VOLUME XIII

IN THE COURT OF QUEEN'S BENCH OF NEW BRUNSWICK

TRIAL DIVISION

JUDICIAL DISTRICT OF FREDERICTON

BETWEEN;

HER MAJESTY THE QUEEN

- and -

ALLAN JOSEPH LEGERE

VOIR DIRE held before Honourable Mr. Justice David M. Dickson, at Burton, New Brunswick, on the 27th day of May, A. D. 1991.

APPEARANCES:

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

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

VERNA PETERSON
COURT REPORTER

VOLUME XIII - VOIR DIRE

May 27, 1991.

I N D E X

LIST OF EXHIBITS

LIST OF EXHIBITS - (CONT'D.)

(VOIR DIRE - R. vs. ALLAN JOSEPH LEGERE)

(COURT RESUMES AT 9:30 a.m., MAY 27, 1991)

(ACCUSED IN DOCK.)

THE COURT: Now we're resuming the voir dire, and the Crown when last we met on the 17th had concluded its case on the DNA aspect of the voir dire and now the defence were going to call a witness, I believe. Mr. Furlotte?

MR. FURLOTTE: Yes, My Lord, call Dr. William Shields.

DR. WILLIAM SHIELDS, called as a witness, being duly sworn, testified as follows:

DIRECT EXAMINATION BY MR. FURLOTTE:

MR. FURLOTTE: My Lord, if I may with the Crown's permission enter Dr. Shields' C.V. as an exhibit?

MR. WALSH: I have no objection.

THE COURT: VD-116. As I have explained to other witnesses the designation of our exhibits as VD doesn't have any medical significance. It refers to the words voir dire.

MR. FURLOTTE: Dr. Shields, would you happen to have an extra copy of your C.V. in your briefcase, by any chance?

A. In my briefcase.

Q. I can give this to the Crown Prosecutor. Dr. Shields how old are you at this time?

A. I have to do some calculations - 42, I believe, maybe 43.

Q. And where are you presently employed?

A. I'm employed at the State University of New York, College of Environmental Science and Forestry in Syracuse.

Q. And what is your position there?

A. I'm a professor of biology.

Q. My Lord, if I may go through some of Dr. Shields' C.V. with him?

THE COURT: Yes, sure.

Q. Dr. Shields, I see for your degrees that you received an A. B. at Livingston College, Rutgers University, New Brunswick, New Jersey, in Biology with Distinction in May of 1974?

A. That's correct.

Q. And you received an M.S., Master of Science, I would assume?

A. That's correct.

Q. At Ohio State University, Columbus, Ohio, in Zoology, in June, 1976?

A. That's correct.

Q. And you received a Ph.D. at Ohio State University, Columbus, Ohio, in Zoology, in June, 1979?

A. Yes.

Q. And dissertation with philopatry, inbreeding and adaptive advantages of sex?

A. That's correct.

Q. Would that Ph.D. have anything to do with population genetics?

A. I hope so. It's probably about four-fifths population and ecological genetics.

Q. Doctor, I see in professional experience you have listed as a teaching associate at Ohio State University in general biology, general zoology, ethology, animal behaviour, ornithology and evolution?

A. That's correct.

Q. That was from 1974 to 1979?

A. Yes.

Q. And again you were an instructor at Wilmington College, Wilmington, Ohio, topics in biology, vertebrate biology, laboratory in vertebrate anatomy.

A. Yes.

Q. Lecturer at Ohio State University at Lima, Ohio, in general biology (Majors: lecture and lab), and again general biology (Non-majors: lecture)?

A. Yes.

Q. And in 1988 you were professor and assistant professor in 1979 to '84 and associate professor from 1984 to '88, State University of New Brunswick, College of Environmental Science and Forest Syracuse?

A. I hope it's the State University of New York. Everything else you said was correct.

THE COURT: It says New York.

Q. Doctor, I see also in your publications that you've published a book?

A. Yes, it was based on my dissertation and it has almost the same title as my dissertation, so it's again mostly population and ecological genetics

Q. And this was in 1982?

A. That's when the book was published, yes.

Q. Published by State University of New York Press, Albany, New York?

A. Yes.

Q. And was that 245 pages?

A. Mm-hmm.

Q. I also see, Doctor, that you have to your credit a number of papers, roughly 36 in number?

A. Thirty-five papers, I think, and one book, yes.

Q. And do any of these have to deal with what material, population genetics?

A. About half of them deal with population genetics or ecological genetic issues.

Q. Doctor, have you ever been an invited lecturer on population genetics, and where?

A. Yes, I have, in many different places. Probably the most fun place was the University of Hawaii, but I've also been invited to speak on such issues at places like Harvard, the University of California at Davis or Santa Barbara, University of Arizona, University of Western Ontario and at Queens in Kingston. Many other places as well.

Q. Queens at Kingston, and that's Ontario, Canada?

A. Yes, it is.

Q. Doctor, I see some of your papers or lectures were what, in inbred populations?

A. I do a lot of writing, reading, and thinking about inbreeding in its general sense. It doesn't necessarily mean the way most people think of it in terms of incest, but rather, population structure.

Q. Population structure. Inbreeding is not another term for incest?

A. Incest is a term for one kind of inbreeding.

Q. And, Doctor, have you testified in court before as an expert witness, and in what areas?

A. Yes, I have. I don't know enough about what this admitted as an expert is but I have testified in a number of courts about population genetics issues, molecular genetics issues, and the statistical issues which are really the same as the population

genetics issues in some senses of DNA typing and forensic systems, and I've testified in both the U.S. and Canada.

Q. And how many courts would you have testified in?

A. Nine or ten.

Q. Pardon?

A. Nine or ten.

Q. Now, Doctor, have you prepared any papers in relation to population genetics as the field of population genetics applies to forensic evidence?

A. I have only prepared one paper and I'm not sure I'd call it a paper. What it is is sort of a - the organization of a paper that I'm planning to write, which I did submit to the U. S. National Academy of Sciences because they had a panel which was considering forensic uses of DNA typing and some of the people who were on that committee that was working on that asked me if I was interested would I submit some information about my experiences in the court room.

Q. And who in particular asked you to submit that paper?

A. Eric Lander suggested that if I was interested that I should. In addition I talked to Victor McCusick who is the chairman of that committee and he said the same thing, and Oscar Zaborsky who is what we call a National Research Council person who was administering the committee.

Q. And, Doctor, I'll show you a copy of the paper. Could you advise me if that's the paper that you submitted to the National Academy of Sciences?

A. Yes, it is.

MR. FURLOTTE: I'd offer this as an exhibit, My Lord.

MR. WALSH: I would have liked -

MR. FURLOTTE: I'll give you a copy.

MR. WALSH: I see it's about an inch thick. I would have liked to have been at least shown it before he tendered it into evidence. I'm going to consent to this. He's asking me to consent to this and I haven't read it. I'm at a very grave disadvantage. I don't want to interfere but I'd like to know what's going in.

THE COURT: As in the case of some of the earlier papers that were put into evidence I will admit it but I'm admitting it simply as evidence that a paper has been tendered. It's not proof of the contents of the paper. It may perhaps provide the foundation for some of the examination. What can you do to get Mr. Walsh provided with a copy, Mr. Furlotte?

MR. FURLOTTE: I have an extra copy I can give him. I just received this myself this weekend.

THE COURT: Well, that's understandable, perhaps, but if you'd see that as early as possible, like later today, at noon-hour perhaps, could he get a copy of that?

MR. FURLOTTE: At break-time this morning I can give Mr. Walsh a copy.

THE COURT: Yes, and if there are matters in that paper that you want to cross-examine on, Mr. Walsh, if it pertained to the question of expertise you might want to do it when that motion is made that the witness be declared an expert, or very possibly - it's more probable that it could be done at the end of the direct testimony, so we'll mark that as

Exhibit VD-117. Two parts, are there, and are they all part of the same paper?

A. Yes, it's the text and the figures, Your Honour.

MR. WALSH: What is the title?

THE COURT: And the title is what?

MR. FURLOTTE: The title is "Problems with Forensic DNA Typing as Evidence in Criminal Proceedings", by William M. Shields.

THE COURT: Make it one exhibit, the one number, VD-117.

MR. FURLOTTE: Dr. Shields, would it be safe to say that the Academy of National Science considered you to be an expert in population genetics when they asked you to submit the paper?

A. That's a strange question to answer, for me to answer. What I would say is that based on the experience that I had with forensic DNA typing based on court room experience and based on my research in population genetics they thought it might be useful for them to see my thoughts on the process and the problems. It's not saying they agreed or disagreed with any of it. I won't know that until I see what the report says.

MR. FURLOTTE: My Lord, at this time I'd like to move to have Dr. Shields declared as an expert witness in population genetics.

THE COURT: Have you any questions, Mr. Walsh?

MR. WALSH: No, My Lord, I have no objections.

THE COURT: Well, I will declare the witness, then, to be an expert in the field of population genetics.

MR. FURLOTTE: And also in molecular genetics, My Lord.

THE COURT: Any questions about that, Mr. Walsh?

MR. WALSH: No, My Lord, I have no objection.

MR. FURLOTTE: And as an expert witness in statistics.

MR. WALSH: I have an objection to that, My Lord, yes. Dr. Shields has pointed out that - my understanding of his testimony is that the statistics essentially form part of the umbrella of population genetics and I don't see why there should be a separate designation for that. It all comes under the umbrella of population genetics.

THE COURT: Aren't we perhaps becoming a little too refined, Mr. Furlotte? It's not going to confine the scope of his evidence if we omit statistics, surely. Whether he's an expert in statistics or not is important only insofar as his expertise in that substrata, sub-field, or whatever you want to call it, that extends to population genetics. If he's an expert in population genetics we're going to hear his evidence on statistics anyway, right?

MR. FURLOTTE: Whatever the Court desires.

THE COURT: We'll qualify the witness as an expert in population genetics and molecular genetics.

MR. FURLOTTE: My Lord, Dr. Shields has never had the opportunity to view the original autorads and I would request at this time that Mr. Bowen provide the originals for the availability of Dr. Shields.

MR. WALSH: We've always told Mr. Furlotte, and the very reason that Dr. Bowen is down here is that if he wishes to see the autorads it doesn't require an order of the Court. Dr. Bowen is here with the originals and he's prepared to in the presence of the doctors keep continuity of the originals, he's prepared to have the doctor review them. I hope

Mr. Furlotte is not now going to ask the doctor to review them on the Court's time.

THE COURT: What did you have in mind here, Mr. Furlotte? They are available in court. I think the Crown has made clear that they are available at all times, but what does -

MR. FURLOTTE: Well, My Lord, the Crown used the originals. Although they didn't put the originals into evidence they still used the originals for comparison purposes.

THE COURT: Well, they're available if the witness wants to refer to those or if he wants to look at them, but I mean, you're not going to spend hours with the witness examining the autorads now, are you?

MR. FURLOTTE: We're awful concerned about time, My Lord. No, I have no intention of spending hours but -

THE COURT: Yes, but it could be done outside the Court's time. As the expression, the Court's time, as Mr. Walsh has used, is fairly important. Well, anyway, what do you want?

MR. FURLOTTE: My Lord, I'd like Dr. Shields to be able to compare the original autorads as to the quality of the autorads for each probe, and it's a matter of just putting them on the light box and saying that either yes, they are good quality, poor quality, or -

THE COURT: Well, Mr. Walsh, you have no objection, presumably, to that?

MR. WALSH: As I indicated, My Lord, I have no objection to Dr. Shields looking at the original. I think the originals would be something he would want to see. I just didn't think that - I thought perhaps we could do this outside the actual court room time to

allow Dr. Shields in privacy to go through with these things in a much easier fashion than I would think his original look through it at this time. It just seems to me a waste of time but if that's the way he wants to proceed, then I'm -

THE COURT: Yes, but Mr. Furlotte now has in mind the actual evidence or the actual testimony dealing with the autorads, is that what you have in mind?

MR. FURLOTTE: Yes, My Lord.

THE COURT: All right. Well, where are they?

MR. WALSH: Dr. Bowen has them, My Lord.

MR. FURLOTTE: Maybe if I had Dr. Bowen's - the Crown Prosecutor could stand here and give Dr. Shields the autorads which I will refer to, it's easier for him to find them than myself.

MR. WALSH: Could I make a suggestion, My Lord? Could perhaps we have a recess and allow Dr. Shields and Dr. Bowen to do it in a confined setting, so to speak, where there's not a whole lot of people watching them and the pauses and the -

THE COURT: Well, what you contemplate and what I foresee is that Dr. Shields is going to want to look at these things privately here for a few minutes at least before he testifies as to their nature and so on, whatever questions he's asked. Perhaps we should have a - Dr. Shields, may I ask you this, what do you want to do with these autorads before you're asked questions about them? Do you want to see them or examine them, or perhaps if it isn't necessary we can go right along.

A. I would just want to confirm. I've seen copies of the autorads and usually they are satisfactory, and

all I would want is just a few minutes to confirm that the originals tell me the same story as the copies did, and it would only take a couple of minutes if you'd want to do a recess, Your Honour.

THE COURT: We needn't bother with a recess, let's do it right here and we'll take the time.

MR. FURLOTTE: My Lord, I'm not worried if Dr. Shields confirms the position of the Crown. As I stated earlier, I'm just seeking the truth in these matters and if Dr. Shields' opinion supports the Crown, then so be it.

(DR. SHIELDS VIEWING AUTORADS.)

MR. FURLOTTE: Dr. Shields, you've compared the originals with the copies that you observed in the past?

A. Yes.

Q. And how would they compare?

A. The same sets of information are available in both the copies and the originals. The copies were well made and therefore I could read them about the same as this, I don't see anything different between the originals and the copies. The originals are always a bit cleaner and a bit easier to interpret, but not in this case exceedingly so.

Q. Now, Doctor, I understand you testified in the Bourguignon case which the R.C.M.P. were involved?

A. Yes, I did.

Q. And they had autorads in that case that you've observed?

A. Yes, they did.

Q. And how would you compare the quality of these test results with the test results in the Bourguignon case?

A. What do you mean by quality?

Q. The quality of the autorads.

A. You'd still have to tell me what you mean by quality for me to answer that.

Q. To be able to read them, I suppose, without difficulty.

A. I think what you're getting at is that the autorads in the Bourguignon case were a little bit cleaner than the autorads in this case. The autorads in the Bourguignon case were, I think I testified, the best I've seen, literally. These are probably closer to the average that you see in forensic cases where there are some minor glitches and problems, but they don't have any serious impact on interpretation. Dirtier, meaning that there are extra bands that are not - they're obviously not the bands that you're most interested in, that they come from either degradation or partial digestion in some cases, or in some cases you don't wash the probe off completely, and that sort of thing happens in a standard way every now and then so that you end up with smokier autorads or lanes that are a little bit more smoky.

Q. O.K., Doctor, what I would like you to do in this case is I would like you to compare probe D16S85, the original autorad, with the autorads of the other probes to see if there's any significant difference in the intensity of the bands in Mr. Legere's lane and in the evidence lanes. Do you think that would be possible on this light box?

A. Sure, although it's really locus D16, it's not probe D16. This is MS1, which is locus D1S7, and there's 3 Prime HVR which is D16.

Q. Now, Doctor, I believe in direct examination the Crown's expert witness found that the autorad for locus D16S85 the bands were too faint to make a proper interpretation for forensic purposes and they ruled that it was inconclusive for that reason. Now what I would ask you to do would be to compare the other locuses with D16S85 to see if they are of greater intensity, and maybe you could do one at a time and state basically what your opinion is, and did I ask you to do this with the copies? Have you done this experiment before with the copies?

A. I have not actually done it. We talked about it but I haven't done it.

Q. O.K., would you do it with the originals, then, please?

A. Well, if I remember correctly, lane 3 is Mr. Legere's lane.

Q. Yes.

A. If I remember correctly, evidence lanes begin here, run out here, and include this one, for example.

Q. That's lane 19, I believe.

A. Lane 19. You can see faint bands in both Legere's and Lane 19 that could be a visual match if you look at them. I'm now talking about 3 Prime HVR which is the D16 locus, and you can see a faint band below it which could be a match to the faint band in Legere's lane as well, and in my lab I might have actually interpreted that as a match. They are certainly light, and I wouldn't argue with someone who said that they would choose to call this inconclusive on

the basis of the fact that they're light. If you look at MS1, D1S7, you can see that it's not quite as light in those two lanes.

Q. O.K.

A. It's still lighter than it is in some of the other lanes but that's not unusual if you're talking about in particular the evidence lanes to have light lanes because there's not as much DNA loaded in those lanes. You want me to look at the other ones, you said?

Q. Yes, so put D1S7 -

A. YNH24 which is D2S44, there the evidence lane looks about as light to me as the D16 does. That's lane 19 compared to this, but I would still call it a match if we're talking about 19 versus here, but certainly it's as light.

Q. It's as light as D16?

A. It's as light but it's better formed. D16 is a little bit misformed as well as being light. The bands aren't crisp bands, they're a little curved and they're a little different, O.K., so that's another potential reason for calling that inconclusive. H30, they're darker. There's also a lot more degradation showing up in some of the lanes.

MR. WALSH: What autorad is that?

A. It's the PH30.

MR. WALSH: The other number for that?

A. D4S139, I believe.

THE COURT: I'm sorry, what was the comment on that last one?

A. They're darker and easier to score therefore, and there's just a little bit more - there's more degradation in these lanes. You can see this black smear that falls out and you can see some extra, I

would call them non-specific bands, that show up in some of the lanes. The one which is D17S79, they're light again; in fact, almost as light as the D16, if you look at just 19 and Legere, 3 and 19, but I would still visually call those a match, and then there's the new locus, D10. I'm not familiar with the probe number for the new D10 locus, is it PY34?

Q. TBQ7, I think.

A. TB, and I seem to have misplaced it. There it is, TB97. Again the evidence lane is light but the bands are well formed.

MR. WALSH: Is this for D10S28?

A. Yes, it is. There are bands there, they're reasonably clear bands and they're well formed bands relative to what happened with the D16. And that's it.

Q. That's it, yes. So I believe, Doctor, if I remember correctly, it was the locus D2S44 and D17 that you thought were of about equal intensity with the D16?

A. I believe that's what I said.

Q. Doctor, next I'd like to compare some slides on the projector. This was, I believe, one of the ones that you said was of the same intensity, Doctor, D17

A. No, D2S44. You've got to go back up, it wasn't this one.

Q. But there was - didn't you mention there was two of them?

A. Yes, I'm reasonably certain I said two, but from looking as you went past, I think that one, for example, is lighter, but go back further. That one

is one, I think. There's certainly the D2S44, you can see how light that is, and it's labelled 135, and 56A and 68A or 69A, so it's lane 3 and lane 19, you can see how light those are on that. There's a band here and a band here that are matching this band and this band. These two aren't that light but these two are very, very light, O.K.?

Q. Maybe if we'll find D16 -

A. You can go to D1S7, you can see that this is also light in the evidence lane, 135. If you find D16 you can show it. There.

Q. Now, this was the one that the Crown's witness says they were too light?

A. Mm-hmm.

Q. And we were comparing this one with the D2S44?

A. D2S44, and in fact, once you take the picture the bottom band sort of disappears. I'm not even sure if this is it or if it's down further, but it's probably right here where this bottom band is supposed to be, but with the photograph they disappear. On the autorads you can still see them.

Q. Now, do you recall which other locus it was that you said was about the same intensity of D16?

A. Go back up again, I don't recall. Well, here, this version of D17S79, that may have been what it was. They may have been two exposures. This is an early exposure and you can see that it is light, very light, O.K., and then the next one that you got to is a re-exposure which is why when we went past it I said no, it wasn't that one because that's certainly not light, O.K.? That is not as light, so with the second exposure on D17S79 it's not nearly

as light.

Q. Now, Doctor, in D17S79 what appears in lane 19, maybe you'd have to come out here, I don't know.

A. No, I can see.

Q. The top band in lane 19 and the top band in lane 17 -

A. Those two?

Q. Yes.

A. Right, what about them?

Q. If there's a distinguishable difference between those two bands, according to the standards of the R.C.M.P., if there's a distinguishable difference with those two bands, would you be able to match the bands in lane 2 - I'm sorry, lane 3, with lane 19? In other words, Doctor, if these two bands are not a match because there's a distinguishable difference, could you say that there was a distinguishable difference between this so-called band and this one here?

A. I don't see a distinguishable difference between these two.

Q. In your lab you would call that a match?

A. Sure. I believe if this is - this is a female fraction from this individual, I believe, and this is the known sample from that same individual; is that correct?

Q. Supposedly, yes.

A. Yes, and there is the top band from Mr. Legere who was matched to this top band, and you can see that they're the same size here as well as here. I would call those a match, but matching this lane to this lane it's not a match, because the lower band is below this and matches this. There is this little curious thing here.

Q. Do you know what that would be, that middle thing?

A. Could be a lot of different things. It could be a bit of a match to this. This might be a mixed sample. It is a male fraction from the same individual and not all the time are male and female fractions perfectly separated, so it could be a mixed sample. It could also be an artifact of different kinds.

Q. Could that bottom one be an artifact?

A. Could be, sure. Could be.

Q. I believe you mentioned in locus D16 that - if I could go back to it - I believe you had mentioned when you were reading the original autorads that the bottom one, although it seemed to line up, aside from being faint that it was kind of blown up or -

A. It's what we would call a not well formed band.

Q. Not well formed, so if I go back to D17 would that bottom one be a well formed band?

A. Well, now, see, you have to be careful about that. If you go back to the previous - this is an over-exposed autorad, and it's over-exposed on purpose. It's over-exposed in a way that will allow for better measurement, if you will, of the bands. If you go back to the previous one where it's not over-exposed, those bands are still there and now they are not misformed, if you will, but as it stands here from this photo, that is misformed, it's sort of a blob rather than a band, but that's what happens when you over-expose. It's not unexpected.

Q. Can you tell, Doctor, whether this band here in lane 17 is a bit higher or lower than the band in lane 19? Any distinguishable difference at all?

A. I would - distinguishable difference is a different question, I'm not sure exactly what you mean by distinguishable difference. I look at those two bands and I would call those a putative match. I think they've migrated about the same distance on that particular autorad and I would want to measure them and see.

Q. So when you say about the same distance -

A. In any lane on any gel you're going to have what we call mobility differences between lanes. There's going to be slight differences in the distance that bands migrate, even when they are identical bands, they're the same DNA molecules. There are a variety of reasons that that can happen. It can simply be a concentration of salts or actual concentration of the gel, a variety of different things can cause lanes to move at slightly different rates.

Q. What if according to the R.C.M.P. standards that slight mobility shift would be enough to call it inconclusive? How would you change your standards in reading or in interpreting the rest of the so-called matches?

A. I'm not sure I - could you repeat the question, what if the R.C.M.P.'s standards what?

Q. If my memory serves me correct when Dr. Bowen was here when Dr. Bowen testified, I asked him if these two were a match and he said no, he could see a distinguishable difference. Like, this one was, I believe, a bit lower than this one here, so he would not call that a match. According to his standards he would not call that a match.

A. It's puzzling to me. If I understand the gels

correctly this is the same individual as this, and here this band, although it's more exposed, over-exposed, so that the band gets broader, appears to be a little bit higher than this between these two. When you have one that's a little bit higher and a little bit lower and they're visually not obviously different, I would call those a match of the band. Not a match of the genotype, but a match of the band, that's what I would call it, and if - see, I'm not sure I - well, I don't understand this notion of simple visual - visually deciding that a very, very small mobility difference on a gel is enough of a difference to call it not a match. I can see doing that with genotypes where you've got one band that's about the same and one band that's very different, I could see declaring those not a match, but I personally cannot see declaring those two not a match simply on the basis of looking at them. I would have called them a match. And then I would have looked at the sizing data to see whether my eyes were telling a reasonable story or not.

MR. FURLOTTE: O.K., My Lord, maybe before we get into the other aspect of population genetics it might be a proper time for a short break?

THE COURT: O.K. All right, you're still on the stand, Doctor, and you shouldn't discuss the case with anyone until all your evidence is complete, as I'm sure you understand.

MR. WALSH: My Lord, if I may, the exhibit that was filed, the -

THE COURT: The copy of the paper?

MR. WALSH: Yes, perhaps if we could make arrangements to

have it photocopied at break-time if you would allow us to have it done?

THE COURT: Oh, yes, surely. Take the original there, or copy, whichever you need. Have the originals of the autorads gone back to Dr. Bowen?

MR. RYAN: Yes, they have, My Lord.

(SHORT RECESS - RESUMED AT 10:55 a.m.)

(ACCUSED IN DOCK.)

DR. SHIELDS RESUMES STAND:

MR. FURLOTTE: O.K., Dr. Shields, now we'll move into the area of population genetics, and maybe you could for the benefit of the Court and us, if you could give a brief description as to what population genetics is and how it applies to the forensic field?

A. Probably what I would like to do is sort of define probability and go from there and talk about why data bases are necessary and why we use data bases to come up with probabilities of what have been called coincidental match and a variety of other things. A probability is a number that gives some idea of the weight, the likelihood of an event happening.

Some of the standard ways we have of talking about probabilities to indicate what they are and how they happen is we'll talk about coloured balls in an urn, for example. We have a jar that has coloured balls in it, and if I were to just take an urn and say that there are black and white balls in it, can you tell me what the probability of drawing a black ball is. If I were to hand it to

a set of people they would look me in the eye and I would hope say they don't know unless they were prescient, unless they could somehow see into the vase. In order to develop a probability you have to know something about the number of events, total, and the number of events of the specific instance that you're interested in. As the example that I was using, if I were to tell someone that there were five black balls and five white balls in an urn and I asked them what's the probability of drawing a black ball, knowing that there are ten different balls and five of them are black, they would say that the probability is five out of ten or one-half, but they do that simply because they know how many balls are in the urn, so they have a count, and that would be the data base for developing the probabilities of pulling a black or a white ball.

You can use the same analogy to illustrate how one goes about using the multiplication rule if you're talking about statistically independent events. You can assume that a black ball - that drawing a black ball is independent of drawing a white ball, as long as when you draw it you put it back in, it's called sampling with replacement, and then the probability of drawing two black balls in a row by that product rule would be one-quarter, one-half times one-half. The reason that happens is simply that half the time the first ball you're going to draw is going to be white, so that half the time it's going to be a failure. Half the time, the other half the time that you draw a ball, it will be black and that will be O.K., for getting two black balls in a row. It's on the first draw half

the time you'll have the black. The second time when you put that black ball back in, half the time you're going to end up with a white, which is again a failure, so three-quarters of the time, half of that half, plus the original half that you failed you will end up with something other than two blacks in a row and you end up one-quarter of the time with one black, so if they are statistically independent events you can multiply probabilities together to come up with what we call the joint probability.

Another analogy that we use, in fact that same analogy can illustrate why the probability for a single genotype at a single locus is 2PQ rather than simply PQ where P and Q are the frequencies of the two alleles. The probability of drawing a black ball and a white ball is the probability of drawing a black first, which is one-half, and the probability of drawing a white second, which is also one-half, so it's one-quarter of the time you'll get that combination, but also one-quarter of the time you'll get a white ball first and a black ball second, and it doesn't matter which way you do it, so you add the two quarters together which is the same as saying PQ times 2, so that one-half the time you end up with a black and a white ball. That's what we call a binomial expansion and how you develop probabilities for single loci. It's exactly the same sort of phenomenon.

Another analogy that helps some people think about it is playing cards. If I ask people what's the probability of drawing an ace from a deck of cards, if they play cards they'll say to themselves,

well, there are four aces and there are 52 cards. If they play cards a lot and they gamble big money on it they'll actually know that that comes out to be one in 13, four divided by 52, so they'll know that the probability of drawing any ace, it doesn't matter what kind, is one in 13, but then I can tell them that I actually cheated a little bit and I'm actually talking about a pinochle deck, and for those who play pinochle, they know that a pinochle deck is different than a regular deck, it includes aces through nines double numbers so that there is actually eight aces and 48 cards, so the probability of drawing an ace from a pinochle deck is not one in 13 but one in six. Those are frequency differences between two populations or two sub-populations. The pinochle deck is the equivalent of a sub-population in all kinds of decks of cards and the regular deck of cards is considered to be a different kind of sub-population with different gene frequencies, different frequencies of the events that they have which are cards, so the question becomes in forensic DNA typing and in lots of other genetic kinds of analyses, how do we go about determining what is the most accurate and reliable probability that we can develop to put a weight on something that's declared to be a tentative match or a non-exclusion. You can use lots of different terms for it.

Well, the way you've got to do that is to sample. If I were to throw ten thousand cards out in the middle of the room and ask somebody to please find out for me what's the frequency of aces through deuces in this particular mega-deck of cards out

there. There are a number of things that they would have to do to do that legitimately, to do that technically correctly. For one, they would have to shuffle the cards, which is what we call random sampling. If they didn't shuffle the cards, decks of cards when they come from the manufacturer are in suits, so that for example, the first ten cards you'd pick if you had no shuffled decks would be all one suit, it would not be a random sample of all four suits, it would be biased to the one suit that exists there, but if you shuffle all of the cards, if you get a random sample, then your expectation is higher that you're going to at least draw some of the different individuals that represent each population.

What determines whether you have a good sample or not are two different things, how random that sample is or how unbiased that sample is if you can't have a random sample, and it might do good to just define random and show why it's not likely to be a truly random sample. A real random sample means that every individual, if we're talking about VNTR alleles as we would be with DNA forensic typing -- if every individual in the population in question had an equal probability of being sampled, everybody in Canada in the Caucasian race had an equal probability of being sampled, that is not in any practical sense likely so the important thing is that it be a representative sample, which means that in the data base are a sufficient number of individuals from all of the genetically different sub-groups that go into making up a Canadian

population and that there are enough of them to represent those individuals at their true frequencies. Well, in order to do that, I've read testimony that suggests that small samples are enough. Well, they are if you're talking about things that vary in a minor way, where there are two or three alleles and that they're all in high frequencies, but in the case of these VNTR loci there are at least 28 bins and if you think about sampling to represent the true frequencies in 28 different phenotypes, which are these bins, then you need much bigger samples than if you were doing it for two bins, heads and tails. The notion here is that simply by chance, even if you have a well shuffled deck, you're going to pick occasionally three aces out of the four and occasionally you're going to miss all of the deuces in small samples, and the more different instances there are, the more alleles there are, the bigger the sample has to be to have a robust estimate of the actual frequencies of the alleles with those phenotypes, and you can actually do some analyses to determine what are robust sample sizes, depending upon the allele frequencies and how many alleles you're trying to estimate the frequencies for. If you do that, if instead of trying to estimate the frequency of the cards, the ten thousand cards that I threw out there, with just fifty which would guarantee that you couldn't get two of the cards in a regular deck of cards, you do it with five hundred, then you're likely to be getting closer to an appropriate sample, and there are statistical tools in population

genetics that allow you to make up for the size of your sample and those are called confidence limits, which I think have been talked about prior to today.

If you have a confidence interval around your frequency estimate it states what the highest and the lowest frequency is likely to be for the ultimate sample if you had a huge sample size, and in fact, as your sample size gets bigger the confidence limits become smaller around your estimate, and that's a good property. What it's saying is that the bigger the sample the better your estimate is, but representativeness of the sample is not the only thing that goes into determining what the correct probabilities are for individuals matching. The other thing that's of critical importance has to do with what we call substructure or sub-population structure or population structure in general, and that is the degree - substructure or population structure can arise for a variety of reasons. The primary reason is non-random mating. It's where individuals tend not to mate randomly, and random there means exactly what I meant before. If we were going to consider the Canadian Caucasian population a random mating population that would be an assumption that every male in the population has an equal probability of mating with any female in the population from coast to coast and Arctic to U. S. border.

Everybody recognizes that that assumption is not likely to - in fact, does not hold, that individuals tend to mate within ethnic groups, they tend to mate in geographical locations, individuals

from a particular part of a country tend to mate more frequently with individuals from that part of the country than they mate with individuals from other parts of the country, and so forth and so on, so that substructure becomes a potential problem in the sense that substructure structures gene frequencies, it changes gene frequencies between different sub-populations. The simplest sub-population to think about and where it all stems from is what we call a family. Since individuals inherit VNTR alleles from their parents, one from Mom and one from Dad, and they inherited it from their parents, siblings have a higher probability of being identical at a set of VNTR alleles than most individuals from the general population.

Thinking about sub-populations is nothing more than saying that there may be random mating groups that are bigger than families, it may include multiple families in that definition, but it may not include the entire mega-population of interest, the Caucasian race in Canada or the native American Indians of Canada and the U. S. or both or separately. When that happens, when non-random mating or natural selection cause frequency differences at different genes across a geno, then willy-nilly it may also cause frequency differences in the VNTR alleles, even if the VNTR alleles are not being selected for directly. They are on chromosomes and they may be at least reasonably closely linked to loci that are being selected and they are on chromosomes that do get transmitted via the process of reproduction, so

that if reproduction is not random, if there's not complete shuffling of the deck in every generation, then some individuals will have higher probabilities of sharing alleles with other individuals than they do with another set of individuals in a different sub-population. In essence, that problem of sub-populations is the equivalent of asking the question, what's the probability of drawing an ace, and the probability is one in 13 in one kind of sub-population, regular decks of cards, and it's a different probability, one in six, in a different kind of decks of cards, in pinochle decks, and if we take pinochle decks and regular decks and mixed them we end up with a third probability that's half of the two, 1/13th and 1/6th, which ends up being about one in 8 1/2, is the probability we get from pooling those sub-groups. Now, what happens when you do that is that you will misestimate the probabilities that are associated with a particular genotype. You will misestimate them by some level or another and the question becomes whether that level or another is sufficient to say that it's inaccurate or unreliable.

Q. O.K., now, Doctor, are you aware of any studies that have been done within the different races in Canada or the United States?

A. Yes, I am.

Q. Are you prepared to discuss your findings?

A. Sure. From having briefly read earlier testimony I think some of this will not be coming as a surprise. I just want to start with an aside, Your Honour, about what statistically significant means

in its many different senses. When scientists are doing comparisons, whether they're doing comparisons of single bins, which is what we have here, bin numbers, frequencies within a single bin, and where the frequencies across a whole distribution of bins, what they try and do is set up what we call statistical analyses that allow us to not just use our eyes but to also come up with an objective way of determining whether the differences that are observed, there are always going to be differences, they're never going to be exactly the same - whether those differences that we observe are meaningful differences or not, and meaningful can have many meanings, and I'll talk about some of them as we go along, but the way that a statistical test works is it looks at the amount of variation. You can see that there's variation between these two bars. What this particular graph illustrates is a comparison between the FBI's and the R.C.M.P.'s Caucasian data bases for the probe or locus D2S44 for Caucasians, and the black bar is the frequency in a particular bin of a particular set of alleles that fall within that bin for Caucasians in the U. S. and Caucasians in Canada from the R.C.M.P.'s data base, which is the white bars.

Just as an aside, the FBI's data base consists of about 210 to 220 FBI agents training from all over the U.S., and then separate samples that were added from Texas and California ard Florida from blood banks to produce a data base of about the same size as the R.C.M.P.'s data base, it's called the FBI Composite or C3 data base, so instead of

looking at this in terms of single pairs, is this different from this or is this different from this or is this different from this or this different from this, there are statistics, and one that I've used is one of them that allow you to look at the entire distribution, and they ask the question, is this distribution, the black bars, different from this distribution, the white bars, in a statistically significant way, and in this particular case there are statistically significant differences when you consider the whole distribution of alleles at the D2S44 locus between the FBI and the R.C.M.P. Caucasian data bases. The reason we say that is because of this number here. This is the probability of being wrong. If you choose to decide, if you end up deciding that those data bases are different, the probability of being wrong is less than one in 100. The probability of being wrong when you conclude that they're different, turned around, even though it's not absolutely correct to turn it around, in essen e what it's saying is that you have about a 99% chance of being correct when you conclude they're different. What it says exactly is that the probability of being wrong, including that they are different, is less than one in 100, so in this particular case for this particular locus there are significant allele frequency differences between Canadians and Americans or U. S. citizens, the other North Americans, in the D2S44 locus.

THE COURT: Mr. Furlotte, these aren't in evidence, are they? Are you putting them in evidence?

MR. FURLOTTE: I will be requesting to put them in evidence.

THE COURT: Yes. Shouldn't they be put in as you go along so that -

MR. FURLOTTE: O.K.

THE COURT: The written transcript will be at least meaningful.

MR. FURLOTTE: Would you - for the court purpose we could either put these into evidence or have them Xeroxed and put the photocopies into evidence.

THE COURT: Do they Xerox well?

A. Perfectly well.

MR. WALSH: I have no objection to the Xerox.

MR. FURLOTTE: Maybe in the break we could have them Xeroxed.

THE COURT: Yes, but can they be marked in the corner with a marking pencil of some kind? The first one would be VD-118.

A. I'm now referring to VD-119 which is for a second probe, the D4S139 locus, and in this particular case you can see that even though there are differences the statistics - statistical analyses tell us that it's not statistically significant. The probability of being wrong in concluding they were different would be one in ten, and for most scientists the area of around .05, five chances out of 100 of being wrong is what we call statistically significant. In addition, some people will say that slightly more than that is enough to be called marginally significant and some people will say, oh, we just use the .05, but at .116 everybody would say that there is no statistical difference in the D4S139 locus between Caucasians in Canada and Caucasians in the U.S. The lower half of that is a third probe or locus, the D1S7 locus, and again there is no statistically significant

difference even though there are differences in allele frequencies between the two, so the first three that I've looked at, one is statistically significant in terms of frequency differences between Caucasians in the U. S. and Canada and two are not, and in VD-120, the last two probes that they have in common that are still being used by both the R.C.M.P. and the FBI, the D17S79 locus is highly significantly different. There's only one chance in ten thousand that you'd be wrong - there's less than one chance in ten thousand that you'd be wrong in concluding that those two distributions are different, and you can see how different they are. There's a very, very big difference in allele frequencies at the most common bin. And finally at the new locus, probe D10S28, there are significant differences between the FBI Composite and R.C.M.P. Composite, with five chances out of a thousand of being wrong if you conclude that they are different. so we would say that those are statistically significant differences. Prior to recently when those data were made available to me as part of this particular case, the R.C.M.P.'s data, I had always testified that I was a bit nervous about the FBI and the R.C.M.P. using straightforward Hardy-Weinberg equilibrium binomial expansions and the product rule to develop their probabilities because substructure could be a problem, and I and others who also have testified in the same vein suggested that we didn't think it was necessarily scientifically correct to make the assumption that there was no variation between sub-populations within races, especially given the fact that the R.C.M.P. and the

FBI and the other forensic groups had already decided that there were at least sufficient allelic differences between the races to develop different data bases for different races in order to ensure that the probabilities would be more accurate than if you just had a giant human data base without regard to racial differences. During the early part, six or seven months ago, some of the data that I will also begin expressing in a few seconds had not yet been analyzed in a way that allowed one to look and see whether there was within race variation in VNTR alleles. That was my first experience in Caucasians illustrating that there might be variation between Caucasian sub-populations, and I personally attribute the difference between Canada and the U. S. to the very obvious difference in the demography of the two countries and the ancestry that's associated with both countries in that about 70%, based on an R.C.M.P. papers, of Canadian citizens are either of French or British extraction, ancestry, and in contrast to the United States I don't think that there's any group, including the British, that have as much as 35% of our Caucasian population, so in my own opinion, I think if those differences are real, and the statistics say that they are, that it probably stems from the fact that Canada is a more homogeneous group than is the United States, and that may be part of the explanation for why there are differences between Caucasians in the U. S. and Caucasians in Canada.

Again very recently some scientists in Great

Britain, a statistician and a population geneticist have come up with what they consider to be a reasonable approach to correct for these particular potential problems of substructure, and what they do is they say that we can look at other genetic systems, even though we don't have enough data yet to completely analyze the VNTR systems we can look at other genetic systems, and we can say what's the greatest amount of substructure that we see in these genetic systems. We can say what's the greatest degree of sub-population structure that we see, and using that as a conservative estimate one can generate a correction factor that changes the frequencies in a way that takes into account, to their way of thinking, the possibilities of substructure in these kinds of forensic DNA typing. The gentlemen's names are Nichols and Balding, and they produced a formula that allows one to calculate by their methodology probabilities of coincidental match. I'm always bothered by the way that those probabilities are presented. To my way of thinking the way they should be presented, the way they should be thought of, is it's the probability that anybody else could have contributed the evidence, that somebody other than the suspect or somebody other than the victim if it's that kind of case, could have contributed the evidence sample rather than saying that it's the probability of - as the FBI still does, or at least did in the last case that I was involved in, of matching the known sample from a victim or a suspect, but in any case that probability that you end up with to weight the match, to come up with some estimate of what's the

likelihood of this match being the result of somebody other than the suspect or the victim, and what I can do then is illustrate what happens to the probabilities when you use different data bases or when you use the correction factor suggested by Nichols and Balding. It will be VD-121, and what I've done is compared the match probabilities that would result using the R.C.M.P.'s data base in this particular case, using the FBI's data base, and using Nichols and Balding's method with the R.C.M.P. frequencies as the base, and what you can see, Your Honour, is that the numbers vary. They vary in what I consider to be a reasonably predictable fashion for all of the loci that are used. The R.C.M.P. produces a set of numbers for all of the loci that are used, the FBI also produces a set of numbers which usually are larger here which means smaller probability, but not always, and Nichols and Balding invariably produce larger numbers. The why is because there's a correction factor that goes into those numbers to make up for the possibility that there's substructure. When you do that this is the final probabilities for two-locus, 4-locus and 5-locus matches. One in 7,400 with rounding for the R.C.M.P., one in 9,000 for the FBI. and one in 4,000 for Nichols and Balding. For the 4-locus match it's one in 5.2 million, and one in 9.6 million, although I read one in 9.9, that must be rounding differences as well, and one in 226,000, Nichols and Balding. For the five locuses, one in 310 million using the R.C.M.P., one in 666 million using the FBI, and one in 5.9 million using Nichols

and Balding. I would just note, Your Honour, that these are extraordinarily, to my way of thinking, different probabilities.

That there is additional evidence for VNTR variation among populations within races can be illustrated by looking at some of the other analyses that have been done, and I'm forced here to use the FBI C3 data base because their raw data came with the location of the samples, and the raw data that I have from the R.C.M.P. did not, but for locus D17S79 what you're looking at is there should be four bars in each bin, the individuals from the California data base, from the FBI's agent data base which was a countrywide U.S. data base, individuals from Florida and individuals from Texas, in that order across, and the little X is the average of those four together and what's used in case work from the C3 data base, and all I would note here is that, one, you can see there are differences from the average depending upon where you are from in the United States, and it can vary by what looks to be reasonable amounts and are statistically significant amounts for this particular locus. Nine chances out of a thousand that you'd be wrong in concluding that the distributions are different, so the reverse of that in concluding that you're right, that you're right in concluding that they're different, so that there are statistically significant differences in allele frequencies including Caucasians from California, Texas, Florida and the FBI's general U. S. population. That would be VD-122.

This is VD-123 and it illustrates the same pattern now. You can see there are differences, this here is the little square that says where they are, but in this case they are not statistically significant, so I would conclude that there are no differences between the Texans and the Floridians and so forth and so on at the D1S7 locus, just as there were no differences between the R.C.M.P. and the FBI data base at that locus. The same is true of the locus D4S139, which I have illustrated here, and this one will be -

THE COURT: VD-124.

A. Yes, 124, and again here you can see visually that there really aren't that much in the way of differences, and in this particular locus notice that California is not here, it's because the California crime labs don't use this locus so that they were not able to contribute a sample to the composite data base, but you'd have a 97% chance of being incorrect if you chose to decide that those were different, that's what that means, so we would conclude that those were the same.

The locus D2S44 which will be VD-125, there are again differences, and California's back in and in this particular case the differences are what we call marginally significant. It's up to the individual scientist who's looking at this sort of thing to decide whether seven chances out of 100 of being wrong in concluding they're different is too much of a chance, and the final locus, D14S13 -

CLERK: VD-126.

A. Again you can visualize the differences, and in this case it says that statistically the difference is marginally significant. A third set of data can be gotten from a paper produced by Dr. Ron Acton of the University of Alabama at Birmingham with a set of co-authors that included Dr. Budowle who's the chief scientist for the FBI's research division, DNA research division, and in fact a lot of the data that you'll see are the FBI's data, but the difference is that the Alabama population is separate and this is all for locus D2S44, and when comparing black and white races in Alabama they report that there are statistically significant differences with some of the frequencies.

THE COURT: That will be VD-127.

A. 128 is a comparison of the whites in Alabama versus the whites in the U.S.A., which is that FBI population of 220 agents, and there are statistically significant differences in those as well. Here you can see some of those, almost 13% there, so forth and so on.

THE COURT: VD-128, the last one.

A. Within races Acton et al compared Alabama blacks to South Carolina blacks and found statistically significant differences. The South Carolina blacks here are the South Carolina population of blacks in the FBI's black data base, the Alabama blacks are Dr. Acton's example.

THE COURT: VD-129.

A. 130 is a similar comparison of blacks in Alabama, the same blacks in Alabama, with blacks in Texas, and again there's a significant difference, and

between the blacks in Alabama and Florida will be the next number, VD-131, and finally, Dr. Acton is reported in a published abstract, although there are no figures with it, that there are statistically significant differences in the overall frequencies, the entire frequencies, between blacks from Northern Alabama and blacks from Southern Alabama.

VD-132 are graphs that I prepared based on raw data provided via the Yee case from Dr. Kidd's study, which I have a copy of, of three Indian groups, two in Brazil and one in the Yucatan in Mexico. Looking at the allele frequencies - this locus is D14S13, again one of the forensic loci used by some for those three different tribes. This is the Mayan, the Surui, and the Karitiana, and I did an analysis on the raw data and also present them in figures and all of them illustrate that there are statistically significant differences between these populations of Native Americans, even though these two come from tribes that are about 600 kilometres apart in South America. That's at that particular locus. This is at a locus that's not yet used in forensics but it is a VNTR locus, D14S1, and it illustrates one of the potential problems with ignoring substructure. It also illustrates one of the statements that I've made that was criticized in earlier testimony at this particular matter, that you can expect that if you take an individual out of his sub-population and test him in another sub-population that that individual will be biased against by doing that form of analysis. There might have been a

misunderstanding of what I meant by sub-populations, but if we're talking about true sub-populations there is going to be a loss of alleles, O.K., there are a number of different things that happen with sub-populations. You don't expect each sub-population to carry as many alleles as the entire what we call meta-population does. When that happens, when there are fewer alleles within a sub-population, the frequencies of the common alleles automatically go up. Because they automatically go up as they do here in this population the probability of matching at that particular locus with that particular allele is very high for an individual from this population much higher for an individual in this population than if we were to test it in either of the other two populations where there are more alleles, and that's the kind of bias that I was talking about in an affidavit that I provided in a different trial.

Q. Is that your explanation, Doctor, as to the criticisms by Dr. Carmody and Dr. Kidd of your -

A. Yes, they criticized my statement - I don't think I said invariably, but I think I said usually, if you take an individual and test them in a data base other than their own sub-population the probability that results will be biased against that individual and the reason why is because if you're talking about true sub-populations that are sufficiently isolated from one another there are going to be higher frequencies of all of the common alleles in a sub-population than there would be in the general population using a mixed population or in a different sub-population. They'll have high frequencies at

different alleles in the two sub-populations.

This one is VD-134, it is a forensic locus comparing those three populations, and again you can see that there's a much higher frequency of this allele in the Karitiana population, and the Mayan and the Surui look a little bit similar although there are differences here, too. There's an allele here that we call a private allele, it only occurs in the Mayan, it doesn't occur in either of the South American populations. Now, if we were to pool these three we would end up with one-third of the probability that it is here, and if we were then to do an analysis in Mexico and say did this Mayan - what's the probability of a coincidental match for this Mayan, we would be using a probability that's one-third of the probability it should be, because in the Mayan population this has a frequency of three times what it does in the general population.

The last one of these, VD-135, is again one of the forensic loci, D2S44, but it just illustrates that there are significant differences in allele frequencies among those.

In addition to the ones that I've illustrated showing differences between - within the black race in the U.S., between whites from Canada and the U.S., within whites in the U.S., between Native Americans within South America and between South Americans and the Yucatan, I've also been given to understand, and I've at least seen the data that illustrates that the R.C.M.P. has found significant differences in allele frequencies between Native

Americans in Eastern Canada and Western Canada. Ontario and British Columbia, I believe, and that those are statistically significantly different.

Q. Doctor, are there any particular conclusions we can draw from the evidence that you submit is evidence of substructure?

A. Well, what I've said all along is that the probabilities that are derived by simply using the binomial expansion, the 2PQ, and the product rule across loci all assume that frequencies of alleles at a locus are statistically independent and that the frequencies across loci are statistically independent and that the data base that you use to generate your frequencies represents the frequencies of alleles in your population of interest, and your population of interest is all of the potential individuals that might have committed a crime, if we're talking about a suspect match or that might have been - contributed a blood sample if we're talking about a victim match. Insofar as there are genetic differences in suspect pools or victim pools, and so far now we're beginning to see data that suggests there are differences at VNTR loci, then simply multiplying the probabilities and simply producing it with the standard population genetics tools produces an inaccurate probability. It's not accurate and it may not be reliable. It may be reliable in some cases but it may not be reliable in other cases, and that's the major problem that I have with it, I don't know how to decide when it is sufficiently reliable in a particular case or when it's not, although there are other forms of evidence

that at least can give you a hint of whether it's reliable or not. I also made the statement, for example, in the Bourguignon case, that I thought that there might be significant differences between the French-speaking Canadians and the English-speaking Canadians. I was aware of no data at the time that would indicate whether that was or was not true, but you did show me the piece of paper that Dr. Carmody produced in evidence.

Q. I believe VD-65, and I'll show it to you again, Doctor.

A. Thank you. Yes, it is VD-65, and I would just note that there's a line for France in which the frequencies of alleles at two of the loci that are currently being used in forensic cases are presented and that the frequencies there are larger for the two alleles that are involved in the Legere case and they do not fall within the Canadian 99% confidence interval, and under those circumstances the French-speaking Canadians who are descendants of the French may indeed have significantly different allele frequencies no matter how you decide to talk about significant differences in allele frequencies, and if they do, then the probabilities that are produced simply by using the Canadian Caucasian data base may indeed be biased against, and those two being much larger suggest that they would be for those two, and under those circumstances I can't sit and say that I'm comfortabl with the probabilities that are produced, that I think that they're reliable and accurate enough tnat I consider them useable.

Q. Now, I notice here in VD-65 which was presented and prepared by Dr. Carmody he has for the Canadian the 99% upper confidence intervals. Now, does that in any way take into consideration substructure?

A. The confidence intervals take into account the sample size primarily. What they're doing is - and in essence that's really all they're doing is saying the bigger the sample the smaller the confidence interval will be around a particular estimate, and in fact if there's substructure what might happen is depending upon which sub-population you sample you'll end up with the same size confidence limits but you'll have a different point estimate in the middle so it does not take into account substructure, confidence intervals do not.

Q. Doctor, I'm going to show you a copy of an affidavit that you had supposedly submitted in the Daniel Vandebogart case.

A. That's a copy of my signature.

THE COURT: VD what? That's in evidence now?

MR. FURLOTTE: It's not in evidence. No, it was discussed much but never put in evidence. Is that a copy of the affidavit that you put into evidence that Dr Kidd and Dr. Carmody had commented or criticized some of your remarks in?

A. Yes, it is.

Q. And what was the basis of that affidavit, what was the purpose of it?

A. It was a re-rebuttal of Dr. Bruce Budowle's testimony in this case which was a rebuttal of my original testimony.

Q. And the substance of the affidavit was to show what?

A. Three things; one - I don't even know if this came up here but the FBI's original data presented to me in the Syracuse case included in it cell line controls without obvious, to me anyway, identifiers that they were cell line controls, and I had asked Dr. Budowle and others why my numbers didn't quite match. I discovered that they didn't match when I discovered that my numbers were slightly different from Dr. Hartl's from the Yee case, and they finally got back to me and said it's because the cell line controls are included, so I removed the cell line controls, re-ran all of the analyses and presented it with the same conclusions I just now pointed to different bins to reach the same conclusions. That was the primary purpose of this affidavit. The secondary purpose of the affidavit was that I did in the time between the original testimony in this case and when I was able to do this re-rebuttal had received from you the data from the R.C.M.P. on their data and I was able to do the analysis that illustrated that there was a significant difference between the R.C.M.P. and the U.S., and that is over and over again what is the "problem" that some population geneticists have with this technique. It's the fact that substructure if it exists, and if it exists at a significant level, significant enough level, will make the probabilities that are produced sufficiently biased in a statistical sense, not a legal sense, Your Honour - excuse me, Your Lordship, that they're inaccurate enough that they're bad, in essence, and also to complain a bit about the treatment that we scientists get from

lawyers, which I think all of us feel.

MR. FURLOTTE: I would offer this into evidence, My Lord.

MR. WALSH: I have no objection, My Lord.

THE COURT: That will be VD-136. What was the name of the case there?

MR. WALSH: Vandebogart, My Lord.

A. New Hampshire vs. Vandebogart.

MR. FURLOTTE: Doctor, do you have any reason to believe that there may be a difference between Canadian Caucasians of British descent and of descent from France?

A. The data that were provided in the handout by Dr. Carmody suggests that it's a reasonable possibility, but there's additional - I don't know whether I'd say Canadians in this case of French descent. I presume from Mr. Legere's name that he is of French descent but I also could talk about it in the context of the band sharing that you see in the New Brunswick population as is evidenced on the autorads produced for this case and the sizings produced for this case.

Q. O.K., in this case, the Legere case, with the evidence that you were given in the autorads and the sizings and whether matching bands were you able to do something with that information?

A. Yes, I was.

Q. And would you tell the Court what you did and what the significance is?

A. What I did is I looked at the autorads and I looked and said how many bands match between individuals who are not related, recognizing that, for example, Donna and Linda as they're listed in the evidence are sisters. Not using that as a comparison but

simply comparing unrelated individuals, Murphy with Linda, Mr. Legere with Murphy, Mr. Legere with Donna, and Mr. Legere with Nina, who I presume are all unrelated pairs. One can use all of the assumptions of the R.C.M.P.'s analysis and production of probabilities to determine the probability that the individuals in question could match at as many bands as they do, and if the R.C.M.P. data base and the frequencies it produces are the right frequencies, then we would have some estimate of how likely it is that all of these could match, so for example, Murphy with Linda -

Q. Now, when you say match, Doctor, are you talking bands match or just that bands fall in the same frequency bin?

A. No, I looked at these autorads last night and these are matches. These are what I would call explicit matches. Visually they are at the same place, looking at the sizings after the visual match -

Q. So it's not just that they fall in the same bin?

A. No, these to me are the same alleles. They migrate - I cannot distinguish them from - I cannot distinguish that they are different alleles, either visually or through the computer analysis, and under those circumstances, for example, Murphy shared four bands with Linda, Legere shared four bands with Murphy - not the same bands, by the way, they're different bands for the different pairs - Legere shared four bands with Donna and Legere snared two bands with Nina, and you can develop the probabilities of those sharing patterns if the R.C.M.P.'s frequencies as produced in their data base are truly representative

of the frequencies of those bands in that population of interest, the New Brunswick individuals who are involved in this particular case as either victims or suspects, and under those circumstances, for example, the probability of Linda's matching Murphy at four bands is one in 10,807, and the probability of Legere matching Murphy at four bands, the four bands explicitly that they match at, is one in 2,749, and the probability of Legere matching Donna at the four bands at which they match is one in 5,616, and the probability of Legere matching Nina at two bands, in this case it was a genotype match as well, is one in nine. Now, what that means is that those probabilities are supposedly independent samples from the general population data base. What's the probability of an individual sharing four bands if this is the distribution of alleles, explicitly these four bands, and in the next comparison if we draw two individuals at random from a data base, from a general population, what's the probability that they will share, and it's those probabilities, and if those are statistically independent events the probability of all four of those events happening, Murphy sharing four with Linda, Legere four with Murphy, Legere four with Donna, and Legere two with Nina, would be once chance in 1,496,600,000,000, which implies to me that there's probably structure in the New Brunswick population, and that the frequencies that are used are not perfectly correct.

Now, one can play, O.K., one can say that Murphy matches Linda, and then I have Legere match

Murphy, and that's not independent, unless all of the bands are different, O.K.? One can do all of that and you still - you can get it down to two bands matching, three bands matching independent, two bands matching independent, and you still have a probability of all four of those events happening that's well above one in a hundred million. In other words, it's supposedly impossible if that's the true data base. What that says to me is that there's background band sharing, there is background relatedness among Murphy and Linda and Legere and Donna and Nina and the other suspects who I finally saw the sizings last night and there's lots of band sharing there as well, and I did the analysis on this set of individuals and it came up to be that there was approximately 3.3 bands shared out of a dozen, so I used all six probes, which is good, it's making that band sharing as small as you can given that population, and if you do that, if you make the background relatedness represent what's done in terms of the band sharing that you observe in this sample, then the probability of a two-locus match becomes one in 44; the probability of a 4-locus match becomes one in 1,910; the probability of a 5-locus match becomes one in 12,633. Those numbers are very, very much larger than any of the numbers using the standard techniques. This is a standard technique, however, just as that is, when you know that there's background relatedness. It is the standard technique used, for example, by Cellmark and the British when they're using multilocus probes. They always have to calculate in the

background level of band sharing in order to determine the weight of how many bands are actually shared in a particular case.

Q. Now, would this be an indication that there would be inbreeding, or just an indication that you couldn't use the general data base that the R.C.M.P. are using?

A. I personally would take it as evidence that there's structure and that the New Brunswick population that these people are sampled from is genetically different from the general Caucasian population represented as the R.C.M.P. data base. They're genetically different probably because of the generic sense of inbreeding, that they have a different pattern of co-ancestry, that they have a higher probability of mating among themselves than they do of having individuals come from outside their group and mating with them. They're not a random mating group, they're a sub-population - part of a sub-population.

Q. Now, the calculations that you arrived at to matching at one probe or at five probes to be something like one in twelve thousand-some?

A. Mm-hmm.

Q. And would that be for unrelated individuals or would that also take in maybe possible relations of Mr. Legere?

A. It takes in what we call a background level of relatedness. It's pedigree unrelated, which is what these people, I presume, are, O.K.? In other words, they're not cousins, they're not second cousins, they're not siblings. What would happen if you had siblings and cousins or uncles and nephews is that

the probability would get bigger again.

Q. And bigger meaning what? Maybe - sometimes we get confused.

A. A larger probability means more likely, it would get closer to one in - well, the probability even if there's no background band sharing of two siblings having identical bands at four loci is one in 256, O.K., so if you were to take 256 pairs of brothers, one of those pairs would likely be identical at four loci. Now, if you had background band sharing as well as sibling relatedness, instead of one in 256 it would get larger, it would become one in 128. That's - please put in the record that I'm doing that out of my head and it's not a number that I would like to say is exact.

Q. So when you quoted the figures of one in 12,000 of sharing five loci that that again would drop down relatively to maybe one in 6,000 or -

A. No, no, no. A brother would be one in 256 even if there were no band sharing, O.K.? It's two different questions.

Q. Now, Doctor, I understood you to say that you were doing something similar to - with the FBI data base as Dr. Hartl did in the Yee case, or did I misunderstand that?

A. What I did is I used the data that were provided. Dr. Kidd finally released those data, released the paper, and I was given a copy of those and I did a statistical analysis using standard bins to see if there were frequency differences between the three Indian populations that he had studied, and there were.

Q. And are you aware of the findings of Dr. Hartl's, that Dr. Hartl did with Dr. Kidd's data?

A. Yes, I am.

Q. And what were his findings?

A. He did the sort of analysis that I just talked about where he looked at the three data bases that you would produce from those three Indian populations, those Native American populations, and calculated probabilities of coincidental match, as it's been called in many cases, or the probability that somebody else could produce the evidence, as I prefer to call it, for the three populations and looked at how it differed between, you know, depending upon which population you used, and he found differences that he considered to be of great import, large magnitude.

Q. Do you know whether or not Dr. Kidd's - how significant Dr. Kidd considered his data?

A. Dr. Kidd has testified that he doesn't feel that the differences are big enough to worry about in a practical sense in forensic settings. Dr. Hartl strongly disagreed and I moderately disagree with Dr. Kidd in the sense that as I said in the affidavit that you put into evidence - I also read that Dr. Kidd criticized this, but I'm not sure why, I wasn't able to get from his testimony why it was incorrect on my part - talking about a difference between one in 50,000 and one in 100,000 of risk of dying from a particular treatment, if those numbers were handed to me by a physician I know which one I would choose, and I think that's a rational choice, and I think that's what we're asking the triers of

fact to do is to make rational decisions based on the evidence.

Another thing that's funny about probabilities that people may not think about sometimes, if you're talking about a probability of one in 10,000 versus one in 10,000,000 and you live in Toronto, if the probability of an event occurring in Toronto is one in 10,000 and there are two or three or four million people, it means that there are a significant number of people who will match if the probability is one in 10,000, and it means that there are not very many people, if any, that will match if it's one in 10,000,000, so under that set of circumstances those numbers have a real practical impact as well, the difference in those numbers.

Q. Are you aware of a letter that Dr. Hartl had circulated after he gave an expert report in the Yee case?

A. You showed it to me.

Q. Yes, and do you know whether or not Dr. Hartl has retracted from his position in the Yee case?

A. What I know for sure from having talked to him on the phone is that he and Dick Lewontin are preparing a paper for science and I think it's actually been submitted that makes similar and even stronger criticisms than he made in the Yee case, so I would say he has not retracted his position.

Q. Doctor, I'll show you Exhibit VD-49A, a paper entitled "Fixed Bin Analysis for Statistical Evaluation", by different authors. Are you aware of that paper?

A. Oh, yes.

Q. And when was that put out for publication?

A. When was it first submitted or when did it come out?

Q. Well, either. When was it first submitted for peer review, do you know that?

A. I believe it was first submitted sometime in late '89. I'm not sure, I'm not absolutely certain. It was revised a couple of times, I do know, and it finally appeared a couple of weeks ago, came out in the May issue of "American Journal of Human Genetics"

Q. Do you know why it was revised?

A. Because like every scientist you always revise. You get peer review and you improve the paper, address some of the criticisms, do your best to improve it.

Q. Do you know whether or not Dr. Lander has taken a different position from the time he wrote the Branbury Report?

A. Dr. Lander wrote an editorial, an invited editorial, that went with the publication of the fixed bin paper as well as another paper by Alec Jeffreys and his group in Britain on forensic use of multilocus DNA typing, and his position -

Q. Are you talking with VD-49A?

A. That's correct.

Q. It was published at the same time?

A. Published at the exact same time, and in it he stated what he liked about what this fixed bin paper was doing and he also stated what he considered to be the remaining criticisms, and they're essentially identical to what he said in the Banbury Report. One of the criticisms that he's made that others have made is that while using a

fixed bin is conservative with respect to defendants, the fixed bin paper and others in testimony have claimed that it's sufficiently conservative to make up for the problems of sub-structure, and he explicitly noted in this paper that accompanies that that's still what we would call a scientist's handwaving, that you can't know whether it's sufficiently conservative until you know how much substructure there is and we don't know that yet, and now that the data are coming in that there is substructure, you need more data before you can do it.

Q. Now, Doctor, the fact that the fixed bin paper has had peer review, what significance does that have as to whether or not it's generally accepted by the scientific community?

A. The fact that it's peer reviewed and published rather than rejected means that it is at least considered warranting further discussion. That's what getting into the scientific literature is about. It is now available for the general scientific community to see it, to judge its merits, to judge the logic of the arguments, to judge the data, but that really only happens after it's published. Prior to that it's a very small sub-set of individuals that get a chance to judge it, so being peer reviewed and published is the first step to acceptance. It's not anywhere near the end step.

Q. Is there any indication as to whether or not the fixed bin paper is going to be accepted by the general scientific community?

A. I know there are a lot of people that are currently writing papers that are critical of certain aspects of it, in particular the population genetics aspects, and in fact what you put into evidence, which is the thing that I sent to the National Academy, is the core of something that I'm going to write in response to that paper. There are others as well, so the only answer I can give you is that it's going to take some time and some argument before all of the kinks are worked out on both sides to everybody's satisfaction, I suspect.

Q. Doctor, in your opinion, how much confidence would you have in the reliability of the approach taken by the FBI and the R.C.M.P. in their fixed bin method to declare calculations of probabilities?

A. Well, I think as I pointed out here, if I do calculations I come up with differences from one in 12,633 for a 5-band match to one in 666 billion I do not find that reassuring in making a decision about what probabilities to use in forensic cases. There are still empirical probability estimates that can be derived from these that almost nobody would argue about, they're just bigger than the ones that are currently presented, and those empirical probability estimates have to do with the fact that if you have a data base you can state unequivocally how many times you've seen a complete genotype that matches one that you're interested in, a suspect or a victim, and you can divide that by the total number of individuals in the data base if you've never seen it before, and that gives you a probabilit that most of the problems - the only problem that

would still be a problem for that probability is if you have extreme substructure, true inbred isolates that are so different from the rest of the population that they couldn't be handled even by that kind of empirical estimate, they'd need their own data base.

Q. Doctor, based on the empirical evidence that you do have before you, would you have any suggestions how the R.C.M.P. ought to alter their method? What has to be done?

A. Well, I mean, I have suggested one, and I suspect that they're doing it, I just - maybe they're not finished yet. One thing that I would do in Canada is certainly have a comparison between French-speaking Canadians and English-speaking Canadians, the two biggest groups, the two most likely on the basis of what I've seen so far that I would predict would be different, and if they are, then you'd need a data base for each rather than a general Caucasian data base. That would go some way towards it. The other possibility is to simply do what they do, and they do it, I think, better than the other forensic groups. They exclude a lot of suspects rather than just say, here's a match, and we have no idea how many other people may have committed this crime. They spend a lot of time on other suspect samples. When you do that the probability, I think, becomes less important, and not having it at all really doesn't make that big a difference.

Q. Now, Doctor, I'm going to recall the evidence given by Dr. Fourney as to the rebinning of the R.C.M.P. population data base, and what I understood his

testimony that when they rebinned it they found that there was five people in the data base who matched across the five probes, so therefore they removed those five on the assumption that they tested the same person twice. Would that be a proper scientific call to make without knowing where the samples come from?

A. No, but it would explain why people have, "never found five-band matches between unrelated individuals", which has been testified to in a number of cases. In my own opinion, I think that unless you know that it's the same individual one could assume that they were actually true random matches and therefore it's not probably appropriate to throw them out. What did happen, and I think why they did it that way, is the FBI did find - were notified by one of the people that provided them with a data base that there were a number of repeats that they discovered, and the FBI went in and found those repeats and removed them and then went into a different data base that they had and found the five-band matches or four-band matches, I think in their case, and removed some of those as well, so it stemmed from the fact that one of the blood banks did tell the FBI that they knew they had the same individuals multiple times, and that's always going to be a problem if you have blood banks because individuals do contribute more than once to blood banks. Some of them do it for money.

MR. FURLOTTE: My Lord, I believe I'm practically finished with this witness and maybe if we had an early lunch break and I may have one or two questions

after lunch and I may not, but I would like the lunch recess to decide.

THE COURT: Yes, that's fair enough. It's quarter past twelve now and it will give you a chance to decide whether you have any more examination. Have you any idea at this time how long cross-examination -

MR. WALSH: Oh, I would think, My Lord, if Mr. Furlotte is done very shortly after lunch I wouldn't expect I'll be too long with Dr. Shields.

THE COURT: Yes, I mean you'd finish this afternoon?

MR. WALSH: Oh, yes.

THE COURT: You wouldn't go over until tomorrow?

MR. WALSH: No, My Lord, I'll make that promise, yes, My Lord.

THE COURT: You better be careful with your promises.

MR. WALSH: I know, My Lord, but I'll make that promise.

THE COURT: I'm just doing this for your benefit, Doctor.

A. I know, I appreciate it.

THE COURT: It looks as though you might be able to get away from our rainy clime this evening.

A. Back to the rainy Adirondacks.

THE COURT: Yes, it will be probably no better there. O.K., we'll recess till one-thirty.

(LUNCH RECESS - RESUMED AT 1:30 p.m.)

(ACCUSED IN DOCK.)

DR. SHIELDS RESUMES STAND:

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

MR. FURLOTTE: Doctor Shields, when you were calculating the improbability of events in the Legere case about Murphy matching Legere and Legere with Donna and

Murphy with Linda did you prepare a transparency or any sheet with data on it?

A. It's not a transparency - actually, yes, it is. Yes, and this particular sheet is missing a zero at the end of one chance in 14966 and seven zeros, there's supposed to be another zero, that's all.

Q. Would you be able to make a correction on that?

A. Actually, if you're going to Xerox it and put that in evidence it's easier to put the zero on the Xerox.

Q. And maybe, My Lord, we could do that so we could put this into evidence and it would be clearer for your notes and maybe for cross-examination.

THE COURT: This amounts to a summary of the evidence that was given earlier.

MR. FURLOTTE: yes.

THE COURT: You haven't seen this yet, Mr. Walsh?

MR. WALSH: No, if it's a summary of what he said I have no objection to that.

MR. FURLOTTE: We can put it back on the overhead and he could just explain it again if the Court wishes.

THE COURT: Mr. Pugh, why don't you take this out, make a Xerox, bring a copy in to Dr. Shields, let him make the correction, and then take it out and make a few more copies. Mark it as an exhibit first, that would be VD-137, and make four or five copies of it and Mr. Furlotte can have one, Mr. Walsh and myself and anybody else.

MR. FURLOTTE: O.K., now, Doctor, there was evidence at this hearing on whether not the probability of factors could be determined as to what the chances were of two hair samples from two different individuals

being at the same place and the same time and that the frequency of the hair sample - somebody else having that hair sample, was one in 4,500.

MR. WALSH: Objection, My Lord, on relevancy.

THE COURT: Well -

MR. FURLOTTE: On relevancy?

THE COURT: Yes.

MR. WALSH: I want to know what -

MR. FURLOTTE: We covered all this in the Crown's case -

MR. WALSH: He covered it on cross-examination over my objections upon objections upon objections where he's trying to equate probability of guilt with probability of whether two samples matched. Dr. Shields is a population geneticist, he's here for the purposes of determining the population genetic issues associated with DNA samples, not for the purpose of determining whether or not two hair samples can be found in the same room at the same time.

MR. FURLOTTE: I don't think it's anything to do with -

THE COURT: No, would you just state your question again. Mr. Furlotte, so I grasp it again?

MR. FURLOTTE: I'm asking the doctor if it would be possible to calculate the frequency that one might expect to find two hair samples from different people at the same time in the same place when that frequency for one would be one in 4,500 for - these would be the probabilities that somebody else out there might have the same hair sample as myself would be one in 4,500. Is it possible to calculate the frequency that myself and somebody else with hair exactly like myself, except for DNA purposes, would be at the

same place at the same time?

THE COURT: We're talking about black and white balls, aren't we, and not hair samples?

MR. FURLOTTE: Well, that's for the doctor to decide, My Lord. That's what I want to ask him this question.

THE COURT: Well, O.K.

MR. FURLOTTE: Are you able to use the product rule in this to come to a figure or would it be one in 4,500?

A. If they're statistically independent I can't tell from the data because I don't know about hair data bases, but if they were statistically independent you would multiply the two probabilities together, which would be an exceedingly low number.

Q. Now, Doctor, last night I believe I gave you copies of the transcript to read Dr. Carmody's criticisms and Dr. Kidd's criticisms on your comparing the FBI data base with the R.C.M.P. data base and I believe you found there was a statistically significant difference and the testimony of Dr. Kidd and Dr. Carmody was that although there was statistical difference in the bin frequencies the end result there was no meaningful difference. Do you have any comment on that and what the real distinction ought to be made because of that finding?

A. The way you've asked that question I'm not sure I can answer it. What I would say is that we probably have a difference of opinion as to what the word meaningful means. I personally do not believe that order of magnitude differences, regardless of how big or small the numbers are, are meaningless even in the forensic sense, as I tried to indicate earlier.

A difference of one in a million and one in ten million to me is a significant difference, both in a practical sense as well as in a statistical sense. and if there are statistically significant differences, then I think that somehow or other those statistically significant differences should be taken into account in the calculations that produce the probabilities of coincidental matches. Dr. Kidd and Dr. Carmody differ in their opinion, and I know other people that share my opinion and I know other people that share theirs.

Q. Under the circumstances where you found the difference would it be proper to use either data base?

A. Proper is a term that makes it difficult again to answer. I'm not sure what you mean by proper. You could use either data base. You could use both combined. I'm not sure you should use either. I can't myself make a distinction. If I were going to use one and only one I would use the one that gave the highest probability because that would be the most in keeping with, I believe, Canada's innocent until proven guilty as well as the U.S.'s.

Q. You said maybe you shouldn't use either. For what reason would you state that maybe it's not right to use either data base?

A. The data that are there, the actual differences that you see, are indicative that there may be greater differences in the particular sample that you're looking at. The fact that there are differences at the level of the whole Canadian population versus the whole U.S. population implies that it's at least possible there may be even

greater differences between New Brunswick and the rest of Canada. Until you know that that's not the case, then the difference between one and I believe it's five million and one in 9.9 million may actually turn out to be a difference of one in 400,000 versus one in 5.2 million, and you don't know.

MR. FURLOTTE: I have no further questions.

THE COURT: Thank you very much, Mr. Furlotte.

CROSS-EXAMINATION BY MR. WALSH:

Q. Dr. Shields, before the break this morning Mr. Furlotte asked you a number of questions related to certain matches or calls that Dr. Bowen made, and you reviewed them. Just so we can clarify it, you didn't disagree with anything that Dr. Bowen - anything that you were referred to by Mr. Furlotte, you didn't disagree with any of the calls that Dr. Bowen had made in that regard, did you?

A. I did not.

Q. In fact, Doctor, one of the witnesses in this particular case, Dr. John Waye, you know him, don't you?

A. I met him at a previous -

Q. In the Bourguignon hearing?

A. That's correct.

Q. And you've alluded to it this morning in relation to Dr. Waye's work. I believe to quote your words you say that the autorads in that particular case were, "They were better run than anybody I've ever seen before".

A. That's correct.

Q. I would take it that you believe Dr. Waye is a

person of great skill?

A. Yes.

Q. And you would value his opinion with respect to forensic DNA typing, would you not?

A. I certainly would.

Q. You would consider his opinions to be of some weight?

A. Indeed.

Q. Thank you. Doctor, as well, and I'll just briefly allude to the Bourguignon hearing, it's been not all that long ago, I believe it was in January you testified in Bourguignon in Ottawa?

A. Sounds right.

Q. And I'll refer you to your Page 124 of your transcript of evidence on cross-examination, and if you remember the statement would you tell me, please, whether or not you remember making this particular statement? I suggest that you did make it. In answer to the question, and the question was, "And that the application in DNA typing forensic purposes is generally accepted". Your answer was, "The application of DNA typing, the molecular portion of it, the running of the gels, done carefully, is acceptable to determine if there is a match or not and I would suspect that almost all molecular geneticists would say that as well". Do you remember making that statement, Doctor?

A. I've made it then and I've made it before and since.

Q. And you would make it now?

A. Yes, sir.

Q. You also, Doctor, at that particular provision - I also note, Doctor, that you've also made the

statement at that particular hearing on Page 136, and the question that was asked of you was, "And, Dr. Shields, you were asked for your opinion with respect to general acceptance in the scientific community and you gave that there was some who obviously dissented. What is your view?" And your answer was, "My personal perspective is that DNA typing is reasonable relevant. and when it is done right even exciting tool to allow for the exclusion and inclusion of evidence". Do you remember that statement, Doctor?

A. I'm sure I made it but I suspect it's taken at least -

Q. No, I'm going to continue. That's one aspect of it. Do you remember that particular aspect?

A. Yes.

Q. And you went on to say, "I personally do not feel that we yet have a data base or a way of generating the probabilities that would allow us to use those probabilities, those matches, as weight for that evidence that a match and an inclusion or an exclusion has occurred". You made that statement then?

A. Yes.

Q. And you would make that statement now?

A. Yes.

Q. That in your personal opinion you do not feel that you have a data base or a way of generating those probabilities at this point in time?

A. Well, I think that actually the recent publication of Nichols and Balding's paper allows one to generate probabilities slightly differently than in

January. This is a fast-moving field and publications are appearing literally on a weekly basis.

Q. O.K., maybe we could just touch on that because I intend to go into that a little bit more depth. Nichols and Balding - correct me if I'm wrong, you referred to a correction factor?

A. That's correct.

Q. And the correction factor is to allow for what? What is the purpose of the correction factor?

A. To correct for substructure.

Q. And that would be related to inbreeding, for example, isolated sub-populations?

A. It would be related to either selection or non-random mating generating allelic differences between sub-populations within what we call the meta-population.

Q. And hence the comparison that you made in one of the exhibits between the Legere case that the FBI, R.C.M.P. and the Nichols and Balding - using the Nichols and Balding correction factor; is that correct?

A. Right.

Q. O.K. Well, we'll get onto that, Doctor, in a short time. I just wanted to clarify that. Doctor - so we'll leave the molecular genetics part of it, the molecular biology part, and I'd like to get into the population genetics aspect because that is the one where your opinion is that we're not quite ready yet, we don't have enough information, is that correct?

A. That's correct.

Q. You're not comfortable is one of the words you used.

A. That's correct.

Q. Again, Doctor, population genetics, it has really two aspects, does it not? Now, correct me if I'm wrong. One of the aspects would be the theoretical or mathematical aspect.

A. That's correct.

Q. The methods you're using are statistical, the methods that are applied in population genetics are actually statistical methods, right?

A. Arithmetic and statistical, yes.

Q. And in that regard population genetics is a single discipline, single disciplinary aspect in that regard in the sense that all population genetics use mathematical formulas and theories that have application throughout the organism?

A. Yes.

Q. There is another aspect, Doctor, to population genetics, and that is the empirical work; am I correct?

A. Indeed.

Q. And when we talk about empirical I'm referring to looking at a particular type of population to see how the theory impacts. Would that be a fair statement?

A. That's one way of making the statement. Another way would be that you use a particular empirical system to test the theory and to inform the theory and to generate new theories.

Q. Yes. to see whether or not the mathematical calculations and the formulas that are adopted, whether they apply to the particular organism that

you're studying? Am I right?

A. Or how they apply, sure.

Q. Or how they apply. I would take it that the empirical work is an important aspect of any population geneticist's work, am I not right? The empirical study is very important?

A. Science works as a discipline, it's a social - social relationships between scientists. There are empiricists, there are theoreticians, and there are some people who do both. All of them together are important in understanding a particular scientific discipline.

Q. But, Doctor, you also do empirical work in your own field, don't you, in the particular population genetic aspect that you apply?

A. Yes, I do.

Q. You do empirical study?

A. Yes.

Q. You also use mathematical models and theories to - when you're looking at your - your empirical work is certainly important to you?

A. Yes, it is.

Q. And important to your work, you know, to make it valid. Your validity associated with the statement that you make regarding the populations that you're looking at, it's important for you to empirically look at these populations, is it not? Am I correct?

A. Yes.

Q. I've read some of the transcripts and you're very particular about the words that are used so I'll try and be careful and you correct me if I use something that has no meaning to you. I was looking

at your C.V., and would it be fair to say, Doctor, that your professional experience, publications, and interest primarily lie with respect to animal populations?

A. Sure, that's fair to say.

Q. In fact, what is your - what kind of animal populations have you studied, Doctor. your empirical work, what kind of population?

A. Swallows, chipmunks, beaver, wolves, beetles, as in b-e-e-t-l-e-s, the insect.

Q. That's why Hawaii is important? Hawaii has some kinds of insects that -

A. Hawaii is wonderful for looking at drosophila. The Hawaiian drosophila are -

Q. And wolves, you've studied Mexican wolves?

A. Mexican wolves, that's correct. I've actually only seen Mexican wolves in a zoo. We studied Mexican wolf blood on gels.

Q. But, Doctor - so I take it, then, you would be considered with respect to your empirical work - what would you be considered in terms of a population geneticist, what kind of sub-specialty would you have under the umbrella of population genetics?

A. Oh, I would say because of the slant of the kind of work I do there are two different aspects of it. One would be conservation genetics. We use RFLP techniques and other genetic techniques to look at the conservation of organisms. We use the systems that I was talking about as model system.

Q. What kind of organisms?

A. Chipmunks, rattlesnakes, endangered species.

Q. So animals as opposed to homo sapiens?

A. Yes, and then the other is we use it for behavioural purposes. We are interested in looking at paternity and maternity and excluding and including individuals as potential parents.

Q. Of the animal populations?

A. That's correct.

Q. Now, Doctor, I take it that there are also population geneticists that do primarily their work, their empirical work, with human populations?

A. Yes, there are.

Q. And as a result there would be those that would be recognized as human population geneticists as distinct from animal population geneticists?

A. Let me just tell you what I would use. I would not use the word population genetics for what you're talking about. When you do the empirical work and run the gels and go out and look at how genes are interacting in the environment a lot of people, me included, would call it ecological genetics or they would call it just evolutionary biology in general, and the population genetics aspects of it are actually the theoretical sides, and that's what I was trying to say, there are some people that are doing purely theoretical population genetics, most of them are Japanese, and there are other people that are doing both, and they come from a variety of different places, and there are some that just do empirical work and literally call themselves ecological geneticists, so some of these distinctions you're making are not ones that I would make.

Q. But there are two distinct - you do empirical work

in your work and population geneticists do empirical study, do they not? They study particular forms of organisms, am I correct?

A. Yes and no.

Q. Yes and no. It's not a very hard question, Doctor. I want to know whether there are population geneticists out there who study animals and whether there are population geneticists who spend primarily their time studying human beings?

A. Well, you just said primary of their time. There are lots of geneticists that spend a lot of time studying humans and a lot of time studying plants.

Q. Let's take a population geneticist -

A. Alec Jeffreys.

Q. Let's take -

MR. FURLOTTE: Let him finish the question, please.

Q. Let's take the position, let's take -

MR. FURLOTTE: Let him finish his answer, rather.

Q. Alex Jeffreys, all right, go ahead, Doctor.

A. He's the one who started forensic DNA typing, I think you know that.

Q. Yes.

A. His lab spends half the time on humans and half the time on birds.

Q. I'm not talking about labs, I want to talk about particular -

THE COURT: Well, you're cutting in on the witness, Mr. Walsh, not giving him a chance to finish completely. You were saying, Doctor, his lab spends half its time on humans, half its time on animals?

A. That's correct.

THE COURT: And then were you going to -

A. And he publishes papers that have to do with whether sparrows are the parents of the kids they're supposed to do, O.K., so is he a human population geneticist or a population geneticist, or a bird?

Q. So you recognize no one as a human population geneticist?

A. Yes, I do. If people work exclusively on humans then I would call them human population geneticists or ecological geneticists.

Q. Fine, and someone who, for example, Doctor, who has done post-doctoral work in human population genetics, someone who has studied human populations for 25 years, would you consider him a human population geneticist?

A. Yes, if they spent 95% of their time working on humans, sure.

Q. Would Dr. Kenneth Kidd, would you consider him to be a human population geneticist?

A. Yes.

Q. And in fact in January, Doctor, all you would recognize him for is a molecular biologist? In Bourguignon you were put the question - the question was put to you who Dr. Kenneth Kidd was and all you recognized him for then was a molecular biologist.

A. He does molecular work in human genetics. He has not developed population genetic theory. I would say that he's better known as a molecular population genetics in humans than he is as a population geneticist.

Q. You're going to make a statement here today, Doctor that you do not consider Dr. Kenneth Kidd to be a human population geneticist?

A. We're having a semantic argument.

Q. Well, I just wanted to get a clear answer.

A. Let me make it easy for you. Ken Kidd is a wonderful scientist, he does excellent work, he's well-known, he's well respected. When you used the word population geneticist what I think of is people like Sewell Wright, people like Haldane, people like Fisher, who developed the theory that then I - and Dick Lewontin is another who's developed theory.

Q. Cavalli-Sforza?

A. Cavalli-Sforza hasn't done that much in the development of the theory, no. He's a human geneticist, probably the best known human geneticist in the world.

Q. That's what I wanted to know, Doctor. You consider Cavalli-Sforza a human geneticist, don't you?

A. A human geneticist, but you're using the word population geneticist in a different way than I do.

Q. Do you remember what kind of book that Cavalli-Sforza wrote, Doctor?

A. What kind of book? He's written a number of different books.

Q. Has he not written a book with respect to population genetics?

A. Sure.

Q. And he's a human population geneticist?

A. Again, using your definition, yes. My definition in that discussion in January of Ken Kidd had to do with people who developed the theory versus people who use the theory. That's all there is to it.

Q. Do you consider Ken Kidd today a human population geneticist?

A. Using your definition, yes; using my definition, no.

Q. What's my definition, I'm confused?

A. Someone who is a population geneticist, who uses population genetic tools and empirical analyses of data using molecular techniques and is a human geneticist. Under those conditions anybody who does human genetics is a human population geneticist.

Q. Would it be an easier definition, Doctor, that a population geneticist, a human population geneticist, is someone who spends primarily all of their time studying human populations as opposed to studying chipmunks and rattlesnakes and barn swallows?

A. No, because medical geneticists spend all of their time studying human populations but I wouldn't consider them population geneticists.

Q. But you would consider someone who spends primarily all of their time studying human populations to be a human population geneticist, would you not?

A. I think I just answered that and said no because medical geneticists spend all of their time studying human populations and they are not population geneticists, in my opinion.

Q. But you would agree that Ken Kidd is a human population geneticist?

A. If by the definition of human population geneticist you mean someone who uses population genetics tools to ask evolutionary questions about humans, yes.

Q. And I take it you would try to get yourself in under that definition?

A. I have done a little bit of that, not like Ken Kidd.

Q. No, you're not going to suggest, Doctor, that you are anywhere in the league of Ken Kidd in terms of a human population geneticist, are you?

A. In terms of a human population geneticist?

Q. As a human population geneticist, as I've defined it, as you say I've defined it, you're not going to suggest that you're of the same qualifications. same experience, as Dr. Kidd?

A. In terms of population genetic theory I'm not that different than Ken Kidd.

Q. You will not acknowledge that Dr. Ken Kidd is a human population geneticist of a rank different than you?

A. A rank different?

Q. Do you consider yourself a human population geneticist, Doctor?

A. No, I consider myself a population geneticist.

Q. Fine, and you would consider Ken Kidd to be a human population geneticist?

A. I think I've answered that question four or five times now saying both yes and no depending upon how you wish to phrase the question.

Q. I see. Demography, Doctor, do you deal with demography in your work?

A. Yes, I do.

Q. And demography, I take it that - you will not agree that there's any such thing as human demography?

A. Sure, there is, people who work on humans.

Q. And would you be considered to be a human demographer or have a specialty or any expertise in human demography?

A. No.

Q. And would you define for us, please, what human demography is or what demography is and what human demography is?

A. Demography is using population dynamics tools to look at how populations - the dynamics of populations If you use population dynamics tools exclusively for human populations we would call you a human population demographer and usually you work for an insurance company.

Q. Oh, you work for an insurance company. Would human demography have anything to do with - or have any application to the questions of substructure?

A. Human demography?

Q. Yes, an expertise in demography, and particularly human demography?

A. Would have anything to do with substructure?

Q. Would it have a bearing on the questions of substructure and stratification, things of that particular nature? Well, let me read you a statement of Dr. Kidd, and perhaps so you won't think I'm using these terms willy-nilly, all right?

A. O.K.

Q. Dr. Kidd testified in his direct examination on May 14th, it is part of his qualifications, I asked him, "Doctor, what is demography, if I have pronounced it right, and what application would that have to population genetics and human population genetics in particular", and he said, "Demography would be the study of population structure with respect to age and sex differences, reproductive patterns, stratification, and in many of those ways it is very intimately related to human population

genetics in terms of issues of stratification, in terms of population size, and in terms of mating patterns, so that much of population genetics applications to humans have to take in account human demography".

A. That's true of other animals as well.

Q. And he goes on to say, "And just as if you were a drosophila population geneticist you would have to take into account the various aspects of drosophila reproduction and migration". Now, Doctor, you recognize, then, that you do not have any kind of an expertise in human demography, do you?

A. Yes, I do, you asked -

Q. No, you've just told me you didn't, Doctor.

MR. FURLOTTE: Let him finish his answer, My Lord.

A. No, I didn't. What I said is I'm not a human demographer. That doesn't mean I don't have any expertise in human demography. All it takes is to be able to read, and if you read and you read carefully you can learn a lot about human demography or any other kind of organism you're interested in.

Q. I see, so you're going to consider yourself, then, as well, someone who has a specialty in human demography?

A. No, as I stated when you initially asked me the question, I do understand demography, I use it when I'm looking at barn swallows, I use it when I'm looking at chipmunks. The demographic principles that you're talking about, whether there's overlap of generations, age of first reproduction, all of the things that go into demography go into the

demography of a plant, a bacteria, or a human. The principles are the same.

Q. And there would be no difference when you applied it to humans?

A. There is no difference when you apply the principles.

Q. The principles, Doctor, but there is - you acknowledged earlier that there was such a thing as human demography?

A. There are people who study only the demography of humans.

Q. Humans, correct, and what we're dealing with here, Doctor, is humans, are we not? The whole issue that we're dealing with here is humans?

A. That's correct.

Q. And I've read a quote to you that you apparently agree with from Dr. Kidd in relation to the application of human demography to the issues that we are involved with here.

A. That's correct.

Q. So you do not - you haven't taught human demography, for example?

A. No, I have not.

Q. And what you're saying is that you have a theoretical understanding of demography generally because you have to apply demography to barn swallows, etc.? Am I right?

A. That's correct.

Q. But there are people who actually develop a greater expertise in a particular area, for example the demography of humans, would you agree?

A. There are people - sure. Yes, sure.

Q. Are you aware of Dr. Ken Kidd's credentials in that particular regard?

A. Sure.

Q. And he has a specialty in human demography over and above what you have actually developed?

A. Absolutely, and Dick Lewontin has a specialty in human demography even better than his.

Q. No, no, but I just want to know about you. No, I don't want to know about Dick Lewontin, I want to know about you.

A. Oh, sure.

Q. But Dr. Kidd would have that specialty over and above what you would have?

A. That specialty.

Q. Yes.

A. He has more knowledge of the empirical data that are associated with humans than I do, without a doubt.

Q. Therefore he would have more knowledge by the very definition, more knowledge of the empirical data related to substructure in the human populations in this world than you do?

A. That I would not necessarily agree with.

Q. Are you going to make a flat denial of that statement, Doctor?

A. Not a flat denial, but I have studied human substructure extensively.

Q. Yes, but what you've just pointed out, Doctor, is that human demography has particular application to the questions of substructure.

A. O.K., I will try my best to explain to you why we seem to be arguing when really we're not, O.K.?

Q. I'm not arguing.

A. Demography is one of the potential causes of substructure. One can go out and look at the alleles and find substructure without understanding why, whether it is purely non-random mating, whether it's selection, how those two interact, whether it's drift. The question of demography only comes in if you're interested in teasing apart the actual causes for the substructure. The causes for the substructure are totally irrelevant to forensic DNA typing. If there is substructure that's what matters, not how it came to be.

Q. Are you suggesting, Doctor, that if you don't know the cause of substructure that has nothing to do - are you suggesting that the cause of substructure is irrelevant to the question of whether substructure exists in the human populations?

A. Yes, I'm saying you can independently find substructure without having any knowledge of how it came to be.

Q. But anyone who had an actual understanding of the causes of substructure would certainly have a better idea of the effect of substructure and the degree, would you not?

A. No, you're wrong. If it's there it will have a consequence on probability calculations as they are practiced in forensic typing regardless of why they are there.

Q. But, Doctor, I thought you - part of your testimony was that we don't have enough data yet, in your opinion, to determine the extent or the effect of substructure.

A. That's correct.

Q. Well, wouldn't you think that knowing or having some understanding of the causes of substructure would be of some benefit in understanding that question?

A. We do.

Q. But you pointed out just a few minutes ago that you don't have to know the causes of substructure.

A. No, all you have to know is whether it exists or not. We know prior to the development of forensic DNA typing that in fact there is substructure in a variety of genetic systems. Protein electrophoresis has illustrated it for a variety of human populations. When you do blood typing, that has illustrated it as well. Over and over again we've seen substructure, we see genetic differences between small tribes of Indians, we see ethnic differences in allele frequencies for a variety of genetic systems. We've seen all of that. What's missing is the evidence about the explicit VNTR alleles that are presented in forensic DNA typing, and what the FBI and R.C.M.P. said initially was - and I think I'm pretty close to quoting - there is no evidence for substructure at these VNTR alleles, even if there is evidence for substructure at the others. Well, it turns out in the past few months there is now evidence for substructure at VNTR alleles.

Q. And you have read, according to Mr. Furlotte, you have read the transcripts of Dr. Kidd and Dr. Carmody.

A. Not the entire transcripts.

Q. Oh, you haven't? You only read a little bit of it?

A. What he gave me.

Q. Well, you must have read other transcripts of Dr. Kidd?

A. I have never read a transcript of Dr. Kidd until this time.

Q. You have never read a transcript of Dr. Kidd's evidence in any court room in the United States yet?

A. I have read reports on his transcripts from the Yee trial.

Q. You have not read the transcript in Yee of Dr. Kidd?

A. Maybe I did, I don't remember. I don't think so.

Q. You have not read the transcript in Jakobetz?

A. No, I have not.

Q. You have not read the transcript in Wesley?

A. No.

Q. Or in Spencer?

A. No.

Q. You realize, Doctor, in Yee Dr. Kidd's testimony with respect to population genetics and the effects of substructure would seem to have been accepted over and above everyone else's? You've read that?

A. Yes, I have, and I also read Dan Hartl's analysis of those data and his conclusions about those data.

Q. Weren't you curious to know, Doctor, what Dr. Kidd's words were in that case, what his testimony was?

A. I have his data.

Q. Weren't you interested in his opinions?

A. I can independently look at what his data means without worrying about his words.

Q. Do you mean that you have never actually read his opinions from his mouth in a court room?

A. That's correct, except I think I read pieces of the

Yee, as I told you, and I read three or four pages, I don't know how many they gave me.

Q. Of this case's testimony?

A. Last week's, that's correct.

Q. So you haven't taken that into consideration or you haven't got all the information from someone like Dr. Kidd to formulate your own opinions, then, Doctor, do you?

A. I have no idea what you're getting at. I have his data.

Q. Well, no, I'll tell you very quickly what I'm getting at. Dr. Kidd in Yee was accepted, his opinion was accepted, over a number of very prominent population geneticists, would you agree?

A. I think I did read the decision, and if I remember correctly, Dr. Caskey's testimony was accepted over a number of particular -

Q. Would you like me to read - are you suggesting that in Yee Dr. Kidd's opinions were not accepted over and above the other experts?

A. What I remember was the magistrate saying that Dr. Caskey's testimony was the most critical to his decision to rule in favour of the prosecution.

Q. I see, so you weren't aware of Dr. Kidd's testimony being accepted in Yee? Is that what you're saying?

A. No, that's not what I'm saying. I read the -

MR. FURLOTTE: My Lord, I'm going to object here because I do not believe the Crown Prosecutor is stating the facts as what happened in the Yee case. My recollection of the Yee case, the judge did not find that he accepted one's word over the over but that he decided it all went to weight.

THE COURT: Yes, well, I think you should, perhaps, be a little more precise in quoting if you're going to examine -

MR. WALSH: Oh, yes, certainly. I've just gone to get the case book. I was kind of surprised when the doctor indicated he'd not read the transcript, so you have not read the judgment in Yee, or have you?

A. No, I did.

Q. You did read the judgment?

A. That's what I just told you.

Q. O.K., and from your remembering or your memory of the judgment, Dr. Kidd's testimony was what? What impact did you get from reading it, what was the impact of his testimony on the judge in Yee?

A. I'm sure it was positive because he did decide in favour of the prosecution. My statement was very simple. What I remember was the magistrate strongly saying that he relied most heavily on Caskey's testimony because Caskey had the most to lose if his testimony was incorrect.

Q. I see, you read Caskey's testimony, then?

A. No, I didn't.

Q. You didn't read his either, then?

A. No.

Q. Well, Doctor, are you suggesting that you have, then, all the information that's necessary for you to come to court here today and give opinions with respect to things like population structure?

A. Absolutely, I presented the data. yes.

Q. You presented the data but you have never actually read these experts' testimony, Caskey, Kidd?

A. No, I've read their papers when they publish on it.

Q. Well, don't you think their opinions as they express them in a court room is something that you should take into consideration when you're weighing your own opinions?

A. Why? I mean I'm here as a scientist. Scientists weigh opinions based on data and what is published and statements that are made that have been reviewed by peers and analyzed in that way.

Q. Wouldn't you be interested in knowing what, for example, an expert has to say about his own data and how that impacts, for example, on something else? Wouldn't that opinion be important?

A. Say that again slowly, please.

Q. Well, let me take you to the Amerindian data that you keep referring to and that we're going to get to in a second. Dr. Kidd gave an opinion in this court room about that, isn't that of interest to you as to the impact that would have on the Caucasian populations in Canada? Wouldn't that have some interest to you?

A. No.

Q. His own data, the interpretation he puts on his own data and how that applies, that would be of no benefit or no interest to you, Doctor?

A. All I can tell you is that in reading Dan Hartl's report, what he said that Ken Kidd said, and reading what I read here that Ken Kidd said in this particular case, over and over again Ken Kidd has said that VNTR variation does not exist or it doesn't exist at a sufficient level and that testimony has changed.

Q. I see, this is what you're interpreting from who?

A. Hartl's.

Q. Oh, from Hartl, oh, I see, and you're interpreting this as opposed to going and finding out for yourself what Dr. Kidd said, is that right?

A. I would presume that Hartl, since it's a signed affidavit, swear to tell the truth, the whole truth and nothing but the truth -

Q. I see, you put a lot of faith in that affidavit?

A. Yes.

Q. Perhaps if you'd just give me a second, Doctor. you kind of took me by surprise when you made your comment there about what your understanding of the Yee case was.

A. I believe you'll find it in a footnote.

Q. Is Dr. Caskey a population geneticist?

A. He's a human medical geneticist, primarily.

Q. Yes, but you indicated that you didn't consider them to be human population geneticists, you didn't consider them to be that. The judge says in Yee, and I'll quote from Page 91, I wonder if this will improve your recollection of the particular case. He says at Page 91 of the - it's the unpublished judgment -

A. I've only been able to see the published judgment.

Q. Well, it would be the same thing, Doctor. "In making my determination I take note of the relative professional standings of the prosecution witnesses and the defence witnesses regarding the band shift issue". Now, that's with respect to the biology, is that not, and he refers to, "Doctors Conneally, Caskey and Kidd have been selected by invitation for membership in the Human Genome Organization and Dr. Caskey is President of the American Society

of Human Genetics. These professional accomplishments are a manifestation of esteem on the part of professional colleagues at the highest level of their disciplines. In addition to the scientific stature and judgment that such election implies, participation in the activities of such organization and affiliation with fellows of that rank gives such individuals, I believe, a somewhat better basis on which to gauge the views of those colleagues about the acceptability of new developments related to their discipline." Do you remember that?

A. Sure, now that you've read it, and if I could I'll find you the quote I'm talking about.

Q. I want to deal with population structure in particular. It says at Page 96: "I find Dr. Kidd's comments about the level of acceptance for the FBI methods for determining match also to be persuasive" -

A. What did he say just before that?

Q. It says: "Many times witnesses have an interest in the outcome of proceedings and consideration of that fact is an important means of evaluating the accuracy of their testimony. The government's witness find themselves in a position defending a process that is under a vigorous attack. As they entered this hearing and throughout their testimony which touched on all pertinent subjects of a scientific dispute they had the ability to express reservations about the extent of their colleagues approval of the Bureau's performance of its case work. In that way they could minimize the potential damage to their professional reputations and stature

that will result if they are ultimately shown to have been in error. They chose not to do so and that decision on their part is a factor in my determination that they accurately express the views of the general scientific community", and then he goes on with Dr. Kidd.

A. And then there's a footnote that says that Dr. Caskey, doing exactly the paragraph you just read, is one of the primary reasons that he made his decision - in a footnote.

Q. With respect to what aspect of DNA typing?

A. The fact that Dr. Caskey was risking a lot to make the statements he did.

Q. I see. Perhaps 97 would help you as well, Doctor. It says; "I likewise find that the FBI method for computing an estimate of the likelihood of encountering such a match in the Caucasian population is generally accepted in the scientific community. In reaching this finding I'd give principal weight to the testimony of Dr. Kidd and Dr. Caskey, though I am fully cognizant of the pre-eminent status and stature of Doctors Lewontin and Lander I do not disregard their testimony or discount its pertinent and persuasive power." So you would -

A. Is that where he said about Caskey the explicit quote that I gave you, where he said that Caskey had the most to risk?

Q. No, there's nothing there. I expect it's in there somewhere, Doctor, but what I'm suggesting is that Dr. Kidd's opinions were certainly accepted over and above - with respect to the population genetic

issues was accepted over and above the other pre-eminent population geneticists that testified in Yee.

A. I can only just state something that I think is reasonably simple to state and perhaps understand. The judge's decision about that is not what matters to the scientists.

Q. No, I appreciate that. I can appreciate that.

A. And scientists tend not to worry about the pre-eminence of other scientists. What we tend to do is to look at the data, look at what the data tells us rather than what people tell us.

Q. But, Doctor, isn't - and we come back to why we get into that case book, reading that particular Yee decision would you not be interested in going to the transcript and finding out what Dr. Kidd said about population structure?

A. I now see what he said in this particular trial.

Q. You didn't read it all, Doctor, you just pointed out to me you read a little bit of it.

A. But it's the piece where he says that he's criticizing me for saying there's a problem and the reason why he thinks - I wonder if he read my entire transcript, by the way - but in any case, the reason that he said there's a problem with what I say is because he doesn't believe that there's a practical significance to the kinds of differences that he "has never stated that there is no sub-structure, that there is lots of substructure but that it's not enough to make a difference", O.K.? That becomes a matter of opinion rather than a matter of what's true or not true. All I've ever testified is that if there is a difference the

numbers are not going to be precise, they are not going to be accurate. Then it becomes a legal decision to make a decision about whether they should be used or not.

Q. But, Doctor, wouldn't you be interested in knowing the opinions, the exact opinions, of a man in a court room who studied human populations for 25 years?

A. Sure. In fact, I called Ken Kidd twice impossible to reach as I am.

Q. But don't you find that would be important to read the actual transcript of his testimony?

A. No, I have his paper.

Q. Of the Amerindians?

A. Yes.

Q. But have you looked at what his opinions were with respect to the effect of that paper on Caucasian -

A. Scientists don't care. That's what we do, that's what peer review and acceptance is, we read the paper which is his opinion, and it's one that's peer reviewed and one he's put out to the fellow scientists.

Q. But what you did with the Amerindian paper, Doctor, is you extrapolated the information there to make a suggestion that that should be applied to Caucasian populations -

A. No -

Q. - that that is evidence of some -

A. - I just put it there that there's evidence of substructure within races.

Q. And wouldn't it be important to know what Dr. Kidd's opinions are with respect to the effect of

his study of Amerindians on the Caucasian populations? Don't you think that would be important?

A. No, because I'm not here to talk about this case. What I'm here to talk about is the general use of the method. Sometimes there are native American Indians involved in these trials and then the Native American differences become critically important, and in fact the R.C.M.P. says we're going to have two data bases, one for Western and one for Eastern; why?

Q. Maybe we could get this out of the road, Doctor. We're not dealing with Mr. Legere here, we're not dealing with someone who's an Indian, are we, or any part of Indian, to your knowledge?

A. To my knowledge, no.

Q. It would be interesting, it would certainly be of some interest to you, would it not, if in fact he had an Indian heritage?

A. If he did, then you'd have to an analysis with an Indian data base.

Q. Exactly, so you don't know that in fact he is an Indian, do you? You assume he's French or has a French background, do you not?

A. In part, from his last name.

Q. And I take it he also would fit within the definition your definition of a Caucasian, would he not?

A. I would have said yes except that I was shown some pictures at lunch.

Q. I see.

A. They were half-Indian and half-Caucasian and you would never have known there was any Indian blood

in them.

Q. Are you suggesting he's Indian?

A. No.

Q. No. What are you suggesting he is?

A. From his last name I suggested French.

Q. And which is? What race would the French belong to?

A. It depends on whether they're Algerians or not. It depends on a lot of different things.

Q. O.K., assume for a moment he's not Algerian.

A. He looks Caucasian to me.

Q. Thank you, Doctor. Would you agree that the Caucasian data base that the R.C.M.P. has is an excellent attempt at a random sampling?

A. I think it's an attempt at a representative sample except that it has probably too few French-speaking Canadians, from what I've been given to understand.

Q. Given to understand. I hope I haven't used a word wrong, Doctor. In relation to some questions on Bourguignon, the question was put to you at Pages 96 and 97: "I want to clear up two things about the data base that you may or may not know. One is it is not strictly from Ottawa, it is called the Ottawa data base because it was generated here in Ottawa", and the answer was, "O.K.", and the question: "But it isn't from the City of Ottawa or anything like that, all right, it was gathered for that purpose trying to get persons from a large number of areas, I suppose across Canada, that may not be exactly accurate but it had the end result". Answer: "O.K.". Question: "Of drawing from people could potentially come from across Canada". Answer "Sure". Question: "All right, what would you call

that in terms of a data base". Answer: "An attempt and it is probably an excellent attempt at a random sample of Caucasians and I don't know anything about English or French-speaking, I would just say Caucasian Canadians from across Canada". Do you remember saying that?

A. Isn't that what I just said?

Q. But when I used the word excellent you mouthed the word excellent as if there was something that was strange to you. It was the exact words that you had used in Bourguignon.

A. This is the first time this has happened to me, Your Honour, and I'm sorry, but I find that offensive. I don't particularly think it's appropriate for you to tell me what I'm thinking.

Q. You just used the expression in the court room, you mouthed the words without saying them, excellent, as if it was a perplexing question, and I wanted to know why you - you used the word yourself, why did you have to react in that fashion?

THE COURT: I hadn't noticed this, I don't know whether you did or not. I haven't been -

A. I don't either, Your Honour.

Q. Would you agree, then, that it is an excellent attempt at a random sample, Doctor?

A. It's an excellent attempt relative to many other attempts that I've seen, sure. If everything that was just said is true, everything that led up to my answer in Bourguignon.

Q. Tell me, Doctor, what is your understanding of the Canadian Caucasian data base? What is it comprised of?

A. My current understanding of the Canadian Caucasian data base is that it's a set of individuals from the armed forces from the Kingston area, I believe, another set of individuals from a blood bank in Ottawa, a blood bank in British Columbia someplace, and maybe another blood bank from somewhere else, and I don't remember. My problem with the data base originally and my problem with the data base now is I'm not sure whether they, one, separate French and English-speaking Canadians, nor am I sure that they have reasonable samples of the entire country. That's exactly what I said in Bourguignon.

Q. O.K., Doctor, if for example the Caucasian data base that was sampled by the R.C.M.P. - if it had as part of the sample population that went into - blood samples came from - if they had an equal percentage of the provinces represented in terms of the general population in Canada would you consider that to be a random sample of the Caucasian population in Canada?

A. If people go into blood banks randomly, if they pick people from the armed services randomly, it would be one of the better and even an excellent approximation of a random sample, yes.

Q. And you would expect to find and the reason you would consider it to be an excellent approximation is that if you were sampling a population of that particular sort you would expect to find randomly an equal representation from different provinces contained within your data base; am I correct?

A. I'm not sure. Could you just restate it again?

Q. All right. If the Caucasian data base that was developed by the R.C.M.P., if where they were

sampling from were the areas that are representative of Canada as a whole, you would consider that to be an excellent random sample?

A. Yes, or a representative sample, rather.

Q. A representative sample, because you would expect to have representatives from different areas of the country, different provinces, different English, French groups?

A. If you can expect that; I don't know.

Q. O.K., well, let's see if we can show you. I show you Exhibit VD-58. Have you seen that before?

A. Last night for about three seconds.

Q. All right, what does three seconds tell you? Take a few more seconds today.

A. That's where I came up with Vancouver, Ottawa, and the Ontario samples. Those were the armed forces, I presume.

Q. Ottawa and Kingston area. You go to the next page you'll see Kingston.

A. Canadian Forces Base, there's the one.

Q. Now, I'll show you this. It's item VD-61. Would you look at that for me, please, Doctor, and tell me if that is of any informational importance to you, Doctor?

A. Sure.

Q. Have you seen that before?

A. No.

Q. Take a second and look at it, please.

A. O.K.

Q. Now, I'll show you VD-60A, or perhaps I'll go through them. VD-59A is Canadian population by province in Canada in numbers.

A. Mm-hmm, O.K.

Q. And look at VD-60A, Canadian population by province in terms of percentage representation.

A. Mm-hmm.

THE COURT: What are you coming to, Mr. Walsh, that 9% of the armed forces at Kingston are from New Brunswick?

MR. WALSH: Well, part of what I wanted to know is how representative he would consider the data base, particularly in light of his opinions this morning, My Lord, and VD-62A?

A. O.K.

Q. And VD-63A. In light of your testimony a few minutes ago, Doctor, you would have to agree that that evidence there would indicate that the Caucasian population of Canada as obtained by the R.C.M.P. is an excellent random sample, representative sample, of Canada as a whole, would you not?

A. Yes, absolutely.

Q. You will note there, Doctor, you will agree that the Province of Quebec has a very good representation on the CFB Kingston sample, do they not?

A. Mm-hmm.

Q. And would you also agree that New Brunswick is adequately represented in this particular sample? Do you not?

A. Depends on how you define adequately but it's represented in the sample at a reasonable rate. It's about the rate -

Q. O.K., a reasonable rate, O.K., and Quebec is represented reasonably? Right?

A. O.K., let me just show you what I'm getting at. How many individuals are we talking about from

New Brunswick when we're talking about how many individuals, six or seven hundred, right?

Q. I just want to know, Doctor, in terms of percentage distribution. I want to know how representative.

A. I've already stated it's a representative sample. You then started to use the word adequate.

Q. O.K.

A. Different words, different question.

Q. A representative sample, right, and what you're getting at, Doctor, is how do we know that we actually have people from those provinces included in the data base, am I correct?

A. No, I've never gotten at that.

Q. So you won't use that as an argument, then?

A. I never.

Q. O.K., so you will agree, Doctor, that if these provinces are adequately represented, right, then you would expect to find representation in the data base, would you not, of each province?

A. Sure, that makes it a reasonable or even an excellent representative sample relative to some others that I've seen, without a doubt.

Q. O.K., and, Doctor, your opinions this morning with respect to going out and sampling the French-Canadian population because there may be some differences between the French-Canadian and the English-Canadian population in Canada, does that data have any bearing on - affect your opinion now in any way?

A. Absolutely not, it is totally irrelevant. What happens is that you may have sitting in this data base people from Quebec who are the equivalent of - the analogy that I was using - pinochle decks, and

people from Ontario who are the equivalent of regular decks of cards, and when you do the whole population you average between the two.

Q. And the same with New Brunswick, Doctor, you -

A. Yes.

Q. So what you're suggesting is - what you're saying, then, Doctor, is that there's not adequate representation, is that right?

A. Adequate representation. What you want is an adequate data base for any potential sub-population.

Q. So the representation, the division of representation on the CFB Kingston base is not an adequate representation of Canada, is that right?

A. Representation -

Q. Is that particular -

A. It's not an adequate sample.

Q. Why? I thought you -

A. For why I just told you.

Q. Well, I thought you talked about this all along, Doctor, that it would be and that it was?

A. It is a representative sample, it is not an adequate sample. I have never said it was an adequate sample.

Q. Why wouldn't it be adequate, Doctor?

A. I just explained it to you, I will try once more. It is at least possible that the Quebecois are genetically different from the English-speaking Canadians. If they are, putting them into a single data base will merge whatever differences there are and having this representative sample of all of the Caucasians is like taking pinochle decks and regular decks of cards, shuffling them together and

saying that the frequency of aces is 12 out of 100. When the frequency of aces in one population is 4 out of 52 and the frequency in the other population is 8 out of 48.

Q. So the fact that there's 20 - according to this information, the fact that there's a birthplace of Kingston military personnel and dependents, there are approximately 20 1/2% from Quebec, and in the Canadian population Quebec makes up 25.8%, that doesn't tell you that you have an adequate representation of the Quebec people in that particular R.C.M.P. data base, is that what you're saying?

A. If what you're trying to do is just come up with how much genetic variation is in Canadian Caucasians. that's exactly how you'd do it. If what you're trying to do, please let me finish -

Q. Go ahead, Doctor.

A. - is develop a probability that someone will contribute a particular genotype to an evidence sample, it is not adequate, if there are differences between the French Canadians and the English-speaking Canadians.

Q. If there are, you don't know?

A. If there are. I do not know but I do know that there are data that say that French -

Q. France.

A. - are different.

Q. From France?

A. Yes.

Q. Right, on two loci?

A. That's correct.

Q. That Dr. Carmody provided, is that correct?

A. Yes, that's correct.

Q. All right, so apart from that you have no evidence that they're different, do you?

A. There's other what I would call circumstantial evidence that they may be different in that there's a difference between the U. S. and Canada. There's also the fact that there's a lot of band sharing when you look at the New Brunswick population represented by this particular case.

Q. And New Brunswick is represented in the sample but not adequately represented, is that right?

A. If New Brunswick differs genetically from the other provinces for whatever reason, then having a very, very small number of individuals, 20 or 30, is not a good sample of New Brunswick's gene frequencies.

Q. What, Doctor, if we made a comparison of the - in the United States you made a comparison between the FBI Caucasian data, the Florida Caucasian data, Texas data. Who else did you compare it to?

A. California for some of the probes.

Q. And you were looking to determine whether or not there was any statistical bin frequency differences?

A. That's correct.

Q. And if you found them, which you did, that's an indication to you that there's substructuring going on, is that right?

A. It's an indication that there are frequency differences between at least two of those populations, which implies geographical differentiation, since we're talking about geographical distances.

Q. O.K., and what did it mean when you compared in the United States, when you compared the FBI with Florida, with Texas, and you found differences. What did that mean to you, what did that tell you as a scientist?

A. It tells me again that the theoretical idea that there's possibly or likely to be substructure, there's likely to be genetic differentiation within human populations as a function of geography and mating distance, if I could use those terms.

Q. And the same comparison between Canada and the United States when you compared the bin frequencies there and found differences that also told you what, Doctor?

A. Same thing, it says that there's evidence that there may be enough genetic differentiation that you have to be -

Q. And you expected that because Canada is more homogeneous than the United States is. Homogeneous means there would be less likelihood of sub-structuring going on in a homogeneous population, am I right, so there would be a less likelihood of substructuring going on in the Canadian population as opposed to the United States population?

A. Yes.

Q. And, Doctor, what if we did the same kinds of tests that you did in the United States and if you compared Canada with the United States? What if we did that with respect to the Caucasian data bases in Canada, between Vancouver, Ottawa, and CFB Kingston, and found no statistical bin frequency differences? What would that tell you?

A. It would tell me that those three populations are likely to be reasonably panmictic.

Q. Meaning?

A. That there's probably travel amongst those areas and the Caucasians that are sampled are interbreeding.

Q. And that there's no substructure?

A. For those three populations, yes.

Q. And if those three populations included - and if one of those populations happened to include representatives from the other provinces that would have some meaning with respect to the other provinces, would it not?

A. Some but not - it depends on the structure. It depends on what we call the population structure characteristic of the different provinces. For example, I mean I can use the U.S. just as easy. West Virgina and Kentucky are notorious for being what we call endogamous, having people who live back in the hollers and interbreed and stay together and they're of Scotch-Irish ancestry, most of them, and they actually show a lot of interesting genetic phenomena because of that, and those two states are likely to be very different from other states, even if you take California and Washington and Oregon and find no difference, or California and Illinois and find no difference, so it depends on the population structure characterizing the particular province in Canada.

Q. Why don't we envision CFB Kingston as kind of a miniature country, all right?

A. It's like the FBI sample.

Q. O.K., it has representatives through Canada, it's kind of a miniature representation of Canada, and if you compared that miniature representation of Canada that's found at CFB Kingston with the Caucasian data at Vancouver and found no bin frequency differences, statistical bin frequency differences, what conclusion would you draw?

A. That there are no statistical bin frequency differences.

Q. Fine, and that means that there's no evidence of substructure?

A. That's correct.

Q. And if we did the same and compared it with a sample population from the capital city and found no statistical bin frequency differences you would have to conclude that there was no evidence of substructure, and in fact -

A. And if you took a population of French-speaking people from Quebec City and compared those to Ottawa and you found no statistically significant differences in allele frequencies. I would say that Canada doesn't have to worry as much as the U.S.

Q. But, Doctor, you're completely discounting the fact that CFB Kingston would have representatives from the Province of Quebec, represenatives from the Province of New Brunswick, representatives from Manitoba -

A. I'll try and show you why it doesn't matter. If we take a big population, we take a population that is, as you're suggesting, homogeneous because it's primarily British, and it has 80% of the decks of cards or 90% of the decks of cards or just 80% are

actually regular decks of cards, and you throw in 20% pinochle decks and then compare that mixture to all regular decks they're not going to be very different, but if you were to take all pinochle decks, French Canadians, and compare those to all regular decks, English-speaking Canadians, there may be a difference.

Q. May be?

A. So it's apples and oranges. Yes, I said maybe. I do not know, I have not seen any explicit data that say one way or the other other than the data I just saw the past two days that say that the French -

Q. In France?

A. In France.

Q. At two loci.

A. At two out of five loci are different.

Q. O.K., and apart from that - are you aware, Doctor, that Dr. Carmody did in fact do these tests between CFB Kingston, Ottawa and Vancouver? Were you aware of that?

A. I was told that he has done those tests, yes. I have not read his analyses of those tests.

Q. Were you aware also, Doctor, that Dr. Carmody did tests with respect to - statistical tests with respect to Hardy-Weinberg equilibrium and statistical linkage? Were you aware of that?

A. I was aware that he had finished the Hardy-Weinberg and that he was still working on the linkage disequilibrium analyses.

Q. And in fact one of the tests that he used - you know Seymour Geiser?

A. Yes.

Q. And one of the tests that Dr. Carmody used was one of the tests recommended by Dr. Geiser?

A. O.K.

Q. The non-parametric median test, were you aware of that?

A. I was not aware of that, I have not read it, no, so now I am aware of that.

Q. Were you aware that Seymour Geiser recommended that as perhaps one way of looking for Hardy-Weinberg equilibrium, testing for correlation?

A. I was not aware of that but I'm not surprised.

Q. O.K., and Dr. Carmody's findings were that there was no high correlation. Does that surprise you?

A. No high correlation with what comparison?

Q. With respect to the Hardy-Weinberg comparison. There was no high correlation with respect to non-random association -

A. - of alleles at a single locus.

Q. At a single locus.

A. I'm not surprised.

Q. And is that an indication to you, Doctor, that there's not significant substructuring going on in those sample populations?

A. No, that's an error that a lot of people have made from the very beginning. Hardy-Weinberg is only one example of what could go out of -

Q. But that is one example, Doctor. I'm not saying it's a complete test, it's one example, though, eh?

A. Yes.

Q. The same as the comparison Dr. Carmody made from the three Caucasian populations, that's another example of trying to determine whether or not there's substructuring going on, is it not, those statistical

tests that he did?

A. Yes, and the tests he did between the two Indian data bases.

Q. And the tests he did at the individual locus, this non-parametric median test that Seymour Geiser has recommended, that's another way of trying to find out if there's substructuring, and he's found none, you're aware of that? Right?

A. No, you're telling me that. I will accept that.

Q. You didn't take that into consideration when you gave your opinions here this morning?

A. What?

Q. You weren't aware the doctor had done these tests, Dr. Carmody?

A. I told you that I was - you keep on changing the question.

Q. You weren't aware of the results?

A. Yes, exactly, I'm not aware of the details of the results. I know that he found - in fact, I knew in Bourguignon that he found no violation of Hardy-Weinberg equilibrium conditions, so I knew that a long time ago.

Q. O.K., did you know that he's also doing work with respect to the linkage equilibrium questions?

A. He told me that he was working on it. I have not seen or heard results yet.

Q. Perhaps, Doctor, we could look - I'll just, so I won't misquote him - he states at Page 36 of his direct examination, Dr. Carmody, "The next thing one wants to know about the data base pertains to the next step in this procedure of calculations, namely the product rule. Multiplying the probabilities

that you obtain from each locus which you are now confident are good reliable estimates because they are fitting Hardy-Weinberg equilibrium you now want to be sure that there are no correlations between what genotype occurs for probe one and probe 2, probe 2 and probe 3, and so on through all the combinations." And the question was, "You want to ensure the difference between each probe, there is no non-random association from probe to probe". And his answer, "That's right, in the same way that one wanted to be sure there was no correlation between the pattern of a band, the two bands at each locus, one wants to be able to be sure that there is no correlation of the band pattern at one locus and the band pattern at another locus". O.K., what do you - and he goes on to say: "To do that test I used a non-parametric test that is a variant of what I used looking at each individual locus. It is not a non-parametric median test - it is a non-parametric median test that I used. It has the ability to pick up strong correlations. It again has a limitation and the limitations are even greater in the case of comparing correlations between probes because the number of categories that you expect is still higher than the number for each individual probe itself", and he did not find - he says, "I have been able to satisfy myself that there are no strong correlations of the genotype frequencies from one probe to another", and I asked him, "If there was, what would you call that term", and he said, "That would be called linkage disequilibrium or gametic phase disequilibrium", and the question was, "And if in fact there is no

association, random association, I take it would be linkage equilibrium". "Yes". So now you know that he's done some work on that particular question.

A. Right.

Q. And that's an indication as well, Doctor, that there's no one indication, one example, that perhaps there is no significant substructuring going on in the Caucasian population, is that correct, in the Canadian Caucasian population?

A. That's an indication that there may not be, but now I would point out that I have a suspicion that were you to ask Dr. Carmody, and certainly if you asked me, if you ran the same test using D17S79 and another locus between the U.S. and Canada you'd discover that there is linkage disequilibrium, or as we say, gametic phase disequilibrium.

Q. I see.

A. Because there are significant allele frequency differences between loci.

Q. If we could get to that for a moment, Doctor, in this - and perhaps before I leave that, and I know Your Lordship will be wanting a break very shortly but I'd like to deal with one issue before we leave that and this is this - what was that correction factor, you called it Nichols and Balding correction factor? Now, the purpose of that correction factor, Doctor, was to correct for substructure caused by inbreeding, sub-populations, and things of that nature?

A. What's what they're trying to do. That's correct.

Q. And in VD-121 you made some calculations with respect to that particular question, so what you're

trying to do there, Doctor, now correct me if I'm wrong, you're obviously quite aware of the fact I'm not a population geneticist, so correct me if I'm wrong - what you're trying to do there is show His Lordship that if there is inbreeding going on in the Province of New Brunswick, particularly in the area which Mr. Legere comes from, that using Nichols and Balding's correction factor those are the frequencies that you would correct for?

A. So you'd end up with one in 5.9 million or one in 226,000, depending upon whether you were talking about a 5-locus or a 4-locus match.

Q. And that is on the assumption that there is inbreeding in the particular area where the crime was committed?

A. That's correct.

Q. And that's the reason you've done it?

A. That's correct.

Q. And part of this background band sharing test that you did was an indication or another way of supporting that in the sense of showing His Lordship that there is some form of inbreeding in the wider sense going on in that particular area, am I right?

A. That's correct.

Q. And assuming for a moment, Doctor, that you had applied Nichols and Balding's correction factor and the figures that you obtained were similar to the figures that the R.C.M.P. obtained in this particular case, and just so we understand each other, assuming for a moment, Doctor, that you had applied Nichols and Balding and when you compared Nichols and Balding's frequencies at the locus were similar to

the R.C.M.P. frequencies, what would that indicate to you?

A. Given the way that Nichols and Balding's correction factor works, that's impossible, because what goes into the formula is the R.C.M.P. frequency, and then that is corrected.

Q. Yes, it's corrected based on what, Doctor?

A. Using - Nichols and Balding suggest using the highest what we call F_{ST}, which is a fixation index. It's the highest level of empirically observed inbreeding you see in human populations. It also corrects for the possibility of what they call non-random mutation of these VNTR probes. Between the two of them what it does is it says - it's in essence a measure of the background correlation of bands.

Q. O.K., it has something to do with the band sharing that you've actually got?

A. Exactly.

Q. This is a way of showing that if you apply Nichols and Balding's correction factor on the background band sharing this is what you're going to end up with, is that right?

A. No, no, no, this is applying Nichols and Balding's correction factor on the R.C.M.P. frequencies.

Q. But, Doctor, what you have to do when you do that, you need a value for the correlation, you need a value for that F letter.

A. Yes, the F statistic, and they suggest .05.

Q. .05, and I take it you need that to carry out your calculations, do you not?

A. Absolutely.

Q. You take Legere's alleles that the R.C.M.P. have

generated, the frequency at the locus ~

A. Again what I would do is take the evidence alleles, but it's in essence you can take either Legere's or the evidence.

Q. What did you do there, Doctor?

A. If I remember correctly, I probably used Legere's because that's what the R.C.M.P. did.

Q. O.K., and what you did is when you got those, then you applied the F value, the value of the correlation. you used what was recommended by Nichols and Balding?

A. That's correct.

Q. And you applied that and you got those particular numbers which are exceedingly higher than the other frequencies, am I right?

A. That's correct.

Q. What if, Doctor, you took a lower coefficient of inbreeding?

A. The numbers would get smaller.

Q. And that's where we're going to go, Doctor.

A. We are?

Q. With respect to this particular - what you're referring to was Nichols and Balding, you're referring to "Effects of population structure on DNA fingerprint analysis in forensic science", are you not?

A. That's correct.

Q. And that's an article that was put into the "Heredity (1991), The Genetical Society of Great Britain", by Richard A. Nichols and David J. Balding, this is the article that you're referring to to do those calculations, am I right?

A. Yes, it is.

Q. And at Page 300 of that, and this is where you got

your .05 correlation factor or your F value, your F statistic. It states: "Cavalli-Sforza and Bodmer (1971) surveyed the literature in which these techniques have been used. The most extreme cases were correlations of 5 per cent; these correspond to severe inbreeding". Five per cent would be, if you were using the F factor, would be .05, would it not?

A. That's correct.

Q. And that is what you used to come up with those particular figures?

A. That is correct.

Q. The most extreme cases of inbreeding ever seen in the world, you used those in those calculations, did you not?

A. Absolutely.

Q. And, "These correspond to severe inbreeding, such as that associated with a tradition of uncle-niece marriages". You have actually, Doctor, in those calculations assumed that the area where Mr. Legere comes from is all made up of uncle and niece marriages?

A. No, I haven't. You haven't read the whole thing. If you like, I'll read it to you.

Q. Well, we're going on, but that is a high - well, you've already pointed out that it's the most extreme case of inbreeding in the world ever seen. .05.

A. That's what they said, we take the biggest one.

Q. O.K. No, they say that is at least the highest they've ever seen in the world, O.K., and you're not going to suggest, Doctor, for one minute, that the Province of New Brunswick is going to anywhere

approximate .05% coefficient of inbreeding?

A. The coefficient of inbreeding is also a fixation index, so it does two different things. If you continue to read, or you let me do it, it will explain to you that it's also to take into account the fact that allele sizes are not distributed randomly in VNTR's.

Q. O.K., let me go on, then. "The largest values found in Europe were an order of magnitude smaller", and I understand from a population genetics point of view when you say an order of magnitude smaller would go from .05 to .005?

A. That's correct.

Q. O.K., that's the largest value ever found in Europe, .005?

A. Mm-hmm.

Q. And you've used .05?

A. That's actually the largest values found in a general population. It's much higher in the British Royal Family, for example but -

Q. O.K., but in Europe generally were an order of magnitude smaller, .005; right?

A. That's correct.

Q. "and more recent surveys show dramatic reductions associated with increased mobility due to modern transport. More typically, values are another order of magnitude smaller." So in populations that would mean that typically they're saying that you would expect .0005, another magnitude order smaller; right?

A. Yes.

Q. "Hence the value 5 per cent appears to be very conservative for any large population and smaller

values would be appropriate in cases where extreme inbreeding is known not to occur." Would you please, Doctor - no, I'm asking the questions - would you please calculate for me using .0005 those figures?

A. I can't.

Q. Can you do that?

A. It's on my computer and I can't do it.

Q. Oh, you've already generated them?

A. You've had somebody do it for you and I'll buy it.

Q. Yes, you've already generated them, Doctor, haven't you? Is that what you're saying, you already have those on the computer, those numbers?

A. These I did on a computer.

Q. But did you use .0005 in your computer?

A. No. If you continue reading in that paper you'll see why they suggest using .05 and why I choose to use .05.

Q. Here, you read the paper and tell the judge why you choose to use the most extreme example of inbreeding every seen in the world to apply to the New Brunswick.

A. O.K., "In the previous two sections we have discussed calculations of match probabilities under hypothesis I^1, ignoring measurement error, and conservative estimates of the parameter F_{ST}. We now turn to calculating match probabilities under I^1, accounting for the measurement error specified by M at (3). Hence we need to consider not only the case that two alleles are the same, but also the case that their lengths are similar. Balazs et al found substanitally different distributions of allele lengths in three U.S. ethnic groups. Their histograms show that the allele lengths have a smoothness property; cells of

each histogram tend to have a similar frequency to neighbouring cells. The size and scale of this effect are summarized in Figure 1, which plots the sample correlation (with respect to the total sample mean) of frequencies of cells separated by given distances. Some apparent smoothing can be attributed to measurement error, as alleles of similar lengths will be confused. However, Figure 1 indicates large positive correlations over distances much greater than the range of measurement error. This smoothing may be a result of the mutation process, which appears to generate new alleles of lengths similar to the progenitor allele", and they cite Jeffreys et al, 1990.

"Hence, given a criminal allele, population structure effects lead not only to a higher probability of observing the same allele in the suspect sample but also the chance of observing alleles of similar length is enhanced compared with that due to random selection in Q." Q is the population of interest. "However, the correlation of similar-length alleles will be smaller than F_{ST} if, as we believe, it is due to the interaction of inbreeding (of magnitude F_{ST}) and other processes (principally mutation) which propagate, but attenuate, the effect to alleles of adjacent lengths. This belief is supported by the data of Balazs et al (Fig. 1).

"Therefore, the probability of match for a single band is conservatively estimated by (5) on replacing the allele frequency p with the cell frequency p_f or p_m and choosing an overestimate of

F_{ST}. Finally, approximating once again the appropriate genotype frequency as the product of the two cell frequencies, the single-locus value R_1 is given by ...".

They then note that they recommend the .05 to take care of both inbreeding and allele size similarities.

Q. Allele size similarities in what regard, Doctor?

A. What I just read, I can explain in just general words, is if you look at variable number of tandem repeats, alleles come with particular numbers of those repeats and that's what determines their length, their fragment length. Turns out that if you look at the distribution of all alleles at a particular locus with a particular probe there are actually correlations. If there's a high frequency allele with a particular number there are also high frequency alleles next to it in the bin, and then if there are low frequency alleles there's low frequency alleles next to it within and without the bin, so that there's actually a higher number of fragments with similar base pair numbers than you'd expect if the number of fragments was randomly distributed of all possible combinations. Because of that you get not just identical alleles occurring more frequently than you'd expect by chance, but also alleles that can't be measured as different occurring more frequently than you'd expect by chance.

Q. And that applies to all the systems, all these RFLP systems, is that what you're saying?

A. Yes, it does, yes, that's what they say.

Q. I see, and that's why you'd use the highest coefficient of inbreeding ever found in the world?

A. It's not just a coefficient of inbreeding, it's a fixation index.

Q. But I mean that's when he refers to the .05, that's what he's been referring to, the correlations of 5%, and that's pretty conservative, is it not, Doctor?

A. Yes, it is.

Q. Doctor, perhaps we'll go on to the issue - I just quickly want to finish up before the break on this aspect and we'll go on to that other issue, but just humour me for a moment and let's deal with this. I'm curious, you've used this 5% coefficient of inbreeding, or it's 5%, it's the highest in the world. They talk about magnitudes lower all the way down to .005 -

A. Again I'm going to disagree. They recommend and they use .05. I didn't choose to use it, they did.

Q. O.K., but assume for a moment, then, Doctor, we don't use what they recommend, we use .0005.

A. I'm here to testify about what other scientists are saying about this process. They recommend using .05. I might actually recommend doing something very different.

Q. Perhaps I'll show you, Doctor, if we did use just .0005 which apparently is the more typically values are another order of magnitude smaller. Apparently from this typically you would expect .0005, right, the coefficient of inbreeding according to this paper, "typically values are another order of magnitude smaller. Hence the value of 5 per cent appears to be very conservative for any large

population and smaller values would be appropriate in cases where extreme inbreeding is known not to occur."

A. If all you're trying to do -

Q. What do they mean when they say, "and smaller values would be appropriate in cases where extreme inbreeding is not known to occur"?

A. Where it's known not to occur, which is not the same thing that you just said.

Q. O.K., so you're suggesting - you're assuming what? What level of inbreeding are you assuming in the Province of New Brunswick?

A. All I can do is state that from the data from this case there's a level of background band sharing that suggests that there's some level of background inbreeding. I could actually calculate what it is, but not instantaneously.

Q. And do you have any feel for how much it would be, Doctor?

A. Not .05, if that's what you're getting at.

Q. It wouldn't certainly be .05 -

A. It would not be .05.

Q. It wouldn't be .005 either, would it?

A. Oh, yes, it would.

Q. Do you think so, Doctor?

A. Oh, yes, when you share this many bands.

Q. O.K., well, perhaps then, Doctor, if you think it was about .005, around there would be probably a reasonable -

A. Reasonable what?

Q. A reasonable estimate of the coefficient of inbreeding in the Province of New Brunswick?

A. Inbreeding by itself, go ahead.

Q. All right, look at these numbers here, Doctor, and tell me whether they look something - if we calculated using .005, and how do they compare to the band frequencies. Tell His Lordship how they compare to Legere's frequencies as determined by the R.C.M.P.

A. They're different, they're smaller, but not as small as the ones that - with the .05.

Q. All right, would you please tell His Lordship what those numbers show?

A. Sure, if you use .005 instead of -

Q. Which is what you believe is the approximation of what you think is the coefficient of inbreeding?

A. No, I said that's a reasonable.

Q. O.K., well, reasonable then, all right.

A. We'll use it.

Q. Let's use it.

A. O.K., instead of one in 79 for the D1S7 it becomes one in 70.

Q. And what did you calculate this morning, Doctor?

A. With .05 it's one in 32.

Q. Continue, and I would like you to do -

A. There are check marks next to mine, do I have to keep on doing mine?

Q. Just go ahead, Doctor.

A. My math was correct for once. Anyway, D2S44, one in 59 was the R.C.M.P., one in 27 was the N. & B. with .05, one in 53 is the N. & B. with .005.

Q. Quite a difference, eh?

A. Absolutely.

Q. Continue, Doctor, please.

A. O.K., would you stipulate to it? D4S139, one in 69. One in 61 at .005 versus one in 28, N. & B.

MR. FURLOTTE: My Lord, if I might object, I wonder if that's Dr. Shields' testimony or some other expert witness that the Crown hired.

MR. WALSH: Well, you don't want to accept those figures, Doctor, they don't look -

A. I didn't say that, I said they looked fine to me. I trust the arithmetic.

Q. O.K., fine, continue, please.

A. Do you want just the bottom line or do you really want me to do each of them?

Q. No, I'd like to know what the R.C.M.P. one is, I'd like to know what you calculated this morning and what's shown there when you use a different coefficient of inbreeding.

A. Sure. By the way, we could use .1 and then you'd be very unhappy, but anyway, D10S28, one in 108 is the R.C.M.P., one in 95, .005, and one in 38, N. & B., O.K., using their recommended .05. D17S79, one in nine for the R.C.M.P., one in seven for N. & B., and one in eight, right in the middle, for N. & B. with .005, and then as noted we have for a 4-locus match, we came up with one in 226,000 for N. & B., one in 5.2 million for the R.C.M.P. without any correction - oh, no, you only have the big one, I'm sorry, so I'll have to do that, 5-locus match. Five-locus match was one in 310 million, R.C.M.P., one in 5.9 million for N. & B. with .05, and you have one in 171 million for .005.

Q. Thank you, Doctor.

THE COURT: You read very well, Dr. Shields, that's the point you wanted me to make, Mr. Furlotte.

MR. WALSH: I wanted to - just so we clarify that aspect of it, Doctor, what we were dealing with here is the number that you got out this morning depended on the actual coefficient of inbreeding that you applied to that particular case, am I right?

A. Of course.

Q. And when you apply a lower coefficient of inbreeding the numbers become very similar to what the R.C.M.P. have generated, do they not?

A. Yes, you can make them even smaller. Actually, you'd never get it smaller.

Q. You said .005 was reasonable, did you not?

A. No, I said it's a reasonable approximation of the degree of inbreeding that might be occurring in New Brunswick.

Q. Fine.

A. It does not correct for the other things that Nichols and Balding's technique corrects for, and Nichols and Balding suggested .05, period. They recognize what you're talking about but they said it and they still say .05.

Q. But tell me what they mean, then, Doctor, when they say, "and smaller values would be appropriate" - here, it says, "Hence the value 5 per cent appears to be very conservative for any large population and smaller values would be appropriate in cases.."

A. That's exactly what they mean. If you're talking about inbreeding by itself, that's fine, smaller values are appropriate. They then continue the paper, you have to read the whole paper -

Q. Oh, yes, you went on to that, but I just wanted to get into the aspect of this particular coefficient of inbreeding that you're dealing with there.

A. No, that coefficient is to correct for both factors, according to Nichols and Balding.

Q. I see, but you didn't tell His Lordship this morning the differences with respect to what happens when you do put in a lower coefficient of inbreeding, right?

A. I used Nichols and Balding's suggestion.

Q. But you didn't explain this morning to His Lordship what would happen if you put in a lower coefficient of inbreeding?

A. Nobody asked me the question.

Q. Do you know what the general coefficient of inbreeding is in the Canadian Caucasian population, Doctor?

A. Absolutely not.

Q. Why? Why wouldn't that be of interest to you? Was that something else that you wouldn't take into consideration?

A. I've no idea. I would wonder if anybody does.

Q. All right. Do you know Dr. Lorne Kirby?

A. Yes.

Q. In fact, you've referenced in court cases his textbook.

A. Yes.

Q. "DNA Fingerprinting: An Introduction"?

A. Yes.

Q. Right?

A. Yes.

Q. And in fact one of the things that you do on quite a regular basis is you say, look, look at - and you compare the Canadian Caucasian population at one locus with particular Canadian Indian tribes, look at the difference.

A. Yes.

Q. You use that as an example of what, Doctor, showing sub-populations, inbreeding substructure?

A. Yes.

Q. Is this Dr. Kirby's book?

A. Yes, it is.

Q. Page 129, is this the particular diagram that you refer to?

A. Yes, it is.

Q. Would you please read at the bottom of - or perhaps I'll read it to you, Doctor, and I don't get into the problem of finding out how well you read.

Page 128 -

THE COURT: Read it a little more slowly because I'm much slower than you lawyers and scientists.

Q. "Small populations, especially isolates, may present a problem in terms of skewed allele frequencies. The statistical power of DNA identity analysis is based on the low probability that different individuals share rare alleles at a number of loci by chance. This is valid for groups such as the non-isolated Canadian population with a low coefficient of inbreeding at 0.00004 to 0.0007." That's even lower, Doctor, than what Nichols and Balding have even testified or written in this particular paper as to what they've seen with respect to the coefficient of inbreeding, am I right?

A. I'm sorry, but the way you read it you lost me, or I got lost.

Q. All right, perhaps I'll let you read it. Pages 128 to 129, it's right under the chart that you keep referring to in the other court cases.

THE COURT: Just hold on a minute and give the witness a chance to read -

MR. WALSH: I was just pointing out, My Lord, where it was.

A. Yes, that's lower than that, but I'm not sure where he's getting his data from.

Q. Well, you didn't have any problem, Doctor, referring to the chart out of that textbook to make your points in other cases. Why are you having problems referring to a few paragraphs underneath the chart?

A. Because the chart is raw data.

Q. I see. I see, so you don't consider -

A. He then goes on to state that there are isolated groups with .02 and .03.

Q. Yes, but not Canadian Caucasian populations.

A. No, of course not, but the difference between these two will result in an F_{ST} that is considerably higher than .00004 or .0007, and I suspect that the allele frequency differences between the two Canadian Indian data bases result in much higher F_{ST}'s

Q. No, no, I didn't ask you anything about that, Doctor. All I wanted to know about the non-isolated Canadian Caucasian population.

A. But, see, I'm suggesting that there is no data about the VNTR's to answer that question.

Q. Well, where do you think Lorne Kirby got these figures, out of the air?

A. I don't know, he doesn't give a citation.

Q. I see, you don't consider Dr. Kirby to be an authority, then, his textbook to be an authority in this particular field?

A. Of course I think it's an authority, but he doesn't give a citation.

Q. You use his book, though, to site particularly the chart out of that book, did you not?

A. Data.

Q. Data, yes, but you consider Dr. Kirby's book to be an authority?

A. To be an authority?

Q. Yes.

A. Yes.

Q. And you also testified this afternoon that you'd be surprised if anyone knew what the coefficient of inbreeding was in the Canadian Caucasian population?

A. I still would be.

Q. You don't think this provides some answer to you?

A. For VNTR's?

Q. This book is on forensic DNA fingerprinting, that's what we're dealing with.

A. Yes, but I think if we read it again it doesn't even make it explicit whether he's talking about VNTR's. I don't think there's enough data yet.

Q. Let me ask you just a simple question and then I'll ask His Lordship for a break. DNA fingerprinting, what particular types of alleles are we looking at?

A. What types of alleles?

Q. Yes, what -

A. Lots of different kinds.

Q. And we're looking at VNTR's, are we not?

A. Not always.

Q. With DNA typing we're not looking at VNTR's?

A. Not always.

Q. In this particular article -

A. Sometimes we're looking at what are called - they're multiple loci rather than single loci. so they're not variable number of tandem repeats, they're repeated throughout the geno, not single locus.

Q. But these highly polymorphic ones -

A. They're still highly polymorphic.

Q. But what we're dealing with here are VNTR's, though, Doctor, are we?

A. Not always. Let me just give you an example. They use a single locus probe, do you remember that one, it's the same in everybody? Guess what the inbreeding coefficient is on that one.

Q. No, I'm talking about - all I wanted to know, Doctor, is whether or not we are looking in this particular forensic application of RFLP typing - whether we're looking at VNTR's, variable number of tandem repeats.

A. That isn't what you asked me, you asked me about the book.

Q. Are we dealing with variable number of tandem repeats when we're dealing with RFLP typing?

A. I can't tell from his quote.

Q. Perhaps I'll let you read it at the break, if you wish. It's up to you. If we could have a break, My Lord?

THE COURT: Perhaps, Mr. Walsh, if you're not going to use some of these exhibits any more they could be got back to the Clerk so that they don't get mixed up.

All right, we'll have a break.

(BRIEF RECESS - RESUMED AT 3:50 p.m.)

(ACCUSED IN DOCK.)

(CROSS-EXAMINATION OF DR. SHIELDS CONTINUES.)

MR. WALSH: Dr. Shields, I caught my wind, so to speak, at break in terms of this -

THE COURT: Not too much, I hope.

MR. WALSH: No, My Lord, I'll be careful.

THE COURT: They get second wind, you know, Doctor.

MR. WALSH: Just on certain points, My Lord. The article that we referred to, the Nichols and Balding, the correction factor, and we've gone on quite extensively with respect to the coefficient of inbreeding and the fact that they've recommended that you use the most extreme ever seen, .05, and you feel based on this background band sharing that you've done that you would - what would be reasonable to you would probably be .005.

A. I'd have to do the real calculations. I think that's a reasonable number to try and see what happens.

Q. O.K., and you said the other aspect that they were looking at, and you kind of overwhelmed me a bit when you were giving me the answer, but it was something with respect to - I understand, Doctor, the other aspect that they were trying to correct for is the problems with respect to the fact that these are continuous allelic distributions as opposed to discrete allele systems?

A. It's actually because it's not quite continuous that they're trying to correct. It's because there's a - you'd probably call it a contagion of sizes, that if

you have a given size of allele you're more likely to have alleles around it in size than you are further from it in size.

Q. The fixed bin method, what if any effect would that have on that particular aspect that Nichols and Balding is also suggesting that you try and correct for?

A. It would depend on the size of the fixed bin relative to the matching window.

Q. You would agree with me, though, Doctor, that the fixed bin approach would have some bearing on ameliorating the problem that Nichols and Balding is suggesting we should try and correct for?

A. If the fixed bin was large enough relative to the matching window.

Q. O.K., and if in fact that was the case, then the only thing that you would have to take into consideration in their correction factor would be the coefficient of inbreeding, am I right?

A. The way you've stated it I would say probably that you're right. I would have to think about it more to give you an absolute definite answer.

Q. And if I am right in that suggestion that would mean that based on what you consider to be reasonable the bin - the locus, the frequencies for the probes that have been generated by the R.C.M.P., and if you used .005 which you consider to be a reasonable coefficient of inbreeding, and you applied the Nichols and Balding correction factor you would in fact have probed frequencies that were very, very similar?

A. It's easier to just use their recommended correction factor.

Q. Yes, but - that's right, just the .05, but if in fact the fixed bin approach, the binning, did ameliorate some of those problems you wouldn't have to go as high, would you?

A. It depends on the size of the bin. Let me just show you and I'll do the best I can to tell you the way I think about it. The way that the bins currently exist both for the R.C.M.P., and I'm more familiar with the FBI so I can say definitely for the FBI, they range from about 6% to around 11% base pairs in size. If you use a matching rule of 5.2%, then actually you need a bin of 10%, 10.4%, to be precise. If you're going to count all of the alleles that could during a second or third measurement contribute an evidence bent, because it could go 5.4% in one direction from a particular band and 5.4% in the other. Given that the matching window used by the R.C.M.P. is 5.2%, all of their bins are in essence no more than legitimate with respect to their matching window. They're not really bigger, in my opinion, O.K., and if they're not bigger they don't correct for what you're talking about.

Q. But assume for a moment that the bins are larger, assume that the bins are larger than the match window.

A. O.K.

Q. Then you would agree, Doctor, that it would correct?

A. It would correct some but not entirely. As they point out in the paper and state very explicitly, it is not just within the same bin, it's also further distant. That correlation that they observe in Balazs et al's data that they demonstrate in that

graph goes beyond bin boundaries when you're looking at, for example, the FBI bins, so it would partially correct for it but not entirely.

Q. O.K., so assuming that it partially corrects for it, then, Doctor, we could actually use a lower coefficient of inbreeding to do our calculations, could we not?

A. Yes, we could. We could, or we could turn it around and say let's do an actual match window frequency and count the number of alleles in a data base that are plus or minus 5.2% from a particular allele in question and use that frequency and use the .05 correction factor. Either of those would be - .005, you keep on wanting to use that, but let me just tell you why I'm hesitant, and I don't think - I'm not trying to naysay you. It has to do with the fact that there's sufficient band sharing from looking at all of the data that I don't think .005 is right any more than I think .05 represents the true inbreeding coefficient. I think it's going to be somewhere in between if we were to just think about the true inbreeding coefficient.

Q. Do you mean, Doctor, if you're just talking about true coefficient of inbreeding that you would -

A. I should - let's be more precise because I'm not talking simply about any inbreeding coefficient. What I'm talking about is F_{ST}, which is the correlation between gametes within a sub-population relative to the correlation between gametes across sub-populations.

Q. O.K., but what you're suggesting is probably somewhere between .005 and .05?

A. Yes.

Q. O.K.

A. Given the amount of band sharing that we see.

Q. So what you're suggesting, Doctor, is that in what you've seen in the area in which you've looked at the samples from the area in which those samples come you believe that the coefficient of inbreeding is higher than has been ever seen in Europe?

A. No, you didn't listen, I guess. I said between .005 and .05. That's less than .05.

Q. .05 is the most extreme case ever seen, am I right?

A. Yes.

Q. .005 is the largest values found in Europe?

A. Not really, if you look at the Ashkenazy Jews it's higher for them. There's a lot of groups in Europe that are higher than .005. It's explicitly higher than those found in European well-mixed populations in cities.

Q. Oh, I'm just reading what Nichols - you've relied on Nichols and Balding, Doctor, and Nichols and Balding have said that, "Cavalli-Sforza and Bodmer surveyed the literature in which these techniques have been used. The most extreme cases were correlations of 5 per cent", and you've told us that means .05?

A. .05.

Q. "These correspond to severe inbreeding, such as that associated with a tradition of uncle-niece marriages. The largest values found in Europe were an order of magnitude smaller", and I understood from you that that would be .005.

A. It also could be .009, it could also be anything .00, so I mean it will vary around .005.

Q. "And more recent surveys show dramatic reductions associated with increased mobility due to modern transport. More typically, values are another order of magnitude smaller", and I had understood from before the break that that would take us right down to .0005?

A. Right.

Q. "Hence the value 5 per cent appears to be very conservative for any large population and smaller values would be appropriate in cases where extreme inbreeding is known not to occur." Now, simply, Doctor, I was trying to determine - you're suggesting that perhaps if we use a coefficient higher than .005 but lower than .05, so you're actually suggestin that we use a coefficient higher than ever seen in Europe but lower than ever seen in the world, is that right?

A. Yes.

Q. Because you believe that the sample population from which these individuals come, that you've looked at -

A. The numbers tell us that.

Q. O.K., based on the numbers, this background band sharing that you applied, that tells you that the coefficient of inbreeding is as high or higher than has ever been seen in Europe? You're nodding your head, for the record, yes?

A. That's correct.

Q. O.K., thank you, Doctor, we'll move on. Now, with respect to inbreeding, this aspect, my understanding from the testimony over the last weeks or so is that one of the indicators of inbreeding is excess homozygosity, would that be an indicator of inbreeding

A. The presence of excess homozygosity can mean increased inbreeding. It can also mean selection for the particular allele in question. The absence of an excess of homozygosity can mean an absence of inbreeding and it can also mean selection, so there are multiple factors that cause chain frequency differences, so you can't say -

Q. But one indicator, one small indicator of absence of inbreeding, would be an absence of excess homozygosity?

A. That's correct.

Q. O.K. Humour me again, Doctor, but when you looked at Mr. Legere's alleles did you see any homozygosity or any excess of homozygosity?

A. You can't really test a single individual for that. I mean, there were homozygotes in that data but I don't know whether there are as many as you'd expect or not expect.

Q. Because he's only one person?

A. Right.

Q. Doctor, isn't it a fact -

A. I do know that it's been reported, for example, that Dr. Carmody has examined the big data base and found no evidence for excess homozygosity, but I also know that the R.C.M.P. in one of their papers reports an excess of homozygosity all of the loci.

Q. But we won't get into that argument. That's part of the Devlin & Risch aspect, is it not, Doctor, that paper that Devlin & Risch put out with respect to -

A. No, no, I'm talking about the R.C.M.P., I'm talking about Waye.

Q. No, I appreciate that, but what I'm saying, Doctor,

is I just want to know whether or not you saw any homozygotes in Legere's alleles?

A. I don't remember but I don't think so.

Q. O.K.

A. I think, if I remember correctly, it was either Donna or Linda was homozygous, and I think maybe Murphy was.

Q. But the populations, at least those samples, are too small to actually give you any idea of whether there's any excess of homozygosity?

A. That's correct.

Q. And isn't it in fact true, Doctor, that the sample that you're referring to for this background band sharing is, to use the words of Dr. Carmody, pathetically small?

A. I don't know what he meant by pathetically. It's small.

Q. Can you make any statistically valid conclusions from such a small sample?

A. I really don't want to do this to you but you better hope you can because that's what you do when you develop the probabilities for forensic analysis.

Q. No, but you're dealing with a sample population of how large that you did your background band sharing on? How many people, Doctor?

A. What are you talking about?

Q. How many people did you look at to develop your theory or to substantiate this background band sharing? How many people did you look at?

A. Murphy, Legere, Donna, Linda, and Nina - five.

Q. And do you think a sample population of five is equivalent to the sample population of the R.C.M.P. Caucasian data base?

A. You're missing what I did. All I did was take the R.C.M.P.'s frequencies, use their logic, and generate probabilities that you'd get four bands to match.

Q. But you have actually taken, though, Doctor, five individuals from that particular area, and based on those five individuals you've extrapolated a theory, and the theory is this high coefficient of inbreeding am I right?

A. The probability that results when you ask what's the likelihood that you'd get this by chance in a small population, in a sample size of the size that we're looking at, is one in trillions. That says that it's probably an incorrect assumption to assume that the R.C.M.P. frequencies are truly representativ of the population from which the five individuals are drawn. Let me finish because I'll explain to you what the problem is. If you have a very, very large sample you can get statistical differences quite easily. When you have a very, very small sample, and that shows the kind of pattern we're talking about, all of the individuals share bands, that's less likely. Only if you were to have that small sample thousands and thousands and thousands of times, and it only showed up once with a lot of band sharing, would you be correct in assuming that because it was a small sample you got a statistical glitch. The fact that it happens with a small sample, and it's true of all five individuals, is to me good evidence for band sharing, not bad.

Q. Well, let me approach it from a different fashion. Doctor, if you tested an individual across multiple

loci and all his alleles were rare compared to, for example, the R.C.M.P. Caucasian data base, what would that indicate to you?

A. That he's a statistically unlikely person.

Q. No, no. but if the alleles are all rare and compared to the bin frequencies of the Caucasian data base of the R.C.M.P., would that give you some concern that perhaps he doesn't reflect the data base, that the data base really doesn't accurately reflect this particular individual?

A. It might if there were other sorts of evidence that implied that he might be from a different race or a different sub-population of the Caucasian race. That might enter my mind, yes.

Q. Yes, that if in fact you looked at an individual - say you looked at me and you found that all my alleles were rare, and as you compared them to this R.C.M.P. Caucasian data base as it presently exists one of the things that would come to your mind is, hey, this person may belong to a sub-population because in fact they have skewed allele frequencies, if I use the term properly.

A. Relative to what?

Q. Relative to your Caucasian data base. Right?

A. Sure.

Q. What if the reverse were true, if all my alleles were common compared to the representative data base?

A. So they all came from bins with high frequencies is what you're saying?

Q. Yes.

A. O.K., what about it?

Q. That is the converse of having rare ones. What would that indicate to you, what is one of the things that

would indicate to you?

A. That is statistically as unlikely as the reverse. That person would not be a good representative of that - or that data base would not represent that person very well either because it should, if it is a representative data base, be random whether that individual is carrying rare or common alleles. If they're carrying all common alleles that makes them different, from a different population, and if they're carrying all rare alleles, that makes them from a different population.

Q. The common alleles, though, Doctor, if my alleles were common and I compared them to a data base and I reflect common alleles in this data base, would it not also indicate, Doctor, that the person that you've tested is a profile of your Caucasian population, is a profile of the people in that particular population?

A. No, let me just show you what I'm getting at. Let's say there's 28 bins, O.K.? Let's say that the high frequency bin is .292, which it is for D17S79, .292, O.K.? That means that 30% of the people will be carrying that particular allele. If an individual has that allele and has the high frequency alleles from all of the bins, all the way through, that person is as rare an event, if you will, because you can multiply it through and find out how rare, as an individual carrying only low frequency alleles. In one case what I would say is that the data base is biased for such a defendant, that they may be from a sub-population with allele frequencies that are lower, and in the other case it's biased against the defendant, if they have all rare.

Q. So if they were common it would be biased in favour of the defendant, is that right?

A. I might reach that as a tentative hypothesis.

Q. And that any gene frequencies or allele bin frequencies that are being generated or profiles that are generated would be over-compensating? It would be a very conservative number in relation to what a true frequency is?

A. It could be. It would depend. But in any case, I mean, to get back to the issue at hand, the question isn't here whether you have one, and that's the key to it, here you have five different individuals that share bands. It's not that they are either rare or common with respect to the data base, it's that they are common with respect to each other, and it's not all of the same loci. If it was only common loci, then maybe, sure.

Q. So this Nichols and Balding factor won't correct for that - it will correct for that problem, won't it? Nichols and Balding, the correction factor will correct for this coefficient of inbreeding that you say is evidenced by this background band sharing?

A. I have a suspicion that if we were to do the probabilities the exact way, it would be different from the way I presented it earlier but I can do it very quickly, that they'd be very, very, very similar, so let me just do that and find out.

Q. Similar to what? No, hold it.

A. The Nichols and Balding probabilities would be very similar to the background band sharing probabilities by themselves.

Q. No, no, what I want to know, Doctor, is the - I don't want to know that question. I want to know about how the Nichols and Balding correction factor, if you used what you say is reasonable, .005 -

A. No, .05.

Q. No, no, but you want to keep using .05 and I want to use .005. You've already used .05. Haven't you?

A. Yes.

Q. O.K., and if we use .005, what you said earlier today would be reasonable, a reasonable figure in relation to what you saw with background band sharing -

A. I also stated that I would rather do the analysis to find out how close or far from that it is, but I mean I said, I admitted it, I said that's a reasonable number, but I don't think it's an exact number. If you let me do this calculation I can tell you.

Q. Go ahead, Doctor, we'll do the calculation.,

A. The background band sharing is 3.3 out of 12, which is .275, Y to the 10th power. One in 404,271. If you're looking at single locus, homozygous potential matches, so for five loci it would be one in 404,271, using the simple 3.3 band share per individual in this population. That's a lot closer to the one in 212,000 or whatever it was exactly, I don't remember, than it is to the one in 5.2 million.

Q. Let me ask you about that again. Let's use your .05 that you used. Doctor, I'm not quite sure of the exhibit number there -

THE COURT: 137 or 121?

MR. WALSH: I think it's probably 121, My Lord.

THE COURT: The comparison of match probabilities?

MR. WALSH: Yes.

THE COURT: That's 121.

MR. WALSH: Even doing that, Doctor, using .05, the highest inbreeding coefficient ever seen in the world, what is across a 5-locus match?

A. One in 5.9 million.

Q. Do you think one in 5.9 million tells you anything about the rarity of the alleles?

A. No, it tells you did it across five loci but that's another story.

Q. Do you consider that to be a low number, one in 5.9 million?

A. Yes, it's a small number.

Q. And if someone was to suggest to you, Doctor, that the probability of finding a match between two sources of a forensic specimen was one in 5.9 million, what would that say to you?

A. What would that say to me?

Q. Yes, what would be the qualitative statement you could associate with that?

A. Maybe you could ask it as a question, I'm not sure.

Q. Well, I'm kind of a simplistic-type person. One in 5.9 million, would you consider that to be common, rare? Would you consider that to be almost proof of the same source, that the two forensic samples came from the same source?

A. No, I would consider it rare, exceedingly rare.

Q. And so even using this .05 correction or correlation factor, the F factor, F statistic, even using that you would arrive at a figure in relation to Mr. Legere

his case, as it compares with source 135, and you come to the conclusion that it's a very or exceecingly rare match; am I right?

A. Without developing any probabilities whatsoever I would have said that. O.K.?

Q. Now, did you make any inquiries, Doctor - I know in Bourguignon you were dealing with an extended family and you're not really dealing with that situation here, are you?

A. What I was told is that two of the victims were sisters.

Q. I see, but in relation to the accused, one of the accused in Bourguignon was part of - the accused and the victim, same family?

A. Same family, and other people that were suspected of the crime.

Q. Cousins and uncles and brothers, you had to take all that into consideration?

A. Yes, that's correct.

Q. Is that a concern of you here with respect to the accused?

A. I have not been told it should be.

Q. So you have no evidence that he has any brothers or twins or anything of that particular nature?

A. That's correct.

Q. But if in fact there was a twin or a brother you would certainly want to know that, that would be important information for you?

A. It would change the probabilities enormously.

Q. And in fact if there was any close relatives, male close relatives, you would want to know that, that would be an important consideration?

A. Yes.

Q. And at this point in time you haven't been told anything of that particular nature, have you?

A. No, I have not.

Q. Thank you. Doctor, I won't play a game of guess where this came from, I'll tell you where it came from. It came from the Streich case. That's a case in Vermont that you were involved in?

A. That's correct.

Q. O.K., and the judge in there at Page 27 attributes a statement to you that, "The FBI's binning procedures generally favour the defendant because the FBI's calculations are based on bin frequencies which are higher than the actual allele frequencies, thereby increasing the probability of a coincidental match". Is that a correct interpretation of the statement you made?

A. That's correct.

Q. And since the FBI and the R.C.M.P. have the same binning procedure, or essentially the same binning procedure, you would also - that statement would apply to the R.C.M.P.'s binning method?

A. I would have to therefore put all of the statements that went around that before I would be willing to have it on the record here, and the statements are very simple. They are conservative relative to other possible ways of developing these probabilities but they are less conservative than in other, O.K., so what I was doing was talking about the relative conservatism.

Q. O.K., apart from the relative conservatism, you have not said in there that it underestimates the frequencies? You don't believe the fixed bin method

underestimates the true frequencies, do you?

A. Yes, I do.

Q. Oh, you do?

A. And I have testified to that.

Q. Well, why did you make the statement that the FBI's generally favour the defendant?

A. Because they were talking about real alleles. What the prosecutor there was has asked me a very simple statement. If we could sequence these genes. knowing what you know about VNTR's, there can be as little as a nine base pair difference in one of these probes and as much as 38 base pair differences, and they are good alleles and you cannot see them on a gel, you cannot tell they're different alleles, but if we could sequence them we would know they were different alleles. Therefore the allele frequencies, the true allele frequencies, if we could get this to be a discrete allele system rather than a quasi-continuous, are such that we could - you'd know that the probabilities, the frequencies of real alleles, were always less than a bin. Under those circumstances, absolutely true, but that's apples and oranges.

Q. But to get to the crux of what we're dealing with here, it's your opinion, Doctor, that the fixed bin method that's been developed by the R.C.M.P. and FBI for forensic use will underestimate true frequencies?

A. Can underestimate true frequencies. Does underestimate true frequencies under two sets of conditions, when there's sufficient substructure, and when alleles for whatever reason bunch up at bin

boundaries.

Q. O.K., and did you see any allele bunching up at bin boundaries in this particular case?

A. The only analysis I've done, it's a long drawn out thing, and this is not what I do for my own research, but I did an analysis of the D17S79, raw data provided by the FBI, and found that there was some bunching up at boundaries such that if you did the analysis you could end up with frequencies that were bigger by actually counting rather than simply taking the biggest bin.

Q. But you haven't done it in this particular case?

A. No, I have not. I don't have the raw data.

Q. Assuming for a moment, Doctor, that we can discount the possibility of bunching of alleles at the bin boundaries of having an effect on underestimating the true frequency, then the only other concern, Doctor, would be substructuring and the effect substructuring would have on the true frequencies and how much binning would compensate for that; am I correct?

A. That's correct.

Q. But you agree that binning is an attempt to compensate somewhat for substructure?

A. I have read over and over again that that's part of the rationale for doing it. I think in my own personal opinion that the bins are a little smaller than would be necessary to do that because of the size of the match windows.

Q. But you would agree that it is an attempt to do that, that is what they're trying to do?

A. Yes, absolutely.

Q. And so your main concern comes down to - if we can discount the possibility of any evidence of bin crowding or boundary crowding we come down to the whole question of substructure, am I right?

A. That's correct.

Q. And it's not so much whether or not substructure exists, but its effect, the extent of it and how it affects these particular frequencies; am I right?

A. Now apparently everybody is agreeing that that's the question, how much substructure exists and whether it affects the frequencies. Until fairly recently there was some question as to whether it existed.

Q. Assuming, Doctor, that there is no substructure affecting the VNTR frequencies and assuming Hardy-Weinberg equilibrium and physical and statistical linkage equilibrium, O.K., those are assumptions I wish you to make and I realize you probably say they're big assumptions, but just assuming, would you agree that obtaining allele frequencies, bin frequencies, by the fixed bin method using the Hardy-Weinberg, then using the Hardy-Weinberg equation to determine probe frequencies, and the product rule to determine overall genotype frequencies would be a generally accepted method of calculation in the scientific community and/or reasonably reliable method of calculation?

A. With one small caveat, yes, the small caveat being that even if you have linkage equilibrium or you can't demonstrate that it doesn't exist and even if you have Hardy-Weinberg equilibrium and you can't statistically demonstrate that disequilibrium exists, there is still the potential that there is sufficient substructure that will not show up in that form so

that the final thing that I would like to see is moderate size samples of appropriate ethnic groups to indicate the degree of substructure directly rather than through the intermediates of the statistics, but all of those things - if you did all of those things, yes, I would agree that that methodology would be scientifically acceptable and reliable.

Q. In essence, satisfied ourselves with respect to the existence of substructure and its extent and its effect on frequencies?

A. Yes.

Q. And if we could satisfy ourselves on that you would agree, with the caveats, but if we could satisfy ourselves with respect to the issues of substructuring if for example His Lordship was to be satisfied that substructuring has been explained to him and the effect has been explained to him to a sufficient degree that he is confident that it doesn't underestimate the true frequencies, you would then agree, Doctor, that the application of the fixed bin method, the Hardy-Weinberg equation, and the product rule would be a valid method of calculation for forensic purposes?

A. I apologize to His Lordship but you asked me a different question. I understand he's got to make the legal decision but we make the scientific decision, and I would be satisfied if all of those things were demonstrated to see it used, but I don't know whether I would be satisfied with the explanations that you just pointed out, so -

Q. Oh, no, no, assuming that the explanations satisfied

you, that's what I want.

A. Then, yes.

Q. So assume for a moment that the explanation satisfied His Lordship, you would agree that that would be an acceptable method of calculation for forensic purposes?

A. It's a strange question.

Q. I don't want to trick you, Doctor, I was just trying to get down to the - we're winding down and I just want to find out what the common denominators are here.

A. If you can demonstrate to the people like myself, and there are others, who feel that substructure is a potential problem in this, that substructure does not have a major impact, O.K., I think we would agree. The question is going to be as a scientist I choose personally, and I did read these pieces of the testimony, to disagree with Doctors Carmody and Kidd that differences of one in a million to one in ten million are not important. I don't find that difference to be what I would call scientifically acceptable, even in forensic practice.

Q. O.K., let's go to that, then, Doctor. You filed an affidavit in Vandebogart which has been entered in evidence here, and the purpose of the affidavit was to show the court there why you should be allowed to get back on the stand to refute some of the testimony of Dr. Budowle; is that right?

A. Mm-hmm.

Q. Correct me if I'm wrong, but part of what you did was to actually take the data from the Legere case and run it through the FBI composite Caucasian data

base which you've termed C3? Am I right?

A. That's correct.

Q. And you come up with, instead of 5.2 million on a match, this particular match 1J, with 56A, 69A - instead of 5.2 million that the R.C.M.P. come up with you come up with 9.6 million?

A. That's correct.

Q. Under the FBI, and you're suggesting - so from the FBI's point of view the probabilities are even lower - lower?

A. Smaller.

Q. Smaller, that you would expect to find the same pattern, am I right, and you're suggesting as well, Doctor, that the difference between - from a statistically significant point of view with these high powers, the difference between 5.2 million and 9.6 million is statistically significantly different?

A. No, I'm suggesting that it's scientifically different that it allows one to make different judgments, O.K., that one would be inclined to conclude that it's a better piece of evidence if the probability is 1.96 million, one in 9.6 million, than if it was one in 5.2 million. That's all.

Q. But you find that there is a statistical -

A. And if it's not, then I would just suggest that we always - and I think now that's now becoming always suggested, that we always take the upper confidence limit on any of these and report that, always report the biggest probability.

Q. O.K., but confidence intervals, O.K., you don't agree then, Doctor, that there's any - let me put it this way, you do not agree that there is no statistically

significant difference between 5.2 million and 9.6 million?

A. Depends on the sample size.

Q. The sample size, you know the sample size.

A. I would have to do the calculations. I think -

Q. They differ by a factor of two, don't they, Doctor, 5.2 and 9.6?

A. Little less than two.

Q. Well, considering the sample sizes of the R.C.M.P. and FBI Caucasian data, you run the data through it, do you consider that to be a statistically significan difference?

A. I suspect if you run the statistics it's not statistically significant.

Q. So, Doctor, why didn't you say that in your affidavit that you filed in the Vandebogart case?

A. Because I don't think that that's what's important. The fact that these vary as much as they do, and that's what goes to a jury, I think is more critical.

Q. Well, what if we applied confidence intervals? Doesn't the confidence intervals allow anyone - we won't talk about a jury, but anyone, to look at the variation of range?

A. Yes.

Q. It's really a scale, is it not, Doctor, to weigh the probabilities?

A. Yes, there are a number of people who've suggested for a long time using upper confidence limits.

Q. And in fact, Doctor, you use confidence intervals yourself in your own work?

A. Yes, I do.

Q. I read somewhere in one of your studies on insects

or one particular form of insects that you actually use confidence intervals when you're publishing your data to show your -

A. What the allele frequencies are.

Q. Yes, the variance.

A. Yes, I agree.

Q. You know that the small sizes that you're dealing with you can't give an exact frequency, you have to give a range of frequency around that? It could be lower than or higher than, am I right?

A. Mm-hmm.

Q. So in this particular case with a 99% confidence interval, that is a pretty good scale to judge how much weight to place on the particular number?

A. That depends strictly on sample size and how well the sample represents the population of interest. You can also put a confidence limit around the one in 226,000, O.K., that's right next to the 5.2 and the 9.6 million.

Q. But I'm dealing with simply the 5.2 million and the 9.6 million that you put down in that affidavit that you swore to.

A. I think I talked about Nichols and Balding in that affidavit.

Q. No, I don't think so.

A. No, I didn't, because the paper hadn't come out yet, you're right.

Q. So you referred to 9.6 million and 5.2 million, right?

A. You're right.

Q. And you actually pointed out in that affidavit that that was, as far as you were concerned, a difference, a big difference?

A. Yes.

Q. But you will say here today that it's not a statistically significant difference?

A. No, I think it's a big difference and it's not statistically significant.

Q. O.K., it's not statistically significant?

A. Right.

Q. Differing by a factor of two at that high power?

A. Right. Unless we were talking about really, really big samples of both, and in fact, if we were talking about big enough samples of both it would be statistically significant.

Q. Yes, but you know the sample sizes you were dealing, you run them through the computer?

A. Yes, but they're still small, so they have big confidence limits.

Q. And which the observer can look and see what the variance is and let them weigh it, is that right? You would agree, Doctor, that perhaps giving the jury, for example, confidence intervals around whatever frequencies are generated would be one way of giving the jury a means of getting a feel for the sample size -

A. If it was around an appropriately conservative estimate, absolutely.

Q. And if you applied the 99% confidence intervals to the calculations you did when you run Legere's through the FBI and you compared it with what was run through the R.C.M.P., it shows that there really isn't any difference, is there, Doctor?

A. No, it does show there's a difference. In fact, if you want to give me Dr. Carmody's little thing I'll

show you the difference.

Q. But I'm talking about 99% confidence intervals around that particular difference.

A. Let me explain to you what confidence intervals are and you'll -

Q. Sure, VD-65, Doctor.

A. Mm-hmm. Well, we only have one confidence limit so I can't do what I was going to do. If you took a confidence limit around 1.52 million, which he does, and you have 1.3 million to one in 17, O.K. -

Q. How many standard deviations would that be?

A. Standard deviations isn't appropriate when you're talking frequencies.

Q. It isn't?

A. No, in essence it's going to be - if you were talking about distributions of measurements it would be the equivalent of about two.

Q. O.K., continue.

A. Well, if it's 99 it's going to be the equivalent of about 2.68, if I remember right.

Q. And if I told you it was three standard deviations?

A. Then it would be 99.7%, but now, what I'm talking about is this ranges from 1.31 million to one in 17 million. It says that 99.7% of the time the true value will go somewhere between one in 3.1 million and one in 17 million. If you did the same thing with the FBI's it would be in the neighbourhood of one in - oh, probably, looking at this, I would say one in four million, maybe one in five million to one in 25 million, and the point I would make there is that even though they overlap there are values that the FBI's could take that do not exist for the R.C.M.P., and vice-versa.

Q. But you would agree with me, Doctor, either way those are very, very rare patterns? The numbers that are reflected there would reflect very rare patterns, would it not?

A. The numbers that are reflected there, absolutely.

Q. Thank you, Doctor. The higher the data base, the more people you have in the data base, the more precise your figures become, the smaller the confidence intervals will go around that figure, am I right?

A. Yes.

Q. You said something in that Vandebogart affidavit that I was just curious about. You looked at the C3 data base, and I'm aware of the problem that you had in actually interpreting the C3 data base because of the cell lines that were in there, but when you did look at it after taking out the cell lines you found that the FBI data base was flawed by measurement error or maybe I'm - perhaps you should look at the affidavit. Bit Quizzical there, I don't want to misquote you. Would you look at Page 4 of that particular affidavit, which is Exhibit 136, and I'm looking at the top paragraph. Would you read me what you say there, Doctor, and we'll have it in the right context? It's very short, I won't -

A. The whole paragraph?

Q. Yes, please, if you wouldn't mind.

A. So you want me to go back here? You want me to start at the page before or just there?

Q. Perhaps -

A. "For example, the frequencies at D4S139 remain stable (Fig. 2) while the changes at the rest are

much larger and statistically significant for three of the loci (Figs. 3 and 4). The flip-flop between bins 5 and 6 for locus D17S79 still exists (Fig. 4) and shows that many individuals were probably near bin boundaries. At the same time the large changes in adjacent bins, 13 and 14 and D2S44, (Fig. 4), cannot be explained as simple movement between adjacent bins. This is especially true since there are no new individuals in the C3 data base as I originally was led to believe so that the observed variation must result from measurement error due to problems with the molecular techniques or protocol and not simply allele sampling error as I originally had believed. The bottom line is that the FBI does appear to have a reproduceability problem which cannot be addressed by noting that different rulers were used between the C2 and the C3 rerun data bases.

Q. Now, correct me if I'm wrong, my understanding is what you were saying is when the new Caucasian data base, when they rerun, and you've assigned it C3 as opposed to C2, but the - O.K., go ahead.

A. No, it's a rerun of the C2. The C3 is a totally different data base, but I originally called their rerun of the C2, C3. That's why the numbers appear two different ways.

Q. O.K., now, what data base did you compare to -

A. The R.C.M.P.?

Q. The R.C.M.P. one.

A. Their full C3 data base.

Q. O.K.. and are you suggesting that there's problems with that? Is that what you're saying there, that there's problems with that C3 data base, that the

bottom line is that the FBI does appear to have a reproduceability problem which cannot be addressed by -

A. No, it's the different C3. Part of the data base in the composite that I used for the comparison, the FBI agents, the one that's marked FBI, was a rerun of their original FBI agents data. Some individuals moved more than one bin, some individuals that were heterozygous became homozygous, some that were homozygous became heterozygous during the rerun, so there were some molecular problems. They are convinced, and I just accept that notion, that the second run was the best molecular technique. That's what they include in their C3 data base and that's what I used to compare to the R.C.M.P.

Q. Were you of the opinion then that the FBI Caucasian data base that you used to compare - was any part of it flawed by the manner in which the -

A. Depends on how you define flawed.

Q. Well, just the basis - the way you've said it here in this particular affidavit.

A. The way I said it in the affidavit - well, what I was implying, what I would still imply, what I would conclude, is that something happened between their first run of the FBI agents and their second run of the FBI agents in terms of the molecular protocol that allowed for the large changes. When you rerun the same individuals twice you shouldn't get changes in frequencies except via measurement error, and initially that's what I thought had happened, but obviously they had some individuals that were mild screw-ups, either the first time they ran them or

the second time.

Q. I see, so you're not concerned here, Doctor, with when you compared it to the R.C.M.P. data base, the FBI Caucasian data base - you're not concerned that the FBI Caucasian data base was somehow flawed so that it wouldn't be a true comparison between the two, would you?

A. I don't know whether you're ever going to have true comparisons between any of them. They say it's not flawed, it's what they use in case work. It's what they use to compare to Texas. They added the Texans, they added the California data base, they added two Texan data bases, in fact, and Florida, and that's their C3 data base, that's what they use in case work, I presume. We all think that it's at least sufficiently robust that it is the probabilities that - tney're going to use it to define probabilities in the States, that's why I compared it to the R.C.M.P.

Q. Being a valid comparison, in your opinion?

A. It's valid in terms of frequencies, yes.

Q. Doctor, would you take that affidavit for me, please, and just flip to the front cover? What's the exhibit number?

A. 136, VD-136.

Q. And this morning you did a part of a slide presentation and you actually refered to the comparisons that you made between the R.C.M.P. and FBI Caucasian data base.

A. Right.

Q. And in fact in that affidavit you attached many of the same charts that you have entered here as

VD-120, 119, 118, etc.?

A. Mm-hmm.

Q. Those were attached to your affidavit, am I correct?

A. That's correct.

Q. And in fact you've also made reference in there to the comparison between the black populations, same references that you made this morning?

A. With the addition of Acton's data from his paper with Budowle et al.

Q. But that was all part of this affidavit that you filed, am I right?

A. Not the part about Acton. That was the black data base from the FBI that I refer to in here.

Q. O.K., but apart from that, that information was all contained in that particular affidavit?

A. That's correct.

Q. What - the presentation that you made this morning, part of the presentation?

A. The R.C.M.P. was, not the look at the Kidd data, not the examination of - I'm trying to remember, do I have the -

Q. Perhaps if you could just go through, Doctor, please, and tell us what's attached to your affidavit I'd just like to know what was in your affidavit, what Dr. Carmody and Dr. Kidd would have seen when they commented on your affidavit.

A. O.K., the only thing in here that's essentially the same is the FBI versus the R.C.M.P.

Q. That comparison?

A. Yes, the new - I mean the new comparison of the Caucasian data base from the FBI, the Texas versus - that's new, that wasn't in here. The Acton data

wasn't in here. I think that's all I - and the graphs of Kidd's data were not in here.

Q. You were aware, of course, that Dr. Carmody agreed with your conclusions in terms of your comparison between the R.C.M.P. and the FBI in terms of the figures that you actually obtained?

A. Yes.

Q. You were aware of that. You were aware of also the fact that Dr. Carmody compared the R.C.M.P. data base with the FBI with Dade County in Florida, with Texas and with Minnesota? You were aware of those comparisons that he's made?

A. Depends on how you define aware. I guess I'm not. I was told that he made other comparisons but I haven't seen it.

Q. Look at VD-65, Doctor.

A. Yes, O.K., Florida, Minnesota, France.

Q. Now, apart from France, the two loci in France, do you think, Doctor, that there is any forensically significant difference in those frequencies?

A. Sure.

Q. When they multiply out across loci?

A. Sure. Just looking at one real quick, I think I would much rather be in Florida if I were Mr. Legere no, the other way around, I would much rather not be in Florida if I was Mr. Legere.

Q. Yes, but the question, Doctor, is with respect to all those, they all demonstrate rare patterns, do they not? They all represent relative rareness of VNTR patterns?

A. Whenever you're dealing with VNTR's you're going to be talking about rare. Even the commonest alleles, with the exception of the monomorphic alleles, occur

at very low frequencies. I mean once you get rid of D16, which everybody is doing, you're talking about 3.3 as being the highest frequency you're going to find.

Q. I just want to get this clarified, both Dr. Carmody and Dr. Kidd recognize statistical - significant statistical differences in certain bin frequencies when you make comparisons?

A. Right.

Q. But they also testified with respect to the fact that when you multiply them across the loci there is no forensic differences. I take it, Doctor, that you don't recognize that concept?

A. Can I put myself in the middle by reading what Dan Hartl says about that?

Q. No, I'd just like to know what you say about that.

A. I personally do think there's a difference, you know I do. I think that, God forbid I should be sitting somewhere else in a court room, I would rather it be accurate going in, getting closer to what's accurate and conservative, as conservative as is humanly possible. If there's any chance of error, err on the side of the defendant, that's my personal opinion.

Q. And if, for example, the estimate was correct. 99.7% confidence intervals around this particular estimate

A. I'd be happy using the upper confidence.

Q. If you had someone look at that and weigh it based on those 99% confidence intervals, is that correct?

A. Yes.

Q. O.K. Doctor, now, correct me if I'm wrong. My understanding of your testimony when it relates to

sub-populations and inbreeding and substructure is that - I wrote down here this morning - you're not comfortable with whether they are reliable or accurate enough, meaning the frequencies that are reported?

A. Right.

Q. That you need more data to determine the extent of substructure, am I right?

A. That's correct.

Q. So I take it, Doctor, you do not believe there is sufficient knowledge yet with respect to VNTR frequencies in Caucasian populations to justify extrapolating the figures in the manner in which it's done, is that correct?

A. In the manner in which it's done I do not believe there is enough data yet.

Q. There's not enough data yet, O.K. You're not saying that it could never be done, you just don't believe there's enough data at this time?

A. That's correct.

Q. So therefore it follows, Doctor, that Dr. Kidd, Dr. Carmody, Dr. Waye, their opinions as to the validity of the figures generated could very well be the correct opinion?

A. You're right.

Q. Therefore, Doctor, the probability of a coincidental match between the semen of the vaginal swabs of Nina Flam and the known standard of the accused could very well be a best estimate frequency of one in 5.2 million male Caucasians, no higher than one in 3.1 million or lower than one in 17 million with 99% confidence limits?

A. If all of the assumptions used to generate that frequency were correct, I would agree, but I believe there's evidence that suggests it's not correct.

Q. No, but what you've indicated, Doctor, is that you believe there's a need for more data before you can actually conclude those?

A. But there are data in this case that tell me that it's not correct, and that's the band sharing.

Q. The band sharing, and you -

A. And the fact that French are different.

Q. O.K., so if we go back to Nichols and Balding and their correction factor and if we did - if we used the lower coefficient of inbreeding than .05 and if we assume that the fixed bin method ameliorates some of the other problems you could, using the Nichols and Balding correction factor, approximate the same frequencies that are now generated by the R.C.M.P. data base?

A. I don't know whether you would or wouldn't. We'd have to do them.

Q. You've seen some of the figures that were generated?

A. Yes, if you used .005, and I've already suggested I don't think that's - you want to know what I think? I'll tell you what I would do. I would take the band sharing which gives a probability for that particular 4-locus match of one in 404,000 and do a 99.7% confidence limit around that. That would be, to my way of thinking, sufficiently conservative.

Q. So do you want to change your opinion now, Doctor, and my understanding was before I started the question was that you didn't believe that there was

sufficient knowledge yet with respect to VNTR frequencies in Caucasian populations to justify the figures that are being generated?

A. That's correct. You didn't say all of the figures, you said the way it's being generated.

Q. And then I asked you the question with respect to the probability of this coincidental match of 5.2 million and you said that's correct.

A. No, I'm not changing my testimony. What I'm saying is that I don't think you can use the simple binomial expansion and the product rule, O.K.. because of the problems of substructure in particular. Given the problems of substructure, if one has independent evidence for how much substructure there is one can use band sharing to generate a new probability of coincidental match that will be sufficiently conservative that it is not likely to be biased in the wrong direction, because as you suggested, just as I admitted, when more data come in maybe Dr. Kidd and Dr. Carmody are going to be right and it really doesn't make any difference, but when more data come in it just might be the case that I'm right and Lander is right and Lewontin is right and it does.

Q. All right, let me ask you this question, Doctor, does it ever enter your mind that perhaps Dr. Kidd is in a slightly better position based on his experience, his areas of study -

A. Than Eric Lander?

Q. Than you, I'm not talking about Eric Lander because I haven't had a chance to cross-examine him.

A. It crosses my mind but I don't believe so because

I've been working on inbreeding and population genetics for all of my career.

Q. O.K., but the other thing, Doctor, is you haven't ever gone out and looked at his opinions, you haven't studied them in terms of what -

A. I've read his papers.

Q. But apart from that you haven't taken into consideration or you haven't seen his opinions that are actually given, have been given in the courts?

A. I have read his papers, I have read a response to his testimony in the Yee case. Having read the paper, having looked at the raw data, having done my own analyses, I agree with the criticism of Dr. Kidd's conclusion that it doesn't make a difference.

Q. But you don't feel it's necessary to actually go and look at his actual opinions, do you?

A. I have his data.

Q. Now, you have his data, Doctor, but you haven't taken into consideration, have you, his opinions?

A. I'm sorry, but I think you misunderstand what science does. Science doesn't care about opinions. Science cares about what the data tell you. If you can take - I mean I can say black is white, but if I can measure it I don't need to listen to what somebody says about something being black or white. If I can measure it with a spectrophotometer that says the light that's coming off of this object is black it doesn't matter what the opinion is.

Q. O.K., I wanted just to establish that. I just wanted to establish, Doctor, that you don't find it's necessary to take into consideration his

opinion, you just want his data?

A. You keep on saying that. I take his opinion into consideration every time I read his papers.

Q. Have you taken into consideration his interpretation of those papers, what they mean in relation to the Caucasian data base?

A. That's what we do is we write papers to give those interpretations.

Q. Have you read his testimony? You have not?

A. No, I have not.

Q. Thank you. The questions pertaining to - I asked you some questions pertaining to the 5.2 million male Caucasians and the confidence interval around that, and that in all likelihood could be correct if there's sufficient data, could be borne out by that?

A. Again, the data in this case tell me that it's not correct.

Q. And that's based on that background band sharing that you've done, Doctor?

A. Background band sharing and the fact that the French VNTR's at two loci are different from the Canadian, the general Canadian data base.

Q. All right, and again you've read Dr. Kidd's opinions with respect to the Amerindian population and what impact that has on the Caucasian populations in this particular case, you've read that?

A. And I agree with him to the extent that Native American populations are likely to be more inbred than Caucasian populations in North America for the very good reason that they tend to be more endogamous, they tend to be less random mating.

Q. So when you look at the Amerindian data you would expect to see that particular types of data?

A. Can I just do something, though? When we're doing a Frye hearing in the States it isn't about the explicit case, it's about the fact that Cellmark and the FBI have one Indian data base, they use one Indian data base and develop probabilities on the basis of that. Yes, the R.C.M.P. does a better job, but they have not to my knowledge yet demonstrated that there's no variation between French-speaking Canadians and English-speaking Canadians or between the people in New Brunswick and the people here. The point that we make with his American Indian data his Native American data, are that there are differences within races of humans.

Q. And that's why this morning you demonstrated the difference between the statistically significant differences in bin frequencies between the blacks, between the Amerindians, the Canadian Native Indians, right?

A. Right.

Q. And do you simply discount the fact, Doctor, that the same kind of tests were done on the Canadian Caucasian populations and there is no differences?

A. No, I say that that's reasonable and that's prima facie evidence that maybe Canada has less sub-structure in their Caucasian population, but I also have evidence from this case of background band sharing and from an affidavit by Dr. Carmody that says that there are significant VNTR differences between the French and the Canadians. They're both Caucasians.

Q. What affidavit are you referring to, Doctor?

A. Well, it's an exhibit. the one we keep on - I'm sorry, it's not an affidavit. It's the one we keep on looking at. What is it?

Q. You're not referring to France, are you, Doctor, the two loci in France?

A. Yes.

Q. You lump in the country of France with North Americans?

A. We're Caucasians, I think.

Q. So in your estimation, your study of worldwide populations, that is a significant difference to you, is it?

A. It falls outside of the Canadian 99.7% confidence interval for those two.

Q. But in your study of world populations, Doctor, that - you do study world populations, don't you?

A. I have looked at data from populations around the world.

Q. As much as Dr. Kidd would have done?

A. Probably not.

Q. No, and you would be interested in knowing his opinion - you wouldn't be interested in knowing his opinions of that particular French data, would you, you make up your own mind?

A. Yes.

Q. That's what I thought. Thank you, Doctor, I have no further questions.

THE COURT: Now, re-examination?

REDIRECT EXAMINATION BY MR. FURLOTTE:

Q. I just have a few questions, My Lord. Dr. Shields, Mr. Walsh was reading to you portions of the transcript from the Bourguignon case and basically testing as to how reliable some of the tests were, and you were advised that in the general scientific community they were determined to be reliable, running the gel tests and such. As far as for the population genetics and the possibility of substructure within the Caucasians in the States and in Canada, was this information available to you when you testified in the Bourguignon case?

A. No, most of the data came after the Bourguignon case.

Q. And Mr. Walsh had explained to you that the population genetics, there was two aspects to population genetics, one the theoretical or mathematical aspect or the formula they used, and then, two, the empirical work, the theory impact which would tend to make the theory valid. As far as the first aspect, the theoretical or mathematical aspect formula, are you an expert in that area

A. We always hate to talk about ourselves - at least I do, talk about ourselves as experts, but I do understand the mathematics underlying most of population genetics.

Q. So basically you use the theoretical or mathematical aspect in your work?

A. Yes, I do, on an everyday basis.

Q. Is Dr. Kidd any different from you in this aspect?

A. I actually would have to talk to him to find out.

I might find out after talking to him that he was as good or better. I might find out that I thought I was a little better than he was in this aspect, but he certainly uses the same tools and techniques that I do, both in terms of demography and in terms of genetics.

Q. What eminent population geneticists would fall under the theoretical or mathematical aspect?

A. Sewell Wright is probably the top name, in my opinion, recently deceased, the father of modern population genetics, along with Sir Ronald Fisher from Great Britain and Haldane from Great Britain. More recently people who have been developing theory include people like Russ Lande and Rick Michaud and Richard Lewontin throughout his entire career developed a lot of theory, Jonathan Rufgarden, there are a variety of names. Most of them have never seen an organism in their entire lives, human or otherwise.

Q. So basically Dr. Kidd, like yourself, are people who use their theories and their expertise so you can get on with your work?

A. In essence we borrow from them to do what we want to do, or we test the theories.

Q. Now, the fact that you deal primarily with animal populations, and Mr. Walsh was getting that Dr. Kidd deals mostly with human populations, would that make Dr. Kidd any more of an expert than yourself to use the theoretical or mathematical aspect of population genetics?

A. I doubt it. I hope not. Otherwise I would probably claim greater expertise than Dr. Carmody since he works on flies and I work on mammals.

Q. Now, Mr. Walsh also asked you if you read the transcripts of other trials where Dr. Kidd testified to see how valid - or whether his opinions were valid or not. I believe you stated you don't subscribe to transcripts from other trials to read his opinion?

A. If an attorney gives me a transcript and given the time I will read it, but that's the only time I read them, if they want me to read it for a particular reason.

Q. And in answering Mr. Walsh you referred that while you didn't read the transcript of the evidence given by Dr. Kidd you had read the affidavit by Dr. Hartl in response to Dr. Kidd's comments on the non-significance of substructuring?

A. That's correct.

Q. And do you have a copy of Dr. Hartl's affidavit?

A. Yes, I do.

Q. And could you read what Dr. Hartl had to say about Dr. Kidd's non-concern about substructuring and exactly what Dr. Kidd's testimony was?

MR. WALSH: I object, My Lord. Unless I'm going to get an opportunity to cross-examine Dr. Hartl I don't see how that affidavit can be properly put into evidence.

MR. FURLOTTE: Well, I'm not putting the affidavit into evidence, My Lord.

MR. WALSH: Well, if he's going to read from it, we can't hold our fingers in our ears. I mean -

THE COURT: Well, let's hear what he had to say anyway.

MR. FURLOTTE: You read a lot of the transcript that hasn't been put into evidence.

A. The data are the data that I presented for the Karitiana, the Surui, and the Mayan data bases, and he states that - this is Dan Hartl stating - "My analysis of these data and the examples provided stand in contrast to the following opinions regarding the data which were stated or implied in court by Dr. Kidd. One, no populations are ever fixed for VNTR alleles. Compare D18S27 and Karitiana where there was only one allele found. The Karitiana and Surui data bases do not differ from one another. Three" -

Q. Dr. Kidd made that statement, that's what Dr. Hartl is saying?

A. That's what Dr. Hartl said he said, and they do differ. "Three, that it does not matter what data base you use for forensic calculations because all the numbers are small and any particular band pattern is uncommon. In the particular example used in this report the accumulated error over three VNTR loci caused by using the Karitiana rather than the Surui data base is a factor of at least 500. In my opinion no credible research scientist would ever treat the numbers one in 213,000 and one in 400 as if they were equal on the grounds that both are small."

Q. And in fields of expertise how would you rate Dr. Kidd to Dr. Hartl?

A. Let me just say that both of them are eminent geneticists. Dr. Hartl is certainly as eminent as Dr. Kidd, and I think my eminence is a little bit less, or maybe a lot less.

Q. Now, Mr. Walsh questioned you also on how Ottawa or

how the R.C.M.P. obtained their data base and that the evidence that you gave in the Bourguignon case was that you found it was an excellent attempt at a random sample.

A. Mm-hmm.

Q. Aside from picking a random sample the way the R.C.M.P. did to assume that maybe they were getting samples from across the country, would it be still legitimate or better or worse if there was a direct attempt and deliberate attempt to make sure you had so many people from New Brunswick, so many people from each province, so many people from French origin and so many people from English origin? rather than just doing it randomly?

MR. WALSH: I object, My Lord. I understand that this was covered earlier this morning. I thought that that was part of the reason he put Dr. Shields on the stand.

MR. FURLOTTE: I didn't cover that aspect - I don't recall covering that aspect in direct examination.

THE COURT: Let's go ahead but I think you are perhaps tending to repeat a little, or get into the same territory. However, let's have this question answered.

A. Probably the best would be to set out and have all the information that you could possibly have, but in many senses that's not necessarily practical. It would be better to actually get them - if you wanted a representative random sample of the whole country you probably should do a lottery and call them on the phone like David Letterman, would you please donate blood today.

Q. Now, Mr. Walsh was questioning about Nichols and Balding and whether to use the .05 or .0005 or -

MR. WALSH: I object, My Lord. Nichols and Balding was raised in the direct examination of Dr. Shields. He was the one that brought it out, he introduced these statistics into evidence. I cross-examined him on that particular area. Mr. Furlotte would like to plow that ground again. I don't think it's proper redirect.

THE COURT: Well, it's a little hard to tell just yet becaus the question hasn't been completed, but I'm inclined to think you are probably going to get back onto the same territory.

MR. FURLOTTE: No, I just never covered in - we put into evidence what his calculations were -

THE COURT: All right, what is your whole question?

Q. Basically, Dr. Shields on answering Mr. Walsh said that he could use .1 and then you'd be very unhappy rather than .05, and I'm just wondering what Dr. Shields meant by that.

A. It was sort of a joke but if you increased the inbreeding coefficient above .05 you would get much, much bigger probabilities rather than smaller and if there were any reason for you to do that, if you had some - for example, the Karitiana, who are fixed for an allele, obviously the inbreeding coefficient there is one, it's not .05, it's not .1, it's not - for that particular locus it's one, so it's as big as it gets.

Q. So the biggest in the world would not be .05?

A. They're probably talking about average across many loci, and I suspect that using the standard tools

until - when that book was published in 1971 that was the highest, but I happen to know for a fact that since then there have been higher.

Q. So that was 1971 that they were referring to that data.

A. Thereabouts. It's also the standard that we all use because nobody has ever published another book to replace it with more modern data.

Q. I believe Mr. Walsh referred that when you used the common band sharing in this case amongst the five individuals on one test gel that you did your frequency calculations with, earlier you said you just visualized the band sharings of the other five suspects and found a lot of common bands there for the Newcastle area, so that would be ten people rather than five that you're basing your common band sharing on?

A. Well, I didn't count them because I didn't have simultaneously all of the gels and I didn't have time to do this, and the sizings. All I noticed was there was still band sharing, more than I've seen in other cases. In the ten cases that I've been involved in, except for the Bourguignon family which was all brothers and aunts and uncles, this case had more band sharing than I've seen. Sorry, the second to most band sharing that I've seen. I saw more band sharing in one case in Syracuse.

Q. And Mr. Walsh had asked you what way would you do it to be conservative, and I believe you answered the way that you would do it would - you'd consider the degree of band sharing that you did calculate

for the Legere case, and I forget which figure you come to, and then you would use the 99% upper confidence interval to come out with a figure, and could you do that for us?

A. No, not sitting right here right now. I don't have the formulas with me.

MR. FURLOTTE: You don't have the formulas. No further questions.

THE COURT: Thank you very much. That finishes with this witness, then, and I guess you're free to go, Doctor. Did you know Woody Hayes of Ohio State University?

DR. SHIELDS: I certainly did.

THE COURT: His sister married Dick Larkin who was the freshman football coach. Did you know him, too?

DR. SHIELDS: I didn't know Larkin. I knew Woody Hayes.

THE COURT: Larkin told me once 57 years ago that I had a great future as a world class high-jumper, and I was going to say that if ever you went to a homecoming there that you might pass the word along that his forecast was a miserable failure.

DR. SHIELDS: I'll do that, Your Honour.

THE COURT: Now, let me see, have you any other witnesses?

MR. FURLOTTE: I have no further witnesses.

THE COURT: You have no rebuttal evidence?

MR. WALSH: If I just had a second, My Lord. I don't believe so, I just want to double-check. No, My Lord, I have no rebuttal.

THE COURT: All right. That, then, concludes this aspect of the voir dire, and the only remaining item is argument on the DNA aspect and I think we talked

about Thursday, June 6th, and if necessary, with the emphasis on if necessary, Friday, June 7th as well. Could that be completed in one day, do you think? Well, I'm available both days and we'll be available.

MR. WALSH: I'm attempting to draft, My Lord, as you suggested the last day, a form of a written outline to follow the arguments. If I'm able to succeed in doing that by then I wouldn't expect that I would be - I wouldn't use up any more than a half a day.

MR. FURLOTTE: I don't expect to use any more than half a day.

THE COURT: We'll probably finish on the 6th, then, so nine-thirty on the 6th, Thursday, the 6th of June.

(ADJOURNED TO 9:30, JUNE 6, 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 3rd day of June, 19 91.

BEFORE ME:

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 #6, Voir Dire, R. v. Allan J. Legere, J.D., May 27/91, 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 held in the above proceeding on the 27th of May, 1991, at Fredericton, 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 27th day of May, 1991.

Verna Peterson