society in Edmonton on DNA and Forensic Science?

A. That is right.

Q. And given a lecture with respect to Case Experience at the R.C.M.P. Laboratories at the 37th Annual Meeting of the Canadian Society of Forensic Science in Ottawa?

A. That is correct.

Q. You have attended workshops on DNA Polymorphisms, in particular the 35th Annual Meeting of the Canadian Society of Forensic Science in Toronto?

A. That is correct.

Q. And the International Symposium on the Forensic Aspects of DNA Analysis, you've attended that as well?

A. Yes.

Q. And the Workshop on DNA: Quality Assurance and Quality Control Programs of the American Academy of Forensic Sciences 42nd Annual Meeting in Ohio?

A. Yes, I did.

Q. And, Doctor, for clarity, in what general field of science do you belong?

A. Biochemistry.

Q. And what relation would biochemistry have to DNA and DNA typing?

A. Biochemistry is essentially the study of the molecules of life. DNA happens to be one of those essential and critical molecules of life that is studied in biochemistry.

Q. And your role at the R.C.M.P. Lab, that is connected

and involved with RFLP typing?

A. That is correct.

Q. And is that the particular form of typing that was conducted in this case?

A. That is correct.

Q. And did you actually perform the case work for the case of The Queen vs. Allan Joseph Legere?

A. Yes, I did.

Q. Using RFLP typing?

A. That is correct.

Q. And your training that you conduct at the R.C.M.P. Laboratory, what kind of typing are you actually doing the training in, training others in?

A. We are training specialists in the use of the RFLP technology.

Q. In forensics?

A. In forensics.

Q. How many DNA typing cases using the RFLP technique would you have conducted in your work?

A. I've accepted 29 cases and completed approximately 20 of those cases.

Q. Those are actually forensic cases submitted to you?

A. That is correct.

Q. Doctor, in your opinion who in this country, Canada, would have done more forensic RFLP typing case work?

A. I'm not aware of anyone having done more than 20 cases in Canada.

Q. Very briefly, Doctor, what does the forensic application of DNA typing entail, particularly the RFLP typing?

A. The RFLP forensic DNA typing involves what Dr. John Waye spoke about in his testimony, particularly

involving, I believe it's Exhibits VD-30 and VD-40? The DNA typing procedure itself, once one has produced autorads the forensic application of DNA typing also involves the interpretation of a match, and by using certain fundamental mathematical formulae one can attach a certain significance to that match after referring to population data bases.

Q. I see, and in the other particular cases in which you were declared an expert did you in fact provide evidence to the Court with respect to your actual typing technique whether or not any matches existed and what the statistical significance of the match was?

A. Yes, I did.

Q. And these mathematical principles that you apply, you said they were fundamental principles?

A. That is correct.

Q. Do you have experience with the issues involving the forensic application of RFLP typing?

A. Yes, I do.

MR. WALSH: My Lord, at this time I'm going to ask that Dr. Bowen be declared an expert in the field of biochemistry and the forensic application of DNA typing.

THE COURT: Have you any questions, Mr. Furlotte, you'd like to put to the witness on the question of his expertise?

MR. FURLOTTE: Dr. Bowen, you said you've - to date you've done about 20 cases of RFLP typing in forensics?

A. I have completed approximately 20 cases.

MR. FURLOTTE: And how many had you completed at the time you did the Lègere case?

A. At the time I began the Legere case I had not completed any cases.

MR. FURLOTTE: Was Mr. Legere the first one that you started?

A. No, it is not.

MR. FURLOTTE: How many had you started before you started Mr. Legere's?

A. Eight.

MR. FURLOTTE: You started eight?

A. Yes.

MR. FURLOTTE: And you never had any of those completed before you started Legere's?

A. That is correct.

MR. FURLOTTE: And how many of those eight went to court?

A. I'm not sure, I'd have to go back and check my records.

MR. FURLOTTE: Do you think any of them went to court?

A. Yes, at least two of them have.

MR. FURLOTTE: At least two of them?

A. Yes.

MR. FURLOTTE: And did you complete those other eight that you had started before Legere? Did you complete them before you completed Legere's?

A. Yes, I did.

MR. FURLOTTE: Were any of them abandoned? Were any of the eight that you started before Legere, were any of them abandoned?

A. Abandoned?

MR. FURLOTTE: That you didn't complete them? That were never completed?

A. I don't believe so, no.

MR. FURLOTTE: Did you find any of them unreliable?

A. No, I did not.

MR. FURLOTTE: They were all - in your judgment they were all reliable tests?

A. Yes.

MR. FURLOTTE: Did you do work in the compiling the data base?

A. Not the particular actually collection of samples and running the data base, no, I did not.

MR. FURLOTTE: Was that completed before you got involved in forensic testing?

A. The compilation of the data base is an ongoing process and it's still ongoing.

MR. FURLOTTE: No further questions.

THE COURT: Nothing else you want to ask?

MR. WALSH: Just one question on redirect. Mr. Furlotte asked you a question with respect to how many actually you had did before Mr. Legere's case, or before you accepted Mr. Legere's - or the Legere case. How many RFLP typing tests had you conducted outside case work?

A. Typing tests as a comparison? I would say hundreds of comparisons.

THE COURT: But when you did hundreds, in what capacity had you done those?

A. These were in the doing of performing technology on various types of substrates such as hair, semen, blood, the repetitive samples and statistical or - not statistical but validation of the technology.

THE COURT: And I suppose in every DNA comparison you do or every DNA typing case, that involves both inclusions and exclusions or inclusions and exclusions result

from your typing, do they?

A. Those are two of the forms of results. There's also an inconclusive result that is possible.

THE COURT: Well, the witness has been qualified, I think, for the purpose of trial as an expert in the field of biochemistry and forensic application of DNA typing. I think those adequately explain.

MR. WALSH: Yes, thank you, My Lord.

THE COURT: May I ask this question? It might save difficulties later. You've been sitting, I believe, through most of the evidence on this -

A. Yes, My Lord.

THE COURT: Or at least the last few days. Is there any area on which questions have been asked or any area covered in the evidence that you feel you're not an expert in and should not be expressing an opinion on? Can you draw the parameters at this point?

A. Well, we have heard testimony from Dr. Carmody with regarding population genetics and statistics that I don't feel comfortable professing myself as an expert in those fields. I have limited knowledge in those fields as it pertains to the forensic application of DNA typing.

THE COURT: You merely accept the formulae that they provide for you, that the population geneticists provide? Where do you get your information from, your probability factors?

A. I use the advice of statisticians and population geneticists such as Dr. Carmody to form my opinions.

THE COURT: Any other field? I'm just trying to think of - well, it may emerge as we go along, perhaps. All

right, the witness is declared an expert.

MR. WALSH: Thank you, My Lord. Dr. Bowen, you actually do as part of your work and part of your case work actually provide statistical significance to the Court with respect to any matches that you do find, is that correct?

A. That's correct.

MR. WALSH: Using fundamental formulas?

A. That's correct.

MR. WALSH: And the data base at the R.C.M.P.?

A. That's correct.

MR. WALSH: And can you give me your opinion with respect to - your opinion as to the reliability of the data base for the purposes you put -

MR. FURLOTTE: Objection. He just stated that it was not his expertise. I don't think he can give his opinion on it.

THE COURT: I'm sorry, you're asking -

MR. WALSH; I'm asking if in his opinion whether or not the data base is reliable for the purposes he's using it for.

THE COURT: Well, he accepts it for that purpose? Say yes quickly.

A. Yes, I do, sir.

MR. WALSH: Thank you, My Lord. Dr. Bowen, you were in court, I believe you said, and you've heard the descriptions of Dr. Waye with respect to the RFLP technique?

A. I heard most of his testimony, yes.

Q. You referred to VD-30 and VD-40 which are the two charts before the Court?

A. Yes.

Q. Is that an accurate summation of the technique itself?

A. Yes, it is.

Q. And could you please, if you would, describe apart from the actual process of actually arriving at an autorad - could you describe what's involved in the interpretation of the autorad that's generated?

A. The interpretation of the autorad is first done as Dr. Waye mentioned as a visual match. One must have the visual match to go on to confirm that. One uses the computer methodology. This computer actually gives you a band size for the individual fragments that you have matched, and using our measurement imprecision we can bin that and then assign a statistical frequency from the bin data that we have in our population data base.

Q. So your match is visual backed up by the computer quantification?

A. That is correct.

Q. Have you been involved in any groups in which you've actually discussed or come out with any statement with respect to how an autorad should be interpreted?

A. Yes, I have. The workshop on statistical methods in DNA analysis came up with a statement on the interpretation of a match.

Q. And were you one of the endorsees of this statement?

A. Yes, I was.

Q. And were you involved in that workshop?

A. Yes, I was.

Q. And did you actually put a publication out with respect to your findings or your conclusions?

A. The statement was published, yes.

Q. I'll refer you to this document, please. Can you tell me whether or not you can identify it?

A. Yes, this is a statement produced by the Working Group on Statistical Standards for DNA Analysis.

MR. WALSH: With the Court's permission I'd move to have this entered, My Lord.

THE COURT: That would be VD-87. What was that called again?

MR. WALSH: It's entitled, "The Statement of the Working Group on Statistical Standards for DNA Analysis". I believe it's August 13, 1990, is the pre-print copy edition, My Lord. August 13, 1990. It's a pre-print of an article to appear in - I believe it's a publication called "Crime Laboratory Digest", a publication of the FBI. Doctor, I'm going to ask you to - I'll refer you to Page 4 of that particular document. Does that particular - is this the section that you're referring to?

A. Yes, it is.

Q. In relation to match criteria?

A. Yes, it is. It's entitled, "The Use of Matching Criteria and Interpretation of RFLP Analysis Results in Forensic Case Work".

Q. And does that accurately reflect your opinion with respect to how a match should be culled from an autorad?

A. Yes, it does.

Q. And that would cover from pages 4 through to -

A. - 6.

Q. 4 to 6?

A. Yes.

Q. And what if any agreement did you reach as to the possible conclusions that can be drawn from the interpretation of an autorad?

A. The possible conclusions were threefold. One could either include, exclude, or reach an inconclusive interpretation of the autorad.

Q. Now, these particular conclusions and this visual matching backed up by computer quantification, I've been referring to an autorad; are we referring to a lane to lane comparison or are you referring to a gel to gel comparison or a combination or what are you referring to in that kind of interpretation?

A. Both forms of interpretation can be used. One can compare lane to lane or gel to gel.

Q. And are those three possible conclusions valid for a lane to lane and a gel to gel comparison?

A. That is correct.

Q. And what do you use in - to do a visual match of an autorad what if any reference points do you use when you're doing a visual match of an autorad?

A. One uses the reference marker system, the molecular weight markers that are incorporated in various lanes throughout the gel as your reference points.

Q. Do you actually have to have both samples in adjacent lanes or can they be in separate lanes on the same gel?

A. They can be in separate lanes in the same gel, spread apart, as along as they are flanked by the molecular weight markers.

Q. Generally how was the typing test that you conducted in this case - how was it done?

A. It was done in accordance with what you see in the charts on VD-30 and VD-40.

Q. And the interpretation that you made?

A. The interpretation was a visual match and it was

then confirmed by the computer.

Q. And how many tests did you actually conduct in this case?

A. The test results resulted in the production of four blots.

Q. What do you refer to by a blot? I'm not sure whether it's the new term that we've actually heard or not but would you please describe or define what you mean by a blot?

A. A blot is a membrane. The Southern blot is the technique that is used as described by Dr. Waye. The membrane itself can be referred to as a blot.

Q. I see, so if I was to refer to VD-40 or VD-30 what would you be referring to as the blot?

A. The blot is made from the gel, it's a replica of the gel. It's the membrane, the nylon membrane here in this particular chart.

Q. All right, for the record you're ferring to VD-30 and you're referring to the bottom of that particular chart where it says nylon membrane agarose gel?

A. That is correct.

Q. And you generated four blots in this particular case?

A. That is correct.

Q. And, Doctor, did you make any matches in relation to this particular case from any of those blots?

A. Yes, I did.

Q. And did you assign any statistical significance to those matches in relation to any of those blots?

A. Yes, I did.

Q. And what data base did you use to assign the

statistical significance?

A. I used the Caucasian data base generated by the R.C.M.P. laboratories. It was dated, I believe, December 3, 1990.

Q. I see, and is that reference to the - I'm going to show you the item that has been marked VD-64 and tell me whether or not you can identify that.

A. Yes, this is the rebin data that I used in the statistical evaluation of this case.

Q. And you were in court when Dr. Carmody testified?

A. Yes, I was.

Q. And what if any relation did the data base that you used in this particular case have to what Dr. Carmody was testifying that he tested?

A. He tested this particular data base.

Q. And the method of calculation that you used to generate the statistical significance, what was your method of calculation?

A. I used the fundamental rules of the Hardy-Weinberg equation and the product rule.

Q. And what if any use did you make of the binning method for determining individual allele frequencies?

A. I used the rebin data in those particular tables and it's a fixed bin technique that we used for generating those tables.

Q. You were again present in court when Dr. Carmody testified and described the method of calculation?

A. Yes, I was.

Q. And was it the same or different than what Dr. Carmody testified?

A. It was the same.

Q. I'm going to refer to VD-54. Would you look at this document, please, and tell me what that is?

A. Yes, it is a copy of my forensic laboratory report with regard to the Legere matter.

Q. This case here?

A. This case here.

Q. Doctor, is there anything that you wanted to comment to the Court about in terms of that particular document?

A. Yes, I've noted since I've released this report that there is a typographical error on the first page.

Q. And would you refer us to it, please?

A. It is found in the general. It's regarding the date that I received the exhibits from Constable R. Britt. They were received on 89-10-25 as opposed to 89-10-29.

Q. And what did you do to confirm that that was in fact the correct date?

A. I went back to my handwritten notes and found that I was in error when I typed this report.

Q. And the results that you generated in this particular case, are they accurately reflected in this particular report, VD-54?

A. Yes, they are.

THE COURT: I wonder if the Clerk could indicate - put the new - there's no serious contestation, Mr. Furlotte, over the date, I gather? I was wondering if we could -

MR. FURLOTTE: I think I missed the gist of that argument.

THE COURT: Well, the witness says he made an error when he typed in 89-10-29, it should have been the 25th day of October, '89. I don't think very much turns on

it, probably, but to avoid later confusion why doesn't the Clerk put 25 after 29 and put your initials on it there.

MR. WALSH: The date that you wish to have corrected, Doctor?

A. May I check that again just before - I believe it was the 29th and I have changed it to the 25th, but I better check that, I don't want to further confuse the Court. Yes, the 25th of October.

THE COURT: Just put 25 with a circle around it next to the 29 there. I'm not changing the report, I'm merely indicating on that exhibit that it has been amended or changed.

MR. WALSH: Doctor, I'm going to refer you to the item that's been entered at this hearing as VD-55. Would you look at that for me, please, and if you would just briefly tell me whether you recognize it and what relation it has to this particular matter.

A. Yes, I recognize it. It is a book containing the duplicate autorads produced from two of the gels, blots in this particular case. The blots are referred to as gel #1, membrane #1, and gel #2, membrane #2.

Q. Gel #1, membrane #1, is the first section of this particular book?

A. Yes, that is correct.

Q. And the typewritten pages, what do they refer to, the two typewritten pages at the very beginning of that item?

A. The two typewritten pages refer to the individual lanes in the autorad or the gel itself as it was originally loaded, and it identifies each sample

as they were loaded in those particular lanes of the gel.

Q. And the second part of VD-55? I'm just going to ask you to speak up a little louder, Doctor, I know you have a low voice.

A. I'm sorry. The second page, gel 2, membrane 2, again identifies the samples as they were loaded into that particular gel.

Q. And I'm going to refer you to the item marked on this hearing 56, VD-56. Would you tell me what that refers to, please?

A. This again contains duplicate autorads. In this case they are autorads from gel #3, membrane #3, and gel #4, membrane #4, which is identified in this particular book as miscellaneous known samples.

Q. Doctor, what kind of samples have you actually in your experience typed using the RFLP method?

A. In forensic case work I have typed blood, semen, hair, buccal swabs. I've attempted to type several other samples but I've been unsuccessful.

Q. Like for example?

A. For example urine.

Q. What kind of extraction methods would you use to obtain DNA or to take DNA from the cells of any of this material; for example, hair root, blood or semen?

A. There are several different extraction methods used for releasing DNA from these various substrates. They're all written down in our protocol manual.

Q. Are the extraction methods that you use, are they - in your opinion what is the reasonable reliability of such methods?

A. They're very reliable in extracting DNA from these

types of samples. That's precisely what they were developed for in the past for extracting DNA from various cell types and that sort of thing.

Q. And are they used by other labs?

A. Yes, they are.

Q. And could you give - for example, what is involved - what is a differential extraction? What does that term mean?

A. A differential extraction is the type of extraction one uses on a semen stain or a vaginal swab where one expects that there's a possibility of having two cell types within that particular sample. With a semen stain or vaginal swab one can reasonably expect to have vaginal epithelial cells from the female and sperm cells from the male, and what one is attempting to do by performing a differential extraction is to separate those two types of cell types so that one can separate the DNA from those two individuals.

Q. Is a differential extraction absolute, is the result absolute? Is there an absolute separation between, for example, the vaginal epithelial cells and semen?

A. No, it is not absolute. In many cases it merely enables one to enrich the various fractions.

Q. What do you mean by that?

A. That there is still some, for example, female component along with the male component but the majority of the female component is with the first fraction or the female fraction.

Q. And what result does that play in terms of the autorad and how you interpret autorads?

A. One can end up with what is a mixed sample in that particular lane and one ends up with extra bands.

Q. Is there anything else related to the methodology of the RFLP typing that could create extra bands?

A. Oh, there are several means that would result in an extra band, primarily the most prevalent reason perhaps is the stripping process itself. Oftentimes one does not completely strip the probe from the previous hybridization, and this will result in bands that are carried through or still seen in the next probing on the next autorad.

Q. And what would you do in a case like that to - what would you do in a case like that where there is a carryover when there's not been a complete stripping from a previous probing?

A. One always documents the order of the probing and one can account for these bands by simply comparing the bands found on a particular probing back to the previous hybridization or probing to see if they do in fact come from that previous probing, and further to that one can retest the membrane with the same probe to ensure that these bands do not appear again.

Q. And is that in your opinion - could I have your opinion as to the reliability of doing that kind of thing?

A. It is very reliable.

Q. What kind of samples were you actually - what kind of substances were you actually dealing with here with respect to the case of The Queen versus Allan Legere and these items that you discussed, the autorads that you've identified?

A. In this particular case I was dealing with liquid bloods, hair, and vaginal swabs and body swabs.

Q. And when you say liquid blood, what do you mean by that?

A. This is a blood sample that has been submitted to the laboratory in a tube.

Q. And what if anything did you have to do with any blood submitted in terms of Kleenex or toilet paper?

A. Yes, I forgot to mention the blood stains. This is a similar extraction to say any stain such as a blood stain that is a slightly different technique in extracting the DNA from it but it was also performed in this particular case, yes.

Q. And your opinion as to the reliability of that type of extraction?

A. That type of extraction has been used in molecular biology for years.

Q. The substances that are displayed in the lanes in these autorads that are set out in VD-55 and VD-56, did you extract DNA from any or all of those particular substances?

A. Yes, I extracted the DNA from all those types of substances for those particular autorads.

Q. And did you have occasion, according to the particular diagram here - did you have occasion to digest any of the DNA that you actually extracted, digest that using any kind of an enzyme?

A. Yes, I digested DNA that I extracted from those exhibits using Hae III, the restriction endonuclease commonly used in North America.

Q. And what if anything did your controls tell you?

A. They told me that the restriction endonuclease

performed its function as expected.

Q. And what about the quantification? Did you quantify any of the DNA that you extracted from the samples?

A. Yes, the DNA was quantified prior to restriction enzyme digestion.

Q. And after you digest the DNA what, if anything, do you do next, Doctor?

A. After the DNA is digested it is first run on a test gel to ascertain that the DNA has digested properly, and then subsequent to that one runs the analytical gel where the remaining portion of that sample is run in an analytical gel for Southern blotting and further analysis.

Q. And is a record kept or did you keep a record in relation to the quantification or the digestion of the samples conducted in this particular case?

A. Yes, all these particular steps are documented.

Q. And how do you go about actually documenting?

A. Gels are photographed after they have been stained with ethidium bromide and records are kept, handwritten notes, on the particular steps used.

Q. Which would be the first of the samples in VD-55 or VD-56 - which would be the first blot that you actually ran in this particular case?

A. The first blot that I actually ran in this particular case is gel #1, membrane #1.

Q. And that was contained in the first section of VD-55?

A. That is correct.

Q. I see, and what if anything did you do with respect to the loading of the DNA that you had extracted from the cells and digested in relation to that first blot?

A. The DNA was loaded from samples that I had extracted from the various exhibits and the DNA was loaded in the order in which one - the typewritten material in this first two pages of this VD-55.

Q. Would you go through that for us, please, and describe and identify what we're referring to in each of the lanes contained in the first blot set out in VD-55?

A. The first lane contained a DNA marker. It is the Brl 1 kilobase marker that is used by the R.C.M.P. It is actually something that we use as a ruler to measure the size of the bands that we generate during this technology.

Q. What if any use do you make of it in terms of your visual matching?

A. It is used in conjunction with the flanking markers to determine the position of the fragments in the gel so it is used as individual match.

Q. Continue, please.

A. Lane 2 contains DNA extracted from Exhibit 157A, which was a known blood sample reportedly from Louis Murphy.

Q. Continue.

A. Lane 3 contained DNA extracted from GT56A and GT69A, which is actually a combined sample of scalp and pubic hair reportedly from Legere.

Q. Now, who combined these hairs and for what purpose?

A. I combined these hairs. There was only three hairs from each exhibit that I was submitted. I felt that there was probably insufficient DNA to run these samples separately, therefore I combined them to ensure that I was capable of getting a result.

Q. And what part of the hair were you actually extracting DNA from?

A. DNA was extracted from the hair root.

Q. Continue, please.

A. Lane 4 contains DNA isolated from Exhibit 115B, which was a known blood standard reportedly from Donna Daughney. Lane 5 contained DNA extracted from Exhibit 140A, which was a known blood standard reportedly from Linda Daughney. Lane 6 contained DNA extracted from Exhibit 1IF. This is a DNA extracted from the vaginal swab, female fraction, and it is reportedly from Nina Flam.

Q. Now, when you say female fraction, if you could just refresh our memories, what are you referring to there?

A. The female fraction refers to the fact that I attempted a differential extraction and this would be the first fraction which should contain predominantly DNA from the vaginal epithelial cells.

Q. Continue, please, Doctor.

A. Lane 7 contains DNA extracted from Exhibit 1I. This again is a vaginal swab reportedly from Nina Flam. This would be the male fraction of that particular extraction. Lane 8 contains DNA extracted from Exhibit 1J. It is denoted 'F' for female fraction. It is DNA extracted from the vaginal swablreportedly from Nina Flam. Lane 9 contains the DNA marker that I mentioned before is just a ruler that we use in our gels.

Q. This is another marker?

A. This is the same marker that we used in Lane 1. We run it throughout the gel as I mentioned previously.

Lane 10 contains DNA extracted from Exhibit 1J, which is DNA from the vaginal swab reportedly from Nina Flam. Again this is the male fraction of DNA from that particular swab. Lane 11 contains DNA extracted from Exhibit 109. This is denoted 'F' for female fraction. It is the DNA extracted from the vaginal swab reportedly from Donna Daughney. Lane 12 contains DNA extracted from Exhibit 109. It is the DNA extracted from the vaginal swab reportedly from Donna Daughney. In this case it is the male fraction. Lane 13 contains DNA extracted from Exhibit 110 and it's been denoted 'F' for female fraction. It is DNA extracted from a body swab reportedly from Donna Daughney. Lane 14 contains DNA extracted from Exhibit 110. In this case it is the male fraction of the DNA extracted from the body swab reportedly from Donna Daughney.

THE COURT: You're saying body swab?

A. Body swab.

THE COURT: B-o-d-y?

A. Yes.

Q. Would you explain what you mean by a body swab, Doctor?

A. Apparently a stain or a semen stain was identified on the body of the individual and it was swabbed by the investigator.

Q. And the difference in your mind between a vaginal swab and a body swab?

A. The difference in my mind is that a vaginal swab is taken from the vagina where a body swab can be taken from the exterior of the skin of the body.

Q. Thank you, Doctor.

A. Lane 15 is the DNA extracted from Exhibit 134. This is denoted 'F'. It stands for the female fraction of the vaginal swab reportedly from Linda Daughney. Lane 16 again is a DNA marker similar to the one, exactly the same as the one in Lane 9 and Lane 1. Lane 17 contains DNA extracted from Exhibit 134. This is the male fraction of the vaginal swab reportedly from Linda Daughney. Lane 18 contains DNA extracted from Exhibit 135. Again it's denoted 'F'. It is DNA extracted from the body swab of Linda Daughney, and again it is the female fraction. Lane 19 contains DNA extracted from Exhibit 135. It is the male fraction of the body swab reportedly from Linda Daughney. Lane 20 contains an allelic control, it's designated NM. In this case it is the female control. Lane 21 again is an allelic control. It is designated L2, and it is the male control, and finally in Lane 22 we have the DNA marker that is the same as the DNA marker in Lane 16, Lane 9 and Lane 1.

Q. What kind of extraction procedure were you using on the body swab?

A. The body swab, as you may have noticed, has a female and male fraction and it was extracted via a differential extraction procedure.

Q. What substance were you working with? What kind of a substance were you extracting the DNA from?

A. I believe it was a swab on a stick.

Q. Containing what? You say a differential extraction you used with what kind of substance?

A. What kind of substance? Oh, it was semen.

Q. O.K. What if any controls or what if any precautions did you take, Doctor, with respect to the loading of

these materials in the lanes you've identified?

A. There are several precautions that are taken that one only has a sample prepared containing a dye, a blue dye in each particular case. One only has enough sample prepared to load one lane. These are in well-marked tubes and as one loads the samples in the lane one can see the blue dye in the lane so one does not apply a second sample to one that has already been loaded.

Q. And what if anything do you do, Doctor, after you've loaded this particular gel?

A. After I loaded this particular gel I ran the gel, I submerged the samples and ran an electric current through the gel so that the DNA fragments would migrate through the gel.

Q. This is the gel electrophoresis that Dr. Waye discussed?

A. That is correct.

Q. And what if any controls - or what if anything did your controls tell you with respect to the gel electrophoresis of the samples that you've just referred to?

A. The controls such as the brome phenile blue running through the gel told me that the gel ran as expected, and I ran it the normal rate and length of time such that I would - it would indicate that the gel ran properly. After staining the gel with ethidium bromide I could see that the gel did in fact run properly, that the lanes were straight, and that the DNA was in the expected position.

Q. And at the risk of using that word, ethidium bromide, when did you actually apply the ethidium bromide,

before electrophoresis or after electrophoresis?

A. Ethidium bromide in our protocols is applied after electrophoresis.

Q. What if any concerns did you have about the correctness of the electrophoresis with respect to these samples?

A. I have no concerns whatsoever.

Q. What was your next step, Doctor?

A. The next step was to Southern blot the membrane to actually transfer the DNA from the gel to a nylon membrane.

Q. And you in fact did it in this case?

A. Yes, I did.

Q. And what if any concerns do you have about the correctness of actually completing the transfer?

A. I have no concerns whatsoever.

Q. Dr. Waye mentioned something about denaturization; how does this or where does this apply in relation to what we're talking about?

A. Prior to transfer one denatures the DNA within the gel. This is done by soaking the gel in alkali, in particular sodium hydroxide, which cause the strands of the DNA to separate such that they can be transferred to the gel in single stranded form.

Q. And, Doctor, was there a record kept of the gel electrophoresis and the other steps that you've described up until this point?

A. Yes, there was.

Q. And what does this record consist of?

A. Again this record consists of handwritten notes on particular forms that we use in the R.C.M.P. and photographs of any stained gels.

Q. Is this the polaroid, I think it was referred to last week?

A. Yes, it is a polaroid photograph.

Q. Is this a reasonably - in your opinion - could I have your opinion as to the reliability of keeping a record in this particular fashion?

A. It's very reliable.

Q. And what did you do next, Doctor, after you actually transferred it to the membrane?

A. After the DNA has been transferred to the membrane, the membrane is dried and then subsequent to that it is hybridized with a radioactive probe in order to test individual loci of interest.

Q. And did you in fact test the blot in this particular case with probes?

A. Yes, I did.

Q. Doctor, do you have the results - after you actually applied the probes what would you do in each case after you applied a probe?

A. After one applied the probe the excess probe that is non-specifically bound to the membrane is washed off under high stringency conditions. The blot is then placed under X-Ray film and the radioactivity bound to that particular blot will expose the X-Ray film and on subsequent exposure one can develop the X-Ray film and produce an autorad.

Q. Doctor, did you in fact do that in this case?

A. Yes, I did.

Q. And with respect to this blot, the first blot?

A. Yes, I did.

Q. And for the purposes of actually relating your results to the Court, how are you going to go about

that today, Doctor?

A. I can relate the results through the use of slides and show the original autorad.

Q. On the light box that you have next to you?

A. On the light box, yes.

Q. What if any difference will there be between actually looking at the slide on the screen of the autorad and looking at the original on the light box?

A. The problem with a slide in particular is the fact that it is a photographic reproduction of the autorad. Therefore, there is some difference in the contrast and the visibility of certain features on the slide that one can readily see on the original autorad.

Q. When you actually generated your report in this particular case, I believe it's VD-54, what autorad - what would you be making your interpretation from?

A. One always makes an interpretation from the original autorad.

Q. I see. What about duplicates of the autorads? For example, the duplicates are filed as evidence; would you ever make an original interpretation from duplicates?

A. No, I would not.

Q. Is there a particular order in which you actually apply the probes, Doctor?

A. There is no particular order established. There is some preference in terms of some investigators in the way they like to proceed. The only concern is that the monomorphic probing and the sex typing have to be the last two probings.

Q. Can you tell the Court anything about the effect of certain probes, whether some are more sensitive or less sensitive than another?

A. Yes, some probes are more sensitive than others, therefore the more sensitive probes should normally be retained until the last several sets of probings.

Q. What if any effect does actually applying a probe and then taking the probe off and applying another one? What effect does that have on the DNA that's in the membrane, fixed on the membrane?

A. As Dr. Waye mentioned in his testimony, stripping process as we're referring to, removing a probe and then re-applying a probe, with each subsequent stripping some DNA from that membrane is lost. Therefore after a series, say 10 to 15 strippings, the sensitivity of detection is less than one would have if the original autorad was in use - original blot was in use.

MR. WALSH: My Lord, I'm just wondering, I'll ask the Court's direction here. Dr. Bowen, I believe at this point in time you would prefer to go to the slide and begin your review of the individual autorads that you generated with respect to the first blot, am I correct?

A. Yes.

THE COURT: Are you going to use both the screen and this at the same time, simultaneously?

MR. WALSH: Yes, now, I'll just ask the Court's direction, My Lord, obviously it's whatever you prefer. There will be a number of autorads that the doctor will be referring to in sequence, sequential order. I'm wondering whether the Court would prefer that the

doctor started now because we certainly won't be able to complete it today, or would you prefer to start in the morning and run through? What would you think would be better, Doctor? Perhaps you could guide the Court on this.

A. In my mind if one wants to look at a series of autorads to get a feeling for the interpretation it is best to view the entire set of autorads at one time.

THE COURT: Well, I think probably that would be the better way of doing it. Is there some other questioning you can go on with tonight for a short time, this afternoon, or do you want to call it off now?

MR. WALSH: I could perhaps ask a number of questions that I could fill in the time a bit, My Lord. I could ask a couple anyway, if I may be allowed.

THE COURT: May I ask this, are you going to have - will there be charts to support the slides and the autorads? Not to support, I mean to eflect the same thing?

MR. WALSH: We have filed as evidence VD-55 and VD-56 which are duplicates of the originals, Doctor, am I correct?

A. That is correct.

Q. Duplicates of the originals of the autorads, so that will constitute the evidence that we wish to have marked at this hearing. The slides are demonstrative evidence of these duplicates. The doctor has the originals under his control and he can have them referred to on the light box. We do not wish, with the Court's permission, to actually enter the originals at this particular hearing because should the Court make a decision at some point that we can

use these before a jury the doctor will need them to prepare further materials.

THE COURT: No, my question was will you have charts in this nature to reflect what is on the slides?

MR. WALSH: Yes, we have one chart here in which the doctor - my understanding the doctor summarized the conclusions that he's drawn from the autorads, at least with respect to the first blot.

THE COURT: Yes, which would reflect the same conclusions as contained in the report, I suppose, except it's put out in schematic -

MR. WALSH Or in a fashion that you can easily look at - perhaps I could ask -

THE COURT: If you want just go as long as you feel is convenient here.

MR. WALSH: Thank you. Doctor, could you tell the Court - you will be referring to it tomorrow but would you tell the Court, please, what probes you used in relation to the first blot?

A. I used the probes, the particular loci that are illustrated in Exhibit VD-27. The probes themselves are for locus D1S7, the probe is MS1.

Q. O.K., I don't think we'll get into that. NS1, what are you referring to?

A. It is the commercial name of the probe. It's M, as in Mary, S1.

Q. I'm sorry.

A. Do you wish to go through all the common probe names?

Q. Yes, just refer to the -

A. O.K., the second hypervariable probe is for locus D2S44. The probe itself is YNH24.

THE COURT: Well, these are just brand names, are they?

A. These are the commercial names for these probes. The third locus is D4S139, the probe is PH30.

Q. Now, D4S139, I believe you were in court when Mr. Furlotte asked a question about that, is that correct?

A. That is correct.

Q. And what if anything did you do as a result of the question he asked?

A. As a result of that question - I had been away on holiday just previous to appearing in New Brunswick and I wasn't sure if there had been any change in the situation at the FBI. I had a colleague of mine contact the FBI to ascertain whether they had dropped the use of D4S139, and they replied that no, they still use it in forensic case work and they are very happy with its sensitivity for use in forensic case work.

Q. Fine. Continue, Doctor.

A. The next probe that is a hypervariable probe is on locus D10S28. The probe itself is TBQ7. The next locus, hypervariable locus, is D16S85. The common name for that probe is 3 Prime HVR. The next probe for a hypervariable locus is D17S79. The common name is V1. And the two control probes that we use in the R.C.M.P. system, the monomorphic probe is D7Z2, and the final sex typing probe, again a control type probing, is DYZ1.

Q. Have these probes been in the arsenal or in the stable of the R.C.M.P. since the beginning of the DNA typing system?

A. We have had all these probes within the R.C.M.P. system ever since we've begun case work. We did not have a data base for locus D10S28 until the past year so that it was not in use for forensic case work up until that time.

Q. Is that D10S28 used by other labs, though?

A. Yes, it is.

Q. Who would use that particular -

A. Several labs use it. I'm aware of, for example, the Centre for Forensic Sciences use it and several labs throughout the United States.

Q. And D16S85, could you tell us, please, Doctor, whether or not that particular probe was used to - whether you use that in your actual calculation of your mathematical significance?

A. This particular probe resulted in an inconclusive result and therefore was not included in the mathematical calculation in this particular case.

Q. But you did actually run the probe on the blot?

A. Yes, I did.

THE COURT: Which probe was that?

A. D16S85.

Q. Perhaps, Doctor, if you would give us some insight as to the conclusions that you'll be telling us about tomorrow. Would you tell the judge what an exclusion means to you in terms of your interpretation and your opinion? What does an inclusion mean to you in terms of when you're looking at a pattern, and what an inconclusive means to you in relation to looking at a pattern?

A. First of all, it might help the Court to understand that it is essentially an exclusionary test. One

is running samples in various lanes of a gel and the test itself is to see whether one can exclude those samples as having come from a single source. By exclusion one sees that the fragments obtained for each of the individual loci are different, they are different sizes, the patterns do not match. If the patterns match one has to continue on to the next locus and the resulting five or six hypervariable loci that we look at in the R.C.M.P. system to determine whether this inclusion for similarity and pattern is obtained with all loci. If this inability to exclude that sample as having come from a common source is present, in fact the bands match at all individual loci, one has to come up with some sort of statistical significance for that match.

Q. What's your initial conclusion before you go to determine statistical significance? What is your initial conclusion from a pattern that matches?

A. The initial conclusion is that these samples could have come from the same individual and that they match, the DNA profiles match. An inconclusive result can result for several means; if only a partial pattern is obtained during the process, for example some bands are lighter or too light to be visualized because there's insufficient DNA present. Another inconclusive result would be due to a partial digestion of the DNA such that the DNA itself was not digested totally as it should have been by the restriction endonuclease. Another inconclusive result would be a result that there is a visual match and yet the bands when confirmed using the computer fall outside the match window.

Q. Doctor, I'm going to refer you to - I hope I'm not too much out of order here but - out of order in terms of the sequence we wish to ask the questions. I'm going to refer you to VD-42, 43 and 44. They are protocols, My Lord. Perhaps I'll show you all three of them, Doctor, and tell me what if any application these documents would have to the testing that you did in relation to the first blot that we've referred to.

A. Exhibit VD-42 is the forensic DNA typing protocols in place in the R.C.M.P. labs in October of 1989. Exhibit VD-43 is the forensic DNA typing protocols as written in March of 1990. There are very minor changes between the two protocols with reference to the October, 1989, protocol, and Exhibit VD-44 is the DNA typing protocol manual for the Biology Section for the R.C.M.P. as of January, 1991.

Q. Why is the last one - Dr. Waye touched on this but why is the last one so much - seems to be, at least, thicker than the others?

A. The last one is thicker because it contains a lot more detail on the individual steps in the protocols. The last one also contains a slightly different methodology as seen in the first two protocols. The reason for the inclusion of more detail in the protocols is, as Dr. Waye stated, the audience changed. The individuals performing the technology such as Dr. Fourney, Dr. Waye and myself, in October, 1989, really knew all the basic steps and were familiar with the technology to the extent that we only needed a very limited sketch of the technology. As we trained more individuals in the technology it became apparent that we had to add more detail for

these people in training so that they could follow the manual more as a recipe book.

Q. Doctor, has anyone looked at the results that you've generated in this particular case, any other scientists have reviewed these particular results?

A. Yes.

Q. I don't want you to tell me what their opinions are, I just want to know if anyone did, and if so, who?

A. Yes, in all forensic case work reports there is - that are submitted by the R.C.M.P. lab - there is at least one independent analyst that goes over the results prior to that report being released. In this case there was an individual at the R.C.M.P. Again there was one or two outside individuals that looked at these results.

Q. Could you name them, please?

A. Yes, the individuals - the particular individual in the R.C.M.P. was Dr. Ron Fourney. The outside individuals were Dr. John Waye and Dr. Ken Kidd.

MR. WALSH: My Lord, I would suggest that -

THE COURT: The name before Dr. Kidd was what?

A. Dr. Ron Fourney.

Q. I understand Dr. Fourney - he's the same gentleman who testified a couple of weeks ago down here.

THE COURT: No, I got him but then you said somebody else between him and - the first outside person.

A. The first outside person was Dr. John Waye. These are people that interpreted the match and the statistics. The statistics alone were interpreted by Dr. George Carmody.

Q. Dr. Ken Kidd, do you know whether or not he has ever been to your lab, in your personal experience and personal knowledge?

A. Dr. Ken Kidd has been at the R.C.M.P. Laboratory in Ottawa on two occasions.

Q. And for what purposes?

A. The first occasion he came to visit the lab to see how we were performing the technology and to discuss various issues that we were dealing with at the time. He also lectured to our first training group at that time. This was in May of 1990.

Q. And is Dr. Ken Kidd on the payroll of the R.C.M.P., so to speak?

A. No, he is not.

Q. I see, and why would you want to refer to Dr. Kidd or why would you want him in your lab or why would you consult with him?

A. Dr. Ken Kidd is an individual that I had met through the Workshop on Statistical Methods sponsored by the FBI. He's an eminent population geneticist that is highly regarded in his field and we were very eager to bring him to our lab so that he could speak and lecture on population genetics to our training people.

Q. Did you ask him for any opinions with respect to any of the things that you were actually doing either in relation to the technology or in relation to the data base?

A. Yes, I did. I personally took him through the lab to show him exactly how we were doing things at that time and had him review the protocols and he has - copies of the data base have been made available to him.

MR. WALSH: My Lord, I think it might appropriate at this point in time if - at this point, I'm sorry - at

this point, My Lord, I would ask if we could adjourn till tomorrow morning. Thank you. If we stay here long enough my English will improve.

THE COURT: At this time we will adjourn.

MR. WALSH: Thank you.

THE COURT: You're still on the stand, of course, and shouldn't discuss the case with anyone until your evidence is completed.

DR. BOWEN: Yes, My Lord.

(ADJOURNED TO 9:30 a.m., MAY 9, 1991.)

IN THE COURT OF QUEEN'S BENCH OF NEW BRUNSWICK

TRIAL DIVISION

JUDICIAL DISTRICT OF FREDERICTON

BETWEEN:

HER MAJESTY THE QUEEN

- and -

ALLAN J. LEGERE

AFFIDAVIT

1. THAT I am a stenographer duly appointed under the Recording of Evidence by Sound Recording Machine Act.

2. THAT this transcript is a true and correct transcription of the record of these proceedings made under Section 2 and certified pursuant to Section 3 of the Act.

3. THAT a true copy of the certificate made pursuant to Section 3(1) of the Act and accompanying the record at the time of its transcription is appended hereto as Schedule "A" to this affidavit.

SWORN TO at the City of Fredericton in the Province of New Brunswick this 21st day of May, 1991.

BEFORE ME:

William J. Culley

A COMMISSIONER OF OATHS

SCHEDULE "A"

RECORDING OF EVIDENCE BY SOUND RECORDING MACHINE ACT

CERTIFICATE

I, Verna Peterson, of Fredericton, New Brunswick, certify that the sound recording tapes labelled #1 through #9, May 7 and May 8/91, J. D. , R. v. Allan Legere, Voir Dire, initialled by me and enclosed in this envelope are the record of the evidence (or a portion thereof) recorded on a sound recording machine pursuant to Section 2 of the Recording of Evidence by Sound Recording Machine Act at the voir dire hearing held in the above proceeding on the 7th and 8th days of May, 1991, at Burton, New Brunswick, and that I was the person in charge of the sound recording machine at the time the evidence and proceedings were recorded.

DATED AT FREDERICTON, N. B., the 8th day of May , 1991.

Verna Peterson