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

TRIAL held before Honourable Mr. Justice David M. Dickson and a Petit Jury at Burton, New Brunswick, commencing on the 26th day of August, A. D. 1991, at 10:00 in the forenoon.

APPEARANCES:

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

Weldon J. Furlotte, Esq., for the Accused.

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Proceedings of October 28 & 29, 1991

Dolores Brewer,
Court Reporter.

COURT RESUMES. (Jury called, all present.)

(Accused viewing proceedings from cell.)

THE COURT: From time to time, ladies and gentlemen of the jury, I have spoken about different things that arise in criminal trials and I have tried to explain some of the purposes and some of the functions of a jury trial to you, or a criminal trial, and I would like just to take a minute to do that at the present time. I think - you may not recall - but way back at the beginning of this trial I said that our system of trial is known as the adversarial system where the presentation of witnesses and their examination and so on is very much in the control of the parties themselves. One party calls a witness and they examine a witness and the other side is given the opportunity of cross-examination, and then if the other side feels there is something to be answered they may call a witness giving perhaps a contrary view of events, or contrary opinions, and the first side or the other side is given an opportunity to cross-examine those witnesses. This is -- The adversarial system is opposed or is a different system than that practiced in some countries. For instance in France they have what is known as an - I'm not sure of the exact name of the system but it's an inquisitorial system where - or a confrontations system almost. In some of their courts there and in some types of trials they'll put two witnesses - two parties together who give different accounts of what happened. This may be in a civil case or perhaps even in a criminal case and they sit down opposite each other

and the parties themselves are the witnesses and they carry on a conversation and they make accusations and counter-accusations, and statements and counter-statements and so on, and they argue and bicker back and forth and the Judge or the Court or the Jury or whatever sits back and they listen and whoever they decide emerges victorious from this confrontation is the victor in the lawsuit. Well that isn't, of course, the system that we follow. We follow the adversarial system where one party presents its witnesses, the other party presents its witnesses.

In this case you have seen here Doctor Carmody now was called. He was examined for two hours last Wednesday afternoon in direct examination by the Crown and then the Crown took another half hour or so after the young lady finished on Thursday morning and he finished his evidence. His evidence, as you will recall, was largely devoted to describing the method of setting up the data base in Canada. He was qualified as an expert in population genetics and, as I recall, that was the description of his expertise, and he told how the R.C.M.P. Caucasian data base was set up and he gave his opinions as to why that would be the proper data base to be used in a case like this. His evidence on direct examination went somewhat beyond that. The Crown had reason to believe in the circumstances that a witness who had testified at the voir dire back in May or in June might be called by the Defence, as a matter of fact the Defence had indicated that he would be called, Doctor Shields this was, and so Doctor Carmody was asked for his opinions or comments on certain

theories that Doctor Shields had advanced in his voir dire testimony and which I suppose he might be expected to advance again if he were called as a witness in this case, and for that reason Doctor Shields was asked for his views on that. The Crown at that point, of course, had I suppose two alternatives. One, they might have said well let's forget about Doctor Shields, we don't know whether he's going to be called by the Defence or not, and there's no obligation on the Defence to tell the Crown in advance what witnesses they are going to call, if any, and they could say let's forget about any theories that Doctor Shields might have that run contrary to Doctor Carmody's and if Doctor Shields testifies and gives different opinions or advances different theories then we will seek leave from the court to call rebuttal evidence and we will call Doctor Carmody or somebody back to rebut those theories. Now, that was one of the things. Now, they can only call rebuttal evidence, of course the Crown that is, with permission of the Court, and the Court doesn't always grant freely the right to call rebuttal evidence. It's only in exceptional circumstances that that is permitted, and particularly where the Crown might have been expected to foresee the type of evidence that would be advanced by the Defence the Court would be inclined to say well why didn't you ask those questions of your witness when you had him on the stand. And that, presumably, is why the Crown in a case like this would put - pose to Doctor Carmody the theories that Doctor Shields had advanced earlier

and ask for his comments on them.

Well now the Defence, of course, as has happened in this case, have cross-examined Doctor Carmody on his general theories and also on his opinions pertaining to the theories of Doctor Shields. The role of Defence Counsel in a case like this, of course, is not to act as a confrontationist and try to beat down the Crown witness and try to change his views. I think it's quite obvious here that Doctor Carmody feels strongly enough about his opinions that he's not going to acknowledge all of a sudden that no, I'm totally wrong in this, but it is the duty of counsel for the defence, of course, to examine into and perhaps bring out any suggestion that the witness might be bias in coming to his opinions or that he has overlooked certain factors that should have been considered, or that his views are out of line with the general thinking on the subject. He goes into those things and then the Defence produces, when its turn comes, it produces its own witness and he expounds his theories. The Crown in this case would be given an opportunity to examine the defence witness and, again, test that witness for those same things. Are there things he's overlooked? Is he bias in coming to that decision, and other factors like that.

In this case Doctor Carmody has been examined very thoroughly, I think, for over 3½ hours probably, I haven't actually taken an account of the time into the thing, and I would say that probably his theories have been tested just about as fully by defence

counsel as they could possibly have been. On Thursday I think the cross-examination perhaps had sort of deteriorated into reciting long portions of the evidence given by Doctor Carmody at a voir dire hearing back in May and sort of saying well how do you comment on that now, and why does that differ slightly from what you may be saying now, and Carmody has answered those questions as they have been put.

On Thursday it had been the understanding that Doctor Carmody's evidence would be completed on that day but he would not be stood down as a witness, his cross-examination would be left open until defence counsel might have an opportunity to consult over the weekend with their defence expert whom they might be calling, and he might wish to ask a few more questions of Doctor Carmody at this time, and then after a brief, presumably, reexamination by the crown counsel that would put an end to that witness and that would be the completion of the Crown's case. And then in the normal course the defence will be asked do you wish to call witnesses and presumably Doctor Shields would be called as a defence witness if the defence at that time saw fit to call him.

On Thursday Mr. Furlotte indicated that he might take somewhat longer than the 15 minutes or half hour which had been suggested to complete cross-examination and might go on all morning this morning, and I must say it's difficult to see where possibly there could be further topics that could be examined but certainly if there are material aspects of Doctor Carmody's testimony which should be examined any

further Defence Counsel has the right to pursue those. But I guess the reason that I'm saying all this is to suggest, Mr. Furlotte, to you that surely in a few minutes and with a few well-directed questions you could complete your cross-examination of Doctor Carmody. You are not going to change his opinions on these things, I would say. You have brought out just about everything; you've put to him about every question you possibly could up to this point; and then get on and if you wish to call your own expert who will give contrary opinions or contrary views on certain aspects of this matter well, good enough, he does, and the jury then would be in a position to -- They'll sit back and they'll have to decide in the long run look, whose evidence do we accept here, and which is the evidence we accept.

So, having said that, I'm not going to say anything more on that point. The Crown will call Doctor Carmody back to the stand and Mr. Furlotte will ask further questions if he has further questions he wishes to ask.

MR. WALSH: Recall Doctor Carmody My Lord.

DOCTOR GEORGE CARMODY, recalled, previously sworn, testified as follows:

CROSS-EXAMINATION CONTINUED BY MR. FURLOTTE:

Q. Doctor Carmody when we left off Thursday I believe you had stated something to the fact that one has to make some decisions based on empirical evidence and that you're using empirical evidence to inform your decision rather than coming upon it from some abstract way from prior principles.

A. I'm using both prior theories in conjunction with the empirical evidence. I don't think it's an either/or situation there, that is that both inform each other, and I'm using the empirical evidence to make my decisions based on how that evidence would jive with the theory.

Q. Right. And the theory, just for a brief review for a minute, the theory is from prior principles that you must be in Hardy-Weinberg, you must have linkage equilibrium --

A. Yes.

Q. -- and there cannot be any significant degree of substructure?

A. Yes.

Q. And that significant degree of substructure would be of a statistical significant degree?

A. Yes.

Q. And in a homogeneous society it would not be uncommon for individuals to have common band sharing in their probe so that there could be legitimate band sharing say in two or three probes.

A. There could be. It depends on the particular probe. I have information on the particular ones that were used in this case and developed a way of predicting how much band sharing one would expect to see.

Q. And it wouldn't be uncommon to share two or three probes in a homogeneous society?

A. It would depend on the probes. I don't have a number. I'd have to resort to some notes in terms of particular probes what the expected amount of band sharing would be and it would depend on a number of

individuals. You're talking, I would take it now, between two unrelated individuals.

Q. Yes.

A. Yes, between two unrelated individuals. It depends on the probe. For some probes one would expect two-thirds of the time in a locus that in fact they would share. For other probes it would happen only 14 - 15% of the time. It depends very much on that bin distribution. If you have very few bins and there is one bin that is very common it means that a lot of people are going to have a band from that particular bin and so if you take two people it's not surprising that they would have at least one of those bands in common, and that is what we would call band sharing. So for some probes in fact it's quite high. I mean it's counterintuitively high to me.

Q. But you can do empirical checks on your data base to see if your model is working?

A. Right.

Q. To see if the theory is working.

A. Right.

Q. I suppose if empirical checks are totally unexpected - the results of your empirical checks are totally unexpected then it might tell you there's something wrong with the model or something wrong with the data that you're using to check the model.

A. That's right. It would lead you to suspect that something needed further reexamination or refinement in theory or looking at some bias, perhaps, in the sample that was chosen, or something like that.

Q. There would be a misfit there somewhere?

A. Yes.

Q. Now, Doctor, if there was a chance of say one in a thousand of an event occurring of say somebody else say sharing a particular band with any individual and you went through your data base and your frequency said that well there's only one chance in a thousand that somebody else out there is going to share these particular bands of an individual, and if you were able to have those two individuals together at the same time, pick them out, and the same occurrence would happen at the same time, the same place, you would multiply for that happening, the probability of that happening you would multiply one thousand by one thousand to get your probability number.

A. Well, if you, prior to the event of having examined those individuals, had made the statement that without looking at any of the data had said that these two people would have these two bands in common then in fact you could calculate the probability of that happening. Typically, in the scenario I think we're talking about, that's not what has happened. What has happened is that you've had two individuals - and I know this is maybe a subtle difference - but you see what I'm trying to distinguish is the fact that if you've never seen what the data looked like and you then predict what the data will look like for a specific instance then in fact you can calculate the probability of that happening. What typically is the situation, however, is that you're standing after the data and you have a retrospective look at the

data, and I know this gets a little bit subtle but there is an important point here, and you're making a prediction about what you've seen already as being there. Now what I'm saying is that you can make that calculation as though you didn't know that in fact that was what you were going to calculate the probability were ahead of time but in fact you know now what you're going to calculate and you're only going to calculate that specific one. What I'm arguing in this case when we get into questions about sharing bands between individuals, we're not so much interested in just the probability that they shared that particular band which they happen to share which you already know they share because you've seen the data now, but in fact you would also be surprised if there had been a match at any of the other bands and you had seen that after you had actually compared the data. And in fact if you looked at the data after you had it and they didn't share any bands and they had two completely different genotypes and you said for some reason it would be unusual but you could say gee, look at that combination of patterns, these two bands are up here and these two bands are down there, they don't match at all, what's the probability of that happening. Well, indeed, if you calculated the probabilities across those it's going to be very rare. So what I am saying is that after you have looked at some data something has happened, some combination of events has happened, and if you look at that particular combination of events it's going to have

a very low chance of happening because any kinds of events could have happened. Some event did happen because you made the comparison. Now, what you are saying is --

Q. Doctor, if I may stop you here for a minute. I don't want to get into the background band sharing aspect at this time.

A. Okay.

Q. We will do that and you will have a chance to explain that after. I want to get into another aspect which might help the jury understand what we're talking about.

A. Okay.

Q. Now, I believe you already mentioned that you were involved in some kind of study with Doctor Gaudette about hair samples.

A. Yes, I was, back in the early 1980's.

Q. Early 1980's. And in the literature by Doctor Gaudette -- he testified in court that the probabilities were one in forty-five hundred of coincidental matches.

A. That's what he had concluded from that study, yes.

Q. Now, he derived his conclusion or calculation based on a sample of 200 samples.

A. Well, as I -- yeah, it was 200 individuals. I think there were ten samples of hair from each.

Q. Well, it was like a data base of 200.

A. Yes, although there were ten hairs from each individual and so therefore there were many, many comparisons made.

Q. And they had the different characteristics of the hair and it's something like the DNA profiling and the calculation of probabilities with DNA profiling?

A. It is similar, yes.

Q. Now, the question back about coincidental findings, if the police were going to, for an example, at the scene of a crime find two hair samples which they're contemporary forensic testing procedures for all intent and purposes they find them identical and DNA testing shows that one would be different than the other, the coincidental statistics - or the statistics of that happening, the proper approach would be to multiply 4500 by 4500, would it not?

A. Well, I feel the number would be 1 in 4500 in that case, not the multiplication of those two because in fact they could have matched on a number of other criteria. But I think the point is is that you could calculate a probability of that happening, yes.

Q. And if the probability is 1 in 4500 of somebody else out in the community having a hair similar to say Mr. Legere then the probability of it being that - that person out there being in the same place at the same time as Mr. Legere you would have to use the Product Rule and multiply across that probability.

A. Okay.

Q. Is that a fair assumption?

A. Yes.

Q. And do you have your calculator with you?

A. Yes, I do.

Q. Would you multiply 4500 by 4500?

A. I get 20 million I guess. 20,250,000.

Q. So the chances would be 1 in 20 million that the hair samples would come from two different people?

A. Well, you see the probability of a match is 1 in 4500. So it's one in 4500 in fact.

Q. And the probability of the hair samples being consistent with each other, the different hair samples found at the scene of the crime being consistent with each other, the chances of them coming from two different people, being there at the same time and same place, would be 1 in 20 million?

A. 1 in 4500.

Q. Why is it only 1 in 4500?

A. That's what the probability of a match is. That's the probability that two hairs match, coming from two different individuals. That's the number that Doctor Gaudet had established.

Q. Okay, let me ask it this way. If the probabilities were 1 in 4500 that it would be somebody other than an accused person, say like Mr. Legere here. He's an accused person, there was hair found at the scene of the offence which are similar to his, okay?

A. Right.

Q. Follow me so far? The chances are 1 in 4500 that it would be somebody else's, is that right?

A. The number of 1 in 4500 which there has been some debate about but I'll take it for a given, is the probability that two hairs taken from the general population from two random individuals are going to match. When you have them both together.

Q. That's not the way I understood it.

A. That's the way I understand that number. And it's not that there's a 1 in 4500 chance that you had this particular kind of hair which matched something else and then had another one which matched something else.

Q. I understood from your testimony and everybody else's testimony that when we come with the frequencies attached to the probes of Mr. Legere as being 1 in 5.2 million or 1 in 310 million, that there's only 1 chance in 5.2 million that it could be somebody else's.

A. Right.

Q. Not 1 in 5.2 million that you could pick two people at random and find a match.

A. No, because that probability is you already have something that you're trying to match. You already have that. You're not taking two random. You are taking that particular genotype, that particular set of bands, and you already have that. You have that set and you say what's our estimate of that particular genotype matching somebody else in the population? That given genotype. You already have it there. You're not taking a random. You have that genotype. What's the probability of finding that identical one once in the population and it's that number is our estimate.

Q. And that's, what I understand of the theory so far, was that right, 1 chance in 5.2 million, we'll take the four probe match, 1 chance in 5.2 million that you are going to find a match matching Mr. Legere's.

A. Right.

Q. Okay. So basically what you're saying, if I searched 5.2 million people I'm going to find one person out of those 5.2 million people that matches Mr. Legere's profile.

A. On average. That's the expectation would be the technical term.

Q. Wouldn't the odds change then that if the first person you pick is going to be that person?

A. No. Has no influence at all.

Q. No influence at all.

A. No.

Q. So the odds are the same whether it's going to be the first person or whether you search 5 million?

A. No, that's not true, because what you're saying when you search 5 million you've already looked at 4.999 million and at each one of those examinations there's a chance of the same number, 1 in 5 million, that that person would match and that's not going to change when you've looked at another individual. If you say well I've looked at 50 individuals, I've looked at a thousand individuals, what's the chance that I didn't find a match in those thousand individuals, you come up with a different number than the 1 in 5 million. When you said I have a group that I've looked at, what's the chance that that 1 in 5 million was included in that group and it gets into a more complicated sort of calculation. But everytime you look at an individual that number is based on a notion that every time you look at a new individual there is that same chance that that individual might match.

Q. All right, let's go back to the analogy of the Lotto 6-49 draw which was calculated as 1 chance in thirteen million nine hundred and some thousand, so we'll say 1 in 14 million. The chances of that draw, going out and picking the winning ticket is 1 in 14 million.

A. Right.

Q. Right. So there's 14 million combinations to get the winning number.

A. Right.

Q. Now, if I go out and buy 14 million tickets all the different combinations I'm bound to win. I'm going to find one winning number.

A. Well, it turns out that if you buy all the tickets in a lottery you're bound to lose because they don't return all the money you've paid for the tickets. So that's one way of guaranteeing that you lose a lottery, just for purposes of advice.

Q. Okay, what about the Florida State lottery where the winning is up to 94 million dollars. If I bought 14 million tickets I'm sure to win. There might be other winners along with me but I would be sure to win, is that not right?

A. If you bought one of every combination you would have to be at least a partial winner, yes. But that you would likely have spent more in trying to win than you actually would have won.

Q. There would have been no guarantee that there would be another winner. That's by pure chance.

A. That's right, in that kind of a lottery, yes.

Q. But when you buy the 14 million tickets you take the chances out of it. You've got a sure thing.

A. You take the chances out of it, yes, and you guarantee a loss, ironically.

Q. When I put the same proposition to you about the hairs, 1 in 4500 and two hairs being identical but definitely from different people being at the same place at the same time, at the voir dire did you agree that you could multiply 4500 by 4500 to get the probabilities?

A. I don't recall, honestly, but when I think about it now anyway, that 1 in 4500 means the chance of having two taken from two separate individuals matching.

Q. I show you on page 151 which I believe is volume VII I was questioning you about the hair samples.

A. Right.

Q. Would you read that portion and tell me if you gave me a different answer at the voir dire.

A. The question was: "And it is proven that they do come from somebody else so that puts both individuals there at the same time. What were the probabilities that both people were there at the same time?" My answer was: "And both left a separate hair sample." Question: "And both left --" Answer: "And there were two hair samples found." Question: "Two distinct - distinctly two different people. No question about it." Answer: "Well, in that case the random match for one is one in 4,500. The random match for the other is one in 4,500." Question: "Could you multiply that?" Answer: "For the joint occurrence of those two, yes, I would think so."

Q. Do you change your mind today?

A. No. No, I haven't.

Q. So you agree --

A. Because that's a different question that's asked there.

Q. That's a different question?

A. Yes.

Q. How is it different?

A. That question is different in -- My understanding of that question is that you already have a hair specimen and you said what is the probability that that matched another hair specimen, and it matched as 1 in 4500. What's the probability that it matched another random hair specimen, that is that you have a standard hair specimen that you were looking for two matches of and you were multiplying it together because both of those had to match this prior stipulated standard hair. That was my understanding of that question and it was not the question that I was answering today, I felt.

Q. Okay, let me put it this way. If we have a standard hair match of Mr. Legere.

A. We have that specimen.

Q. We have that specimen.

A. Okay. So there's no 1 in 4500. That is a specimen.

Q. That's a specimen. No one in 4500. We find at the scene of the crime a different number of hairs which are all similar to Mr. Legere's. 9 hairs I believe. A DNA test is done on one of those hair samples which the statistics say it's 1 in 4500 that it could be somebody other than Mr. Legere.

A. Right.

Q. Right. How would you calculate the statistics that it could be two people there, that the different hairs found are from different people?

A. My initial answer I think would be that it would be 1 in 4500 that it would be from a different person, that that hair that matched - that the DNA didn't match, is that what I understand what the scenario is?

Q. Say if the scenario was that the hair didn't match Mr. Legere. Say it came from John Doe.

A. The hair -- Well, the DNA from the hair.

Q. The DNA.

A. The DNA from the hair. Okay.

Q. Well, hopefully, if the hair -- If the DNA didn't come from Mr. Legere hopefully the hair didn't come from Mr. Legere.

A. That would be my presumption.

Q. Safe assumption. Again, if the hair was proven to be John Doe's rather than Mr. Legere's --

A. Right.

Q. -- what would be the probability of there being another person there besides John Doe with hair similar to Mr. Legere? Do you multiply 4500 by 4500?

A. I think it's still 1 in 4500. I'm trying to analyze the scenario there because there are some subtleties in this that it's not quite the probability that there was somebody else there. It's the probability that there was a hair there that didn't match the others in terms of their DNA when they matched on all other criteria and Mr. Legere's hair being present there was no --

Q. Well we don't know if Mr. Legere's hair there as being present. We're just using Mr. Legere's hair as a standard.

A. Well then the chance of an individual chosen at random to match Mr. Legere's hair is 1 in 4500.

Q. And the chance of going out and picking another individual to match Mr. Legere's hair again is one in 4500?

A. Yes.

Q. So the chances of picking two individuals out there to match Mr. Legere's hair would be 4500 times 4500?

A. That's right, or the 1 in 20 million.

Q. It's like the Lotto 6-49. Everytime you want to pick a winning number you have to multiply the probabilities of each draw.

A. Yes.

Q. Before I get into background band sharing, the field of population genetics, whether you're -- You're in the experimental field --

A. Yes.

Q. Not the theoretical field.

A. That's correct.

Q. A population geneticist in the experimental field it doesn't matter whether you're studying plants, animals, insects, humans, you all use the same general theory from the theoretical --

A. We use the same general theory. There are some theories that more specifically apply in the case of plants for example. Plants can - many plants can self - they can mate with themselves for example, which you don't get in most animal populations and

so forth so you have to allow for things like that, and in fact there are some plants that just self, or predominantly self, and so forth. So there are some species specific aspects of population genetics but the overall theory and certainly things like Hardy-Weinberg equilibria and linkage disequilibria are quite general and apply to virtually all species.

Q. And substructuring?

A. And substructure, although in many species we know from the biology that it's unlikely to be important, in other species it might be more important than other species, but in general it's one of the aspects of population genetics that is looked for when one is studying virtually any species, yes.

Q. And the general dispute among scientists over whether or not Hardy-Weinberg and the Product Rule can be used, who would be the proper people to settle that dispute?

A. Well, my sense is that it's going to require more data and that typically would fall in the area of people who collect data and I would put that more in the experimental camp. I think the theory is there. On the other hand, some of the answers are going to come not just from collecting empirical data but by doing computer simulations, for example, taking existing data and resampling it. We have a technique that's called bootstrapping and so forth where you take the data that you have and you pretend that that's what the universe is and you sample from that data, so it's a process where you take the data that you do have and you keep resampling it to give you

an idea, or you hope an idea, of what would happen if you took further samples from the real world. So those sorts of types of experiments, whether you call that theoretical or experimental empirical, I think is really a question of the particular person doing it. I know experimental people who do that kind of computer simulation and I know theoretical people who do that kind of computer simulation and indeed there's not a hard and fast line that one can draw and always put into one set or the other any particular individual. There are many people who have their feet in both camps and in fact straddle that area. So it's not a -- It's a fuzzy border between the two areas.

Q. But it will take somebody with a lot of knowledge about population genetics and experimental tests and --

A. Yes, it would take people with knowledge of the areas and what has been done and what needs to be done, yes.

Q. You wouldn't feel comfortable if I went in and settled your dispute for you?

A. Hardly.

Q. Nor would you expect any common people to be able to settle your dispute?

A. That's right.

Q. Now, you recall at the voir dire my going through all the different sizings for different probes that were run in the first gel with you and comparing Mr. Legere's bands with the bands of Donna Daughney?

A. Yes.

Q. And you calculated out the probabilities for me of Mr. Legere, using the R.C.M.P. data base, you calculated out the probabilities of Mr. Legere by chance sharing the same bands as Donna Daughney.

A. Sharing the particular bands, yes.

Q. Yes.

A. I recall that calculation.

Q. And your calculations you come out that there was only one chance in 1.8 million that Allan Legere could share the same bands, I believe it was four or five, with Donna Daughney.

A. That particular set. In fact as I recall it, that was the probability that in fact you had two people chosen at random that would have that particular match for that particular band.

Q. And aside from Mr. Legere sharing a good number of bands with Donna Daughney he shared a fair number of bands with Linda Daughney?

A. I don't recall the specifics but, yes, I'm sure that there were some bands shared with Linda Daughney.

Q. And the bands that he shared with Linda Daughney were not all the bands that he shared with Donna Daughney. They were different bands involved.

A. I think so. I don't remember the specifics but I'm willing to agree that that probably is the case.

Q. And aside from Donna Daughney and Linda Daughney Mr. Legere shared a lot of bands with the other suspect, Lewis Murphy.

A. There was another individual that there was some sharing with, yes.

Q. And Lewis Murphy also shared bands with the Daughneys that he didn't share with Legere?

A. There was bands being shared between different individuals, yes.

Q. And Mr. Legere also shared bands with Nina Flam. There was one probe that he matched both bands, is that right, Doctor?

A. I don't remember the specifics of the individual matches but I know that there were bands shared there. I don't remember the exact numbers in those particular cases.

Q. There was a lot of band sharing.

A. Okay.

Q. Between those individuals.

A. There were a lot of band sharing. I'm not sure it was greater than you would expect however.

Q. You're not sure.

A. Nope.

Q. But it's very possible.

A. Not from the calculations I have done, no.

Q. We'll get into those, Doctor. When I had you do the calculations and to look at the band sharing that Mr. Legere had with the Daughney girls it looked as if Allan Legere was more related to Donna Daughney than it looked as if Linda was related to Donna Daughney, didn't it?

A. That could be. I don't recall the details of that but I'll be willing to concede that.

Q. Isn't that an odd occurrence?

A. No.

Q. It's not an odd occurrence for an unrelated person to share more bands than a related person?

A. Not necessarily. I've done calculations and if you look at the amount of expected band sharing it's significantly high, actually.

Q. So 1 in 1.8 million is not an odd occurrence?

A. Not in the analysis of this kind of data, no.

Q. If Mr. Legere was compared to say 10 or maybe even 20 people of the community that the same frequencies kept occurring would that kind of evidence suggest that we might be dealing with substructure?

A. If that higher frequency continued through through a larger sample yes I would conclude that there was something abnormally high and something strange in that population that you were sampling that was not like the R.C.M.P. data base population.

Q. Were you in court when Doctor Kidd testified?

A. Yes, I was.

Q. Do you recall me asking Doctor Kidd how common would it be that if you drew 5 people at random from a data base how many bands could you expect them to share?

A. I think I recall but I don't remember specifically. I have done some calculations and I can give you results.

Q. But do you recall the answer he gave?

A. I don't recall specifically. I think he said that you had 1 or 2 - a probability of 1 or 2 or something like that. I don't remember what he said.

Q. Something like 1 and he said a probability of 2 or 3, I forget the word he used, but it would be something out of the ordinary.

A. Um-hmm.

THE COURT: I think we should bear in mind here that you people may be talking about different things on different occasions. Doctor Kidd was talking about single band sharing. Are you talking about single band sharing or double band sharing?

A. I'm talking about single band sharing but in general when I'm using the term I mean single or double or triple or quadruple. Anything outside of non-band sharing. I'm distinguishing just those two categories where you don't share anything or you share at least one or more.

MR. FURLOTTE: I believe Doctor Kidd's testimony was that if you picked two people out that you might expect them to share one band on a probe. That would be a normal occurrence. For them to share two or three it would be uncommon, and to draw five people and for the average for those five people to be two or three bands would be something unthinkable.

A. I don't recall his specific answer to that.

Q. But are you telling me now that it would not be uncommon to draw five people at random for them to share two or three bands?

A. That's right.

Q. So you differ from Doctor Kidd's testimony.

A. In that respect because I have actually done the calculations and I have looked at the data and if you took people at random from the R.C.M.P. data base it's surprising that some of those loci how often you would expect two random individuals to share bands. It's a lot higher than you intuitively would think.

Q. At some of the loci.

A. At some of the loci, yes.

Q. What about across all of them? The average across all of them? You wouldn't expect that.

A. On average it's still pretty high. I have the numbers, actually. I could go through the --

Q. Yes, we'll go through them, Doctor. So are you saying that at the voir dire when you testified you found that it would make you wonder about it if you had that kind of common band sharing but today it doesn't make you wonder any more?

A. It doesn't make me wonder now because now I've figured out how to analyze it.

Q. Okay. Now, you mentioned about your empirical test to test your model, your theory. Have you drawn 5 or 10 people at random out of the R.C.M.P. data base to see if you would get the common band sharing that you found from the Newcastle region?

A. I don't have to, actually, because I can approach it analytically and predict how many I would expect to see, analytically.

Q. So are you saying you don't have to test your theories?

A. No, I say I do have to test them.

Q. You're saying you do have to?

A. I do have to.

Q. Have you tested it?

A. I've tested it against the sample and I know analytically it's the right result.

Q. Again, you have the prior information here to see if you are going to get reproducible results. Wouldn't it be proper for you to go back to the R.C.M.P. data

base and start drawing out nine or -- In this case you used 9 individuals?

A. Right.

Q. From the Miramichi area. Wouldn't it be proper to go back to the R.C.M.P. data base and draw out nine individuals here, nine individuals there at random, and then check to see if you have that same kind of band sharing?

A. That's what I intend to do.

Q. It hasn't been done yet?

A. It hasn't been done yet.

Q. So you have nothing to support your opinion really?

A. Yes, I do. I have the --

Q. The figures.

A. -- the analysis of the formula.

Q. Would you expect to ever to be able to convince the scientific community that you were right without testing your opinion first?

A. I know the derivation of the formula is correct and I know that that would be accepted in a peer review journal with experts who are knowledgeable in probability theory and algebra to corroborate that in fact it is correct. I have had several people look at it and gone through the derivation with them and they concur that the analysis is correct.

Q. What do you call several people, and how qualified are they?

A. Well, I would say I have checked it out with three people, one person being Doctor Kidd, and in my mind he's qualified. In fact --

Q. So is Doctor Kidd now contradicting what he testified to earlier?

A. When he testified he hadn't seen the formula and he didn't know about it at the time, and I think what the formula predicts is, as I would say, counter-intuitive. There is actually expected, really, to be more band sharing than one would have had the intuition about, including my own intuition before I derived the formula.

Q. I understand you are aware of Doctor Hartl checking the FBI's - the reproducibility of the FBI's data base?

A. I read a commentary of his or a report that he submitted to a case in Ohio back some two years ago where he analyzed what had been done there, yes. I don't remember all the specifics of it but I do remember reading that.

Q. And the DNA was rerun on the FBI agents that had been put into their data base?

A. Yes.

Q. And on the rerun --

MR. WALSH: Well, unless Doctor Hartl is sitting back here somewhere and I'm going to get a chance to cross-examine him Mr. Furlotte is not entitled to testify as to what, if anything, Doctor Hartl said about the FBI data. That is an improper use of information on cross-examination I would submit, My Lord.

MR. FURLOTTE: My Lord, this witness just finished testifying that he checked his results of background band sharing with three other people and they con-

curred with him, and he checked with Doctor Kidd. Hearsay evidence is nice when the Crown wants it in but whenever -- You know this is a two-way street here.

THE COURT: There was a question put to the witness who were the three people you checked with and he hasn't been given an opportunity to answer that question totally. He said Doctor Kidd but the question then wasn't pursued as to who the two others were.

MR. FURLOTTE: Well, he didn't finish --

THE COURT: Are you pursuing it? Are you following that up? Do you want to know who the other two people were?

MR. FURLOTTE: That will be found out in due course.

MR. WALSH: The issue here though, My Lord, is he's off onto another area all together. He's off onto asking him about Doctor Hardlt. That's an improper use of cross-examination. My understanding, My Lord, is when Doctor Carmody - he can certainly refer to others and adopt that as his opinion but Mr. Furlotte cannot through his mouth get the evidence of some other person who is not present in this courtroom in as evidence and that's what he is doing here.

MR. FURLOTTE: Well, My Lord, I just find it funny how the expert witnesses can refer to somebody else --

THE COURT: Well, go ahead, ask your question.

MR. FURLOTTE: -- to share their opinion but they're not allowed to testify as to those who opposed the --

MR. WALSH: My Lord, as you are aware, it is not a matter of me making something up, and if Mr. Furlotte finds it funny, my understanding of the law in this regard

it's about a hundred and fifty years old so I don't think that there's anything funny here nor do I think what I've raised here is something I've made up. It's something that's in the books and on the law. It's common --

THE COURT: We went into this matter rather fully last week on Wednesday or Thursday and -- Go ahead if you want to examine this witness but you can't be presenting evidence on behalf of Doctor Hardlt here, as Mr. Walsh points out Mr. Furlotte.

MR. FURLOTTE: On the reliability of the R.C.M.P. data base it's only - the DNA has only been run once, isn't that right?

A. The R.C.M.P. data base most of the samples have only been run once, yes.

Q. They didn't run the DNA the second time to see if they would get the same results.

A. That's correct.

Q. With the experience from the FBI I believe tests have been done on different occasions.

A. Um-hmm. With the FBI there was one sample where I think that was done. I know of examples at the R.C.M.P. where they have also rerun samples. It hasn't been done on the entire data base but there's no reason to do it on the entire data base. If one was looking at it in terms of efficiency rather than rerunning the same specimens again it would be more productive and useful in fact to look at different specimens and then in fact to see whether there was any difference between the two groups that you ran rather than to spend your time redoing and redoing the same ones.

Q. Okay. So you say there was no reason to run the R.C.M.P.'s over the second time. If Doctor Hartl found that the FBI in their second time running that they could only identify 16% of their FBI agents -- Rather than identify all of them all over again they were only able to identify 16% of them on the second run why wouldn't it be feasible and necessary for the R.C.M.P. --

THE COURT: Well, you're getting into evidence again. You're giving Doctor Hartl's evidence about --

MR. FURLOTTE: Well, My Lord, I'm not offering it for the truth of it, I'm offering it for the experiments that were done and possible problems with data bases.

MR. WALSH: I'll register an objection, My Lord. Mr. Furlotte completely and utterly in my humble opinion misunderstands the way he can use this kind of information on cross-examination and I can only reiterate my objection to the method that he has adopted.

THE COURT: Well, perhaps I could ask the witness this. Are you familiar with the experiments that Mr. Furlotte is referring to?

A. To be honest, quite vaguely. I don't remember the specific numbers. I'm willing to concede, if you will, or to say that in fact there was some discrepancy when they reran some specimens but I don't remember why that was or how it was resolved. I know it has been resolved and in my opinion it's historically interesting fact but has no present-day relevance.

MR. FURLOTTE: Do you know how many times the FBI did run their specimens in their data base to check for reliability?

A. I don't know.

Q. But they have done it more than once?

A. I don't think they have run every one of them more than once but I'm not sure of that. I know of examples where the same specimens - a subset of those were run a number of times. I know of instances where the same set of specimens, close to 200 of them, were run both by the R.C.M.P. and the FBI to establish that in fact there was no difference where you ran it, and even though there were differences in the protocols that you came with the same results.

Q. Do you know whether or not there was a statistical significant difference found between the FBI's two runs?

A. I don't know. I know there were some discrepancies but I don't remember the number and I don't know how many were run and I don't know what the resolution of that was. I know now that it is not any longer considered to be a factor in any of these calculations or -- As I said a minute ago, I think it is now a dead issue.

Q. Okay, Doctor, just two more questions before we get into the background band sharing and the calculations that you derived. There are a considerable number of eminent scientists in the field of population genetics that disagrees with those scientists in the forensic community, is that right?

A. There are some.

Q. A considerable number?

A. I would have to have a specific number there if I were to answer. I would say there are some. More than one.

Q. Did you agree in May of this year when you testified on the voir dire that there was a considerable number?

A. If that's what I said at that time that's what I said. I would say now there are some.

Q. At page 190, volume VIII, and I asked you was there a considerable number of eminent scientists in the field of populations, what was your answer?

A. When you said "So there are a considerable number of eminent scientists in that field of population genetics that disagrees with those people in the scientific community", and I said yes.

Q. So now you want to retract that to just being that there is some?

A. There are some. Because I'm not sure now that I've had some courtroom experience that one has to split hairs as to what considerable means, and you would have to define for me what you meant by considerable.

Q. Enough to cause concern, Doctor.

A. Give me a number.

Q. Is there enough to cause you concern?

A. No.

Q. Was there enough to cause you concern in May of this year?

A. No.

Q. Doctor, I notice on P-167, I believe in your testimony you said at one time you didn't find there was a statistical significant difference between the R.C.M.P. data base and the one from Montreal?

A. On that exhibit? That there were at, as I remember two of -- I think there were only four probes that I could check there in the data that I had at the time.

Q. With Montreal there's five. I'm not talking about the one in Northern Quebec.

A. No, no, this is the one from Montreal which is the only one that I have seen and the only one that I know of, and that there were when I did bin frequency comparisons, and it was not for all of these five loci in fact because at the time I did not have the D17 so I only did it on four, and of those four there were two that showed statistical difference in bin frequencies, and you see the result of doing the calculation on a population that the two of the four probes that I tested there were statistically significant differences. You come up with a number that is, I would say, insignificant from the number that you came up - that I came up with in the R.C.M.P. data base.

Q. But even for the D10, the R.C.M.P. and the Montreal, the Montreal doesn't even fall --

A. Is outside that 99% confidence interval.

Q. It's even outside the 99% confidence interval.

A. It is. In that particular case.

Q. So the one in the R.C.M.P. is 1 in 108 and Montreal is 1 in 71.

A. Right.

Q. And when you add the wide confidence interval it's outside that.

A. That's right, because that's one of the probes that in fact when you compare the bin frequencies there's a statistically significant difference in the profile between the two.

Q. And I believe also in this to get your confidence intervals, the 1 in 3.1 million to 1 in 17 million which surrounds 1 in 5.2 million, why is it so higher on the up side, say between 1 in 5.2 million to 1 in 17 million, and low on the lower side of 5.2 million?

A. I understand that's difficult to realize why that is but in fact if you expressed these numbers as a decimal, that is you divided 1 by 5.2 million, you would come up with a decimal that would be .000 whatever. You come up with that. If you expressed these as decimal fractions rather than as a fraction as I have here but as decimals, in fact the distance between the lower 99% and the upper 99% if you looked at it in terms of the decimal expression of those is identical, and it's just that then when you take the reciprocal of that which is what you do to express it this way it gives that apparent asymmetry. But if you were to express these as a decimal fraction you would see that they were symmetrical around that point estimate. And I know it's the way arithmetic works when you make fractions of things.

Q. Did you kind of average in -- Did I understand on your direct testimony that you kind of averaged in the lower figure to get the 1.31 million rather than use the 56 times 44 times --

A. That's right. I used the proper statistical combination of those. I did not just multiply the lower 99% on all of those together because that is going to give you a number which is much, much wider in terms of being more frequent than in fact the real 99% confidence interval is. It's more conservative. I have no objection to people who do that. Doctor Kidd did it. It's a fast and easy way to take these calculations and multiply them through but that's not what I did here.

Q. The formula that you put together to calculate the degree of band sharing you might find at random pick of 9 individuals in the R.C.M.P. data base --

A. Yes.

Q. You used that formula on the 9 individuals from the Miramichi which were in the number one gel of the R.C.M.P. in this case?

A. They were amongst the autorads. I have to confess that the data that I used for this were given to me by Doctors Bowen and Fourney from those autorads. I personally did not inspect the autorads. I'm taking the numbers that they had and worked with those, and I provided those to Doctor Shields as well. I think that we agree on those numbers.

Q. Okay. And do I understand that it was just on the morning that you testified last week that you were able to pull out of your head some kind of a formula to calculate the frequencies of 9 people sharing these bands?

A. Yes. Over the, actually, four day period before I - three day period before I began testifying and in conjunction with Doctor Kidd, actually, we going back and forth developed this formula jointly, and it was just on that morning that in fact through a fax a few times back and forth between myself and Doctor Kidd after he had stood down from testifying that in fact we came up with the solution that we had been seeking to get.

Q. And after you had the benefit of Doctor Shields' testimony in May of this year this formula that you come up with to, I suppose, counter Doctor Shields' testimony is an eleventh hour miracle.

A. Well, I don't know if it's a miracle but it certainly is later than I would have ideally liked to, because if I had been able to come up with that formula a month or two ago there are a number of other things I would have liked to have done and in fact have done some further analysis of many other data bases using that formula and even applying the formula to this Miramichi data base in a much more precise way which I have not done yet.

Q. Would you admit, Doctor, that if you had not been able to come up with this eleventh hour formula that Doctor Shields' testimony would have caused the R.C.M.P. great concern?

A. I don't think so because even without that formula there is other analyses that I have done that really corroborate to my satisfaction that the sample of nine unrelated individuals on those autorads are consistent with being taken from the R.C.M.P. data

base. That there is no statistical deviation of those either on the bands that they have, on the fact of whether there's an amount of homozygosity versus heterozygosity that would lead me to suspect that if we took a larger sample from the Miramichi that it would differ from the present R.C.M.P. Caucasian data base.

Q. Doctor, I believe after you testified last week that you provided me an explanation of the formula that you arrived at and the figures?

A. Yes.

Q. So that I could fax this to Doctor Shields?

A. Yes.

Q. So that he could have a look at it.

A. Yes.

Q. And is this what you had faxed to Doctor Shields - or what you had given me to fax to Doctor Shields?

A. Yes, it is.

MR. FURLOTTE: My Lord I would like to enter this as an exhibit.

THE COURT: That will be D-12.

(Clerk marks document entitled "Band Sharing Between Unrelated VNTR Genotypes" exhibit D-12.)

THE COURT: Should we give this to the jury to read now or what is the best time? Is this the hieroglyphics of the formula or --

MR. FURLOTTE: I doubt if the jury would be able to understand it without any explanation.

THE COURT: Well, it's in evidence; they've got to understand it. They've got to be given the opportunity to understand it. Whether they do or not is --

Why not have this witness read out that. It's in your writing, Doctor?

A. It's in my writing and proceeds on for about four or five pages My Lord. I'm happy to follow the Court's wishes.

THE COURT: Why not have this -- Rather than have the jury read this document either now or later wouldn't it be the best thing to have the witness read the matter. It may mean something. I have my own suspicions about that. No reflection on the jury intended. But I think this would be the best way perhaps to acquaint the jury with that document.

MR. FURLOTTE: I agree, My Lord. I thought you meant give it to the jury without an explanation.

THE COURT: Oh no, no, no. No. I'm not talking about an explanation. I'm just talking about conveying the content of the memoranda to the jury. Let's do this. Let's have -- Is this agreeable to counsel?

MR. FURLOTTE: I'm just wondering how long you want to go on before you break.

THE COURT: Well let's do this before the break and that will give them something to think about during the break. They can even take it with them perhaps and have it with their coffee.

Why don't you sit down, Mr. Furlotte, and rest your bones while the Doctor reads this. It's going to take a little while.

A. So this proceeds on for five pages and I start with the heading being "BAND SHARING BETWEEN UNRELATED VNTR GENOTYPES".

"An argument can be made that increased amounts of band sharing between individuals is evidence of population substructure and/or inbreeding. In order to evaluate whether or not a level of band sharing is high, we need to estimate the expected degree of band sharing in a random mating population."

Now I go on to a derivation of the formula that is going to allow me to do this.

"Let the bin frequencies for a VNTR locus be given by: P_1, P_2, P_3, ... P_n."

These would be the frequencies of the bins that you had estimated from your population sample.

"The population is in Hardy-Weinberg equilibrium so the expected genotype frequencies are give by P_i^2 for homozygotes (that is to have two bands from the same bin it would be frequency of that bin multiplied by itself for all of the bins) and $2P_iP_J$ for heterozygotes."

That is if you have a band in one bin and a band in another bin the frequency of that happening is the probability of one times the probability of the other multiplied by two because you could have it coming from mother and father in both ways.

"We can calculate the probability of not sharing a band by considering two mutually exclusive, exhaustive cases."

There's two ways that you could approach where you are comparing two individuals that did not share a band. The first case is where your first individual is homozygous, that is has a single band so both bands have come from the same bin. In this case:

"No bands will be shared if the second individual contains only bands in bins other than that of individual #1."

Thus the probability of no bins being shared is the sum of all of the probabilities of getting that particular homozygote, which is P_i^2, times the

probability of 1 minus that probability squared because you have to have the other individual not having that band at all, so the probability of that is the summation of the P_i^2 times the $(1-P_i)^2$ over all the different bins. That's one case. So that would be the probability of not sharing if you had the first individual homozygous and then whatever the other individual was. That's the probability of that.

Case number 2 is where individual 1 is a heterozygote. So individual 1 has two bands.

> "No bands will be shared if individual #2 contains only bands that are not in the same bins as both bands of individual #1."

Thus the probability that no bands are shared in this case is the double summation over P_i and P_J of $(2P_iP_J)$ times the quantity $(1-P_i-P_J)$, that total quantity squared, summed over all of the combinations of where P_i -- where i does not equal J. It's algebra. It looks intimidating. The ideas, for people who work in this area, are relatively straightforward, and so far as I understand in my discussion with Doctor Shields on the phone since I last testified he agrees to this approach too.

> "Now we can derive an expression for the probability of sharing at least one band between two random individuals since,"

the probability of sharing a band is just 1 minus the probability of not sharing a band. It seems quite evident that either you have to share a band or you do not have to share a band. So that's what we mean by exhaustive. We've looked at all the possibilities. Either you share or you don't share.

It's as simple as that. And you have to fall in one place or the other so those two probabilities have to add up to one because one of the situations has to hold. So I can calculate then the probability of sharing a band by subtracting the probability of not sharing a band, which I have just calculated in those two cases, from one, which I do, and so the probability of sharing at least one band, could be more than one, is equal to 1 minus the summation from 1 to n of P_i^2 times $(1-P_i)$, quantity squared, minus the double summation of $(2P_iP_J)$ times the quantity $(1-P_iP_J)^2$ summed over all the cases where i does not equal J. So that's the formula.

THE COURT: They've followed everything so far.

A. Now, when we have K individuals, K could be some integer number, we have 5 individuals K is equal to 5, if we have 25 individuals K is equal to 25. The number of pairwise comparisons we can make if we have K individuals is given by K times 1 minus K divided by 2. In this particular application if we have 9 people there are actually 9 times 8 divided by 2 or in fact 36 possible pairwise combinations. It comes about because if you have 9 individuals you can compare individual 1 with individual 2, individual 1 with 3, 1 with 4, 1 with 5, 1 with 6 all the way up to 9, 2 with 3, 2 with 4, 2 with 5. If you enumerate all those, it's where this formula comes from, you have 36 combinations of pairwise comparisons when you have only 9 individuals. And that's a little bit surprising sometimes but when you think about it it's the case.

So that's K times (K-1) over 2.

"On the autorads run for the Legere case, I had John Bowen score the 9 unrelated individuals:

183
185B
188B
191A
195C
157A
56A-69A
115B
1IF."

So those were the nine individuals known in this code, in fact I'm not even sure which of these numbers applies to which particular individual by name in any case.

"This resulted in $\frac{9 \times 8}{2} = 36$ pairwise comparisons. For the six probes he reports the following number of pairwise comparisons."

So he went back to the autorads, and I asked him to do this, and scored for each of these 36 pairwise combinations for each of the loci how many times of those 36 comparisons you got a band being shared, at least one band being shared. For the D1S7 locus it was 4; the D2S44 it was 5; the D4S139 it was 8; for D10S28 it was 7; for D16S85 it was 11; for D17S79 it was 19. So that's the observed. That's what you observed with this sample of nine individuals. You had those numbers. Those numbers of 4, 5, 8, 7, 11, 19, they seem high.

"To calculate the expected number of pairwise comparisons that share at least one band we need to plug the observed bin frequencies into the previous formula."

I'm just going to spare you that rereading of the formula.

> "This is only feasible using a computer program, but a reasonable approximation can be obtained by calculating the expected value when all n alleles (when all bins) are equally frequent. This is done for n = 2 - 10, 13, 26, 50 in table 1 (page 4)."

And I have a table here where I have calculated the expected amount of band sharing in pairwise comparisons for the cases where you had two bins, three bins, four bins, five bins, six bins, all equally frequent. And I have that tabulated here and those numbers range from in the case where you only have two bins you expect 87½% of the time that if you took two people at random that they would share a band all the way down to the case where if you had let's say 26 bins, 26 equally frequent bins, that you would expect only 14% of the time when you took two people at random that you would share a band. But still the numbers run from a high 87% of the time. Most of the time if you had only two bins you would expect - and those bins were equally frequent, you would expect there to be band sharing to the case where you have 26 bins where still 14% of the time, that's like 1 time in 7, that's I think counterintuitively high it seemed to me for 26 bins but that's what the formula predicts.

> "We then use the observed homozygosity at each locus to find the effective number of alleles (n_e) for each VNTR probe. The value of n_e is used to then estimate the expected frequency of band sharing for that probe from table 1."

Table 1 is the table that indicates for equally frequent bins what the expected band sharing frequencies are.

So from that for each of the probes I did a calculation. For the D1 locus, for example, you would expect using this approach 27% of the time when you compare individuals they would share a band. For D2 you expect 27% of the time. For D4 41% of the time. For D10 7% of the time. For D16 41% of the time. For D17 58% of the time. Almost 60% of the time for the D17 locus when you looked at two people they would share a band. Very high.

"Since 36 pairwise comparisons were made for each probe,"

which I have later refined because it turns out that for two of the probes only 28 comparisons are possible because the data is not available for that probe on one individual, in this document I have for D1 we observed 4, we expect 9.8. For D2 we observed 5, expect 9.8. For D4 we observed 8; we expected 14. So it's fewer than we expected. For D10 we observed 7; we expect 5. A little bit higher. For D16 we observed 11; we expected 14. For D17 we observed 19; we expected 21. These numbers, just a parenthetical remark, My Lord, actually have been modified. I sent further information to Doctor Shields and I have refined my calculations beyond this particular one, so the numbers are a bit different in reality when you do the calculations using the adjusted numbers that John Bowen had given me, and there's another way of adjusting that I'll go into a little bit later. But these numbers I don't mean to take as sort of the absolute ultimate answer, but the point is in this the observed number that you saw of band sharing was really for most of these probes not statistically

different from what you really would expect. Okay? Which was what my conclusion. And the last page on this, the fourth page, is the table that I tried to summarize for you.

> "CONCLUSION: There is no evidence in this sample from the Miramichi that this group of 9 unrelated individuals has any more band sharing than a random sample of 9 individuals would have from the populations sampled for the R.C.M.P. data base.
>
> This sample of 9 individuals cannot be used to argue for substructure and/or inbreeding in the area from which they derive."

And then I signed it with the date and I have my telephone numbers on there for a person to be able to contact me if they needed further explanation.

THE COURT: Well, I think we will stop there for a recess.

JUROR LANCASTER: Excuse me, My Lord, can we have a couple copies of that to look over and try to absorb some of it.

THE COURT: Yes. I'm sure counsel would not object to that. Why not have the clerk run off copies of this. Make sure they are accurate copies of the original. Mark "Copy" in the corner so they won't be confused with the original. And Mr. Sears will bring it in to you as soon as they are available. Is that agreeable?

JUROR LANCASTER: Thank you My Lord.

(RECESS - 11:00 A.M. - 11:30 A.M.)

COURT RESUMES. (Jury called, all present. Accused viewing proceedings from holding cell.)

THE COURT: Okay, Mr. Furlotte.

CROSS-EXAMINATION BY MR. FURLOTTE CONTINUED:

Q. Okay, Doctor Carmody, in your formula and explanation of the band sharing between unrelated VNTR genotypes could you tell me why you developed the effective number of alleles? Why you use the effective?

A. I am using the effective number of alleles because the formula requires very lengthy computations to use the actual bin frequencies and that can only be done after I write a computer program to do it. It's not practical to do all the exact calculations using the actual frequencies in the bins on a hand calculator. And using these effective number of alleles, the effective number of alleles defined in population genetics is basically the number of bins that you would have of equal frequency that give you the same amount of homozygosity/heterozygosity that your actual bin frequencies give. So it's a number that is used extensively in population genetics as a way of mathematically calculating things where you don't know the specific or it's more complicated if you use each bin frequency being different. My sense is that using the effective number of alleles is the closest we can approximate the correct answer of this formula without going through the extensive lengthy computations that would be required to use the actual bin frequencies. And essentially what it does is it compensates for the fact that if you have a locus where you may have ten bins but 50% of the time the bands fall in only one of those bins that means that most of the time you are going to get a band from that bin and only rarely are you going to get it from the other

bin. So that though you have indeed 10 bins the effect at that locus is as though you had fewer bins but that they were all equally frequent, and the effective number of alleles is in a way of establishing that correspondence. It's the number of equally frequent bins that give you the same amount of expected homozygosity as the actual uneven distribution that you have in the bins that in fact you use. And so I did it as a shortcut and I recognize its limitations and I recognize the fact that it is not the actual calculation using the actual bin frequencies. I would argue, however, that the number that you get using the effective number of alleles is going to be very close to the number you would actually get when you did the real calculations using the actual bin frequencies.

Q. Okay. And I notice also in your argument you state that in order -- In D-12 you state: "In order to evaluate whether or not a level of band sharing is high, we need to estimate the expected degree of band sharing in a random mating population."

A. That's right, because that's the hypothesis that I'm testing. You see the hypothesis that I'm testing is that this sample came from a completely random population, from a population that showed no sub-structure, from a population that was like the population that we derived the R.C.M.P. data base from.

Q. Okay. And this formula that you put together applies to a random mating population.

A. That's right, and that's the prediction - that's why we're testing that hypothesis you see. That's the hypothesis we're testing. Because if you had the hypothesis well this is not a random mating population it's very difficult to test that because then you would have to stipulate well what do you mean and to what degree is it not random mating. So the real virtue of having a no hypothesis that everything is simple and random is the easiest thing to test, rather than saying well it's not random because then you have to specify exactly to what degree is it not random, and you can choose all sorts of levels of the parameter, whereas when you say it's random there's one fixed prediction from that and it's the simplest model. It's the no hypothesis we call it in hypothesis testing.

Q. And basically that's what the scientists are trying to show that there is substructure; they're trying to show as to what degree there may be non-random mating.

A. That's right. That if the results showed disagreement with the predictions from this approach it would not be consistent then with this hypothesis and you would reject that hypothesis.

Q. Now, do you believe that the listed number of homozygotes are a true representative in your calculations?

A. In fact the numbers that I have used and in fact the further numbers that I have sent to Doctor Shields are slightly modified from the numbers in that submission because there was further work done and in fact I did calculations further using the expected

homozygosities rather than the observed homozygosities. So that the numbers -- My final numbers in fact differ slightly from that, and in conversation with Doctor Shields of which there were two by telephone since I last testified and one this morning, it's clear, and I fully agree, that one should use the expected homozygosities rather than the observed homozygosities which I've done in further calculations. And I believe Doctor Shields has used as well.

Q. So you have used the expected there now?

A. I have used the expected now, yes.

Q. In your original calculation you used the observed?

A. The observed, which is incorrect.

Q. Incorrect. But all the data in the R.C.M.P. data base is using what? - observed or expected?

A. Well, there's in fact both pieces of information there, and the reason I used the observed in that particular submission was that that one was easily and more readily available because it's right there as a number. To get the expected I had to do some further calculations and in the pressure of time to get that to Doctor Shields I did the simple expedient of using the simpler of the two knowing clearly that it was not the best estimate to use but I used it.

Q. Now, in these do you multiply those together when you calculate the frequencies or the probability of expected band sharing?

A. I just calculate the expected probability for each of the loci separately. That number of the observed or expected in this case, which I ultimately used

expected homozygosity, is used to estimate the effective number of alleles which is then looked up in that table that I did the calculations for that are in that submission, and that table is the same table that I have used subsequently using effective number of alleles derived from expected homozygosities to then used the number that comes out of that table, so in the column where you have a number that is the expected amount of band sharing that you would expect to see at that locus, that is the number that derives and lines up with the effective number of alleles that you would have given that expected homozygosity.

Q. Okay. Did you fully explain why you can't use the actual number of bins?

A. The reason I couldn't is because I don't have enough time to do that. It would take me a week or two in fact to develop a computer program that would do those calculations. There are a lot of calculations that have to be done there. It doesn't seem that many but you have to multiply in a number of those cases in the formula different bin frequencies by one another and multiply them by themselves in some cases, and it's just not practical for me to do it on a hand calculator without spending three or four days.

Q. But the only way to develop this accurately or reliably is to use the observed bin frequencies?

A. That's correct. So that these numbers are an approximation but that in my opinion they are going to be very close to the number that you would get when you use the actual bin frequencies.

Q. So I'm just wondering as to why you would draw these very strong conclusions with inappropriate data.

A. Because we know - and in population genetics theory we know that using effective number of alleles in these kinds of formulas will be giving you numbers that are very close to the frequencies when they actually jump around. It's used quite extensively. The effective number of alleles is used quite extensively in population genetics to calculate inbreeding coefficients, to calculate effective population sizes, to calculate amounts of genetic drift that can happen, and it's a standard simplification that is used in population genetics.

Q. And, again, I believe your calculations of the number of observed - numbers of pairs that shared at least one band you say you got that from Doctor Bowen?

A. The observed number of actual shares in those pairwise comparisons I got that from Doctor Bowen. I had the set there. When he was back in Ottawa and I saw him on Friday while I was back in Ottawa he went through the data again and there was a slight change there which I submitted to Doctor Shields by fax on Friday.

Q. Is this what you faxed to Doctor Shields on Friday?

A. That is correct.

Q. I believe there might be a small difference here where Doctor Shields may have marked something in, this last column that are --

A. Yes, that's right, and we discussed this, he and I, over the phone and that results from the fact that

when we scored 9 individuals we included as one of the individuals Donna - one of the two sisters, Donna. These have to be unrelated so we didn't use the other sister. You can also do the same calculations if you include Linda and not Donna. And so the numbers that he has added here are the numbers you would get for the observed number of pairs that matched if you used Donna in the 9 person data base and not - if you used Linda in the 9 person data base and not Donna.

Q. So you agree with those numbers?

A. I agree with those numbers. And they are slightly different, and they are different in some cases, surprisingly so, from using Donna.

MR. FURLOTTE: I would like to enter this as an exhibit also My Lord.

THE COURT: D-13. Further modification of formula.

A. That's not a modification of the formula, My Lord, it's of the observed data in the 9 person sample you could take a 9 person sample and one of those 9 people could be Donna but then you would want to have them all unrelated so you have to choose either Donna or Linda. We did it using Donna. You could also have a 9 person sample if you take Donna out and put Linda in it.

THE COURT: Yes, but I mean it's a modification of your formula paper or message.

A. Yes. Because in fact I've done the calculations, as I believe Doctor Shields has, using the data base with the one individual changed in both cases.

THE COURT: I was just looking for a short title to put on the exhibit list. Modification of formula paper.

MR. FURLOTTE: I will show that to you Doctor. Doctor, I will also give you D-12 and maybe you could show us or state where the numbers have changed and by how much.

A. Okay. In the case of the first probe, the D1, and I'm looking now on page 2 of my original communication with Doctor Shields, where we had scored - or Doctor Bowen had scored four pairwise comparisons of the 36 that had a match that now becomes 3 in the case of the data base of 9 with Donna in it and becomes 7 in the case of the data base of 9 where Linda is in it and not Donna.

Q. So four changed from a three to a seven - from a three and a seven?

A. Four changed to a three in our original data base and it changed to a seven if you put Linda in there and took Donna out.

Q. Okay.

A. For the D2 locus we originally had - and Doctor Bowen had said there was five matches, or comparisons where there were matches, that went in the revised data that we provided to Doctor Shields, it went to fourteen in the case of the data base containing Donna and it went to twelve in the data base containing Linda.

Q. And that's quite a change in this one.

A. So it had gone up - it had, oh, more than doubled.

Q. Almost tripled in the case of Donna?

A. Almost tripled in the case of the data base with Donna, yes. And this was because in fact when the original scoring was done the original scoring was

done here in Fredericton by Doctor Waye and Doctor Bowen when I asked them for this data and they did it strictly in their hotel room using visual match criteria. They went back when Doctor Bowen got to Ottawa and used the match criteria that's used by the R.C.M.P. of the 2.6% window and using that 2.6% window in fact you call more things matches and shares then you would visually. So the reason that this went from five to fourteen or twelve was that if you were to look at these on the autorad you would not call them a shared band because they would be slightly different, but they wouldn't be different enough by the match bin criteria that the R.C.M.P. uses to call it different, so that they use that criteria of the match bin of 2.6% to tell whether it was a shared band or not when in fact visually it's not a shared band. Nevertheless we put it in because that's the proper thing to do statistically. So that went up from five to fourteen, and in the case of the data base without Donna and with Linda in it it goes up to twelve.

In the case of the D4 locus where they had originally scored eight visual shares that went up to ten in the case of the data base with Donna in it, and goes up to twelve in the data base with Linda in it. So in both cases eight went up. It went up to ten and it went up to twelve in the case of the second data base.

In the case of D10 we originally had recorded - or they had originally recorded or reported to me seven. That now becomes eight in the data base with

Donna and remains eight in the data base with Linda. So it remains the same but it has gone up by one in both those cases.

In the case of D16 we originally had reported eleven and these are now out of twenty-eight possible pairwise comparisons because there are only eight people in this data base now because we don't have the information from the autorads on D16 and D17, so there's only eight people and so eight times seven divided by two is twenty-eight comparisons that can be made. So in the twenty-eight comparisons of D16 we had originally - and they had originally scored eleven, that now becomes seven in the case of the data base with Donna and becomes eight in the data base with Linda. So in that case the original number eleven now has decreased to seven or to eight so it's gone down in that case.

In the case of D17 where they originally called nineteen comparisons of the twenty-eight being sharing a band, that becomes twenty-three when you use the 2.6% match window criteria, so nineteen goes to twenty-three in the case of the data base with Donna and it goes to twenty-two in the data base with Linda. So in both those cases it's gone up from nineteen in one case to twenty-three and the other to twenty-two.

So as a result of this, in the majority of cases for these six loci the revisions are such that the number of pairwise comparisons that show a band being shared by the match bin of 2.6% criteria has gone up in the majority of cases although in some it has gone down.

Q. The only one it has gone down in is in the D16.

A. No, D1 has gone down in the case of the one in the original one but it has gone up in the case of the other one. I think if anything what this data is telling me, just looking at the numbers, of let's say we have just comparing the two data bases of nine individuals where there are eight that are held constant and you are just swapping one or the other one in, in one case you get three being shared, in the other case you get seven. So just by changing one individual in nine in that data base you go from three to seven out of thirty-six. That sort of tells somebody who is trying to analyze this data if you have a sample and if you by changing one individual in that sample can get that kind of a change, it's telling you that you need a bigger sample. Okay. That's what it's telling me. In the case of other loci, D2, where it's fourteen and twelve well that's not too much different and that's kind of the difference you would expect. In the case of D4 you get ten and twelve. Again, that's maybe not too different. In the case of D10 it's the same, eight and eight. In the case of D16 it's seven and eight. In the case of D17 it's twenty-three and twenty-two. Those sorts of changes are what you would typically expect when you swap one person for another in a data base of that size sample it would seem to me, but in the case of the D1 where you double by just changing one individual in that data base it's saying to me as a statistician that, hey, this data base, you know, we have to be very, very cautious of drawing any inferences from

this small a size data base. That the conclusions we're going to draw when the number can double or halve, depending if you just change one individual in that data base, is saying that you need a larger data base.

Q. But Doctor you're really only changed that drastically in the D1S7?

A. That's right.

Q. You go from a three to a seven.

A. That's right. Which is more than doubling.

Q. The other ones are much closer. The D2 you're only out by 2; the D4 you're out by 2; the D10 they both have 8; the D16 you're only out by 1; and the D17 you're only out by 1.

A. That's right, and they can go up or down. They're not always going in the same direction which is telling you something too. That would be a kind of pattern that one would expect if indeed these were randomly chosen. One would expect that kind of variation to happen. The variation of going from three to seven does seem quite large to me actually for that locus and shows how sensitive this sample of nine is to the particular people who are in it.

Q. Okay. Now, before you revised your data and came up with the bigger numbers I suppose, what analysis did you use on the original data to reach your conclusion that there is no evidence for substructure and/or inbreeding in the area from which they were derived?

A. I used, actually, three approaches. I first went back and I said well before we even look at band

sharing if we took these nine individuals and considered them to be a data base does the pattern of bands that those nine individuals have look like the pattern of bands that we have in the R.C.M.P. Caucasian data base. And there is a statistical test, a likelihood ratio test, that can be done to compare the frequency of the bands you have in that set of nine with the frequency of the 974 individuals that we have in the R.C.M.P. data base, and for all of those loci, the D1, the D2, the D4, the D10, the D16, the D17, there is absolutely no statistical difference in the frequency of any of the bands in that sample of nine whether you include Linda and not Donna or you include Donna and not Linda. So that says that that sample of individuals could statistically be drawn from the R.C.M.P. data base and it's consistent. You cannot see any difference. Now, I have to concede that when you have a sample of nine you would have to have a very extremely different sample in order to pick up a difference from comparing a sample of 974 individuals to a sample of 9 individuals. I would be the first to admit and say that goodness, you are very unlikely to have seen a difference. But the first thing that I did was to do that test. It's a rigorous statistical test and you can calculate it and you can see that in fact there's no deviation. In fact for most of the loci something like 80% of the time you would expect to get a pattern like you got. So that was the first test I did. The second test I did in these samples of nine in each of the two alternate ways of doing

the data base was to compare the expected amount of time that you would see an individual that had just the single band. That's what we call homozygosity. To look and see whether there was any increase or decrease in the expected level of homozygosity in this sample of nine individuals compared to what we would predict if this sample had been drawn from the R.C.M.P. data base, and there was none. At none of the loci was there a statistically significant deviation. Now, I have to concede also in this case that with a sample of nine you really don't have enough to do a powerful statistical test. So there's limitations there. And you would only see a significant difference if there was a very, very strong deviation. But nevertheless there was no pattern that would suggest anything but having drawn this sample from the R.C.M.P. data base in either the bin frequencies or in the levels of homozygosity/ heterozygosity. Okay? Two of the tests that I used on the big data base I applied to this very small data base.

I then did the comparisons at each locus. I said at D1, for example, I compared the observed number of times of the 36 comparisons that we saw a band being shared, which was 3 in the case of the data base with Donna. We expected to see by the formula I developed and using the effective number of alleles that was appropriate for this locus - we would expect 7.75. Okay? This comes out to be a fractional number because that's the way the calculation comes out. It doesn't have to be a

whole number like an integer which the observed number has to be. You either observe 3 or 4 or 5 as an integer. So you observed 3, you expected to see 7, so in fact in that data base you have an under-representation, actually, of the number of band shares, which you would expect, statistically. That's not significantly different. If you compare what the expectation was in the data base with Linda you would expect to see 7.75 there too. You observed 7. Bang on statistically, okay? In fact there's no statistical difference for that one.

Looking at the D2 locus, okay, you observed in the case of one data base 14, in the other data base 12. In both those cases you would expect to see by the formula 9.85. So is 9.85 really different from 14 or 12. If you do the statistical test appropriate for that, the so-called chi-square test, you find no evidence of statistical signficance. Okay?

The D4 locus, that's two loci down, the third locus at the D4 locus you expect 10 in one data base, 12 in the other data base. Sorry, those are the observed. You observed 10 and 12. What do you expect by the formula? 11.88. Pretty close, right? Well, if you do the statistical test they're not statistically different. That's three loci where there's no statistical difference for the amount of band sharing. For the 4th locus, D10, you expect to see 8 in one data base, 8 in the other data base. What do you predict? You predict there should be 7.75. 7.75, is it different from 8? I think it's clear it's not. Statistically it's not.

Looking at the D16 locus, okay, you observed 7 in the case of one data base, 8 in the case of the other data base. What do you expect? You expect to see 18. You expect to see many more than you actually observe, okay. Well, that's telling you that in fact it's under-represented. There's no more band sharing there than you would expect to see by chance. In fact there's fewer. And it's statistically significantly lower which makes you kind of wonder, hey, maybe there is something funny going on at this locus and in fact maybe there is, I don't know. But in any case, there is no information at that locus that you have too much band sharing. If anything, you have too little.

At the last locus, at the D17 locus, you expect to see in one data base 23, in the other data base 22. You expect to see 16. 16.35 is the actual number. That turns out to be statistically significantly different. That is that at that locus and only at that locus, and the one locus out of six, that's the only locus where you have more band sharing than you would predict statistically by this hypothesis. Okay?

So to summarize that, of four of the six loci there's absolutely no evidence that this sample is any different than if you had taken it from the R.C.M.P. data base. For the 5th locus - that's four out of six - for the fifth locus you see that in fact you have too few bands being shared than if you took it from the R.C.M.P. data base. We're just saying that it's different statistically and

you kind of wonder why that is. I don't have an explanation why that is. My explanation would be, and my advice would be, hey, taking a sample of 9 is too small a sample to do anything that has any meaning in it, we need larger samples, and we can't draw inferences from a data base of nine people. And it's only at one locus of those six loci that in fact you have more bands being shared than you would predict by the theory that I developed. Okay.

So that's the conclusion that I used to draw the inference that in fact this data base certainly does not convince me that there is any significant difference in it that would lead me to suspect that this could not have been drawn from the R.C.M.P. data base. That those deviations in the case of one locus going in one direction and in the case of the other locus going in the other direction, is telling me that in fact to do anything that is statistically appropriate with this data I need a larger sample or I need more samples of the same size to compare a lot of individual samples that are all that same size. So my analysis of the hypothesis that there is an increased amount of band sharing for these VNTR loci in this sample of nine random individuals I would say I stand on, that there is no evidence that I can see in this that would support that notion. There are some statistically significant differences but I would say what they're telling me is that I don't have a large enough sample.

Q. Doctor, if you don't have a large enough sample now, now that there are statistical significant differences, why is it that you had a large enough sample last week on Thursday to show that there wasn't any statistical significant difference?

A. Well, I'm actually -- It may sound like I'm saying a different thing but I'm saying the same thing. I'm saying now that in fact the way these numbers - and I would have said then if somebody asked me, and in fact I said in the voir dire that doing this kind of analysis on a sample of nine individuals is a pathetically poor sample, and those are my actual words that I remember verbatim. It's a pathetically too small sample. I would, as a statistician, be reluctant to draw any conclusions that I would be willing to stand behind from this size of a sample and particularly by doing this kind of analysis.

Q. It may be a pathetically small sample to form a population data base for any small community but when you're testing empirical tests to see if the data fits the theory there is no need of large samples.

A. Oh yes there is, and this is telling me that that's exactly what is needed in this case. That if I wanted to test the hypothesis of increased band sharing in this area I couldn't do it on a sample of this size.

Q. You're testing in this case Mr. Legere's sample with a pathetically small sample.

A. I have a sample from an individual --

Q. From the Miramichi area.

A. And I'm comparing that to the 974 individual Caucasians in the R.C.M.P. data base and that sample of 974 is a very adequate sample.

Q. You do admit that your original conclusions was based on wrong data?

A. My original conclusions based on wrong data? No, I'm not sure what the wrong data is. I mean my conclusions on that original data that I supplied to Doctor Shields on Friday was in fact the same conclusion that I'm drawing now, that there were some loci there that differed but that in those cases you were getting fewer - in most cases fewer shared comparisons than you would expect.

Q. Now that you have the correct data on band sharing rates would you reach the identical conclusion that you did last Thursday or would you now admit that evidence exists which is consistent, not necessarily proves, but is consistent with Doctor Shields' suggestions?

A. I would say that the data are consistent with both it being a sample from the R.C.M.P. data base as well as Doctor Shields' opinion that in fact there might be some band sharing. That I think that you would need to get a larger sample to decide that question ultimately and finally. I would say that there is enough information in the analysis so far that would lead me to be very chary of drawing any conclusions that I would be wiling to stand behind. That I think it's perfectly consistent with there being no substructure in that area. It could also

possibly be at maybe one locus or maybe two of those six that there may be some effects that in a larger sample might be drawn out, but on the basis of this size sample I would be reluctant to draw what we would call in statistics a robust conclusion.

Q. But you were pleased with relying on that small size sample last Thursday when you drew your original conclusions that there is no excessive amount of band sharing in that area?

A. Well, I would still say that certainly for five of the six loci there's no evidence of excessive amount of band sharing. It's only one of the six. And then that is sort of consistent with a very small sample like this having just that happen by accident of the sampling, and particularly I see that when if you swap one individual for another in that sample of nine the inference changes slightly for the one locus, the D1 locus, and if it can change for that one I'm not comfortable drawing strong inferences from this size data set.

Q. Okay. But the expecteds that you stated, they don't match. The expecteds don't match the observed.

A. The expecteds don't match -- only match in four of the six. That in two of the six there are statistically significant deviations. In the case of one locus you have too few band matches. In the case of the D17 locus you have too many. And the only evidence that I see in this data that are consistent with there being any band sharing are for the D17 locus.

Q. But you were all pleased with your data last Thursday because there was no statistical differences. Because you had the wrong data and there it was a beautiful test.

A. No. In fact the data showed statistical differences but the differences were as much on the side as having under-representation as over-representation. And the other thing you can do, which we can talk about the statistical propriety of doing this, is to take all the data and amalgamate it together and say well look we have these different loci we're looking at individually, what if we put it all together and looked at it as one kind of sample from the human genome. And if you do that the observed number of matches, as in the case of one data base 65 and in the case of the other one 69, the expecteds are 72.09. And that's not statistically different. So when you look at the data in total it doesn't give any overall expression to there being any more band sharing then you would expect. In fact in total there's less band sharing present than in fact you would predict if you lumped all the data together. Now, I understand why statistically it is not strictly proper to add these categories together when you already know that there are some statistical differences with two of them but what I am saying is that if you hadn't done that previous analysis and you did that you wouldn't find any difference overall in the entire data set. The single locus that goes up is balanced off by the single locus that goes down and the other loci are bang on.

Q. Okay, Doctor, does statistical analysis take sample sizes into consideration during the test of the hypothesis?

A. Yes, it does, and it should compensate for the size of the samples.

Q. So we know the size of the sample in this case, nine samples, they are statistically significantly different and --

A. In the case of two.

Q. And that test of statistical differences has taken into consideration the size sample and it still fails.

A. It does factor in -- I would say it's not that the test fails. The test in fact corroborates the no hypothesis for four of the six, and for only two of them is there any difference and because the difference goes in opposite directions it makes me very suspicious of drawing any strong conclusion from that. It's telling me that if the phenomena that your hypothesis is claiming is true here, that there is an increased amount of substructure or inbreeding going on, that that should have its influence at every locus, not just at a single locus, and it wouldn't go up at one locus and down at another locus. That it's saying that there are some phenomena going on here that we still don't fully appreciate and understand the biology of that are not necessarily at all related with inbreeding, sub-structure, whatever you want to call it.

Q. Do you agree now then that there is more band sharing in the nine that you have done than you would expect by chance based on the R.C.M.P. data base?

A. Only at the D17 locus. Only at one locus of the six.

Q. And is that because the sample size is too small?

A. I'm not sure, and the only way I can know that is in fact to take a larger sample or take more samples of the same size.

Q. But the sample size didn't change from last Thursday till today?

A. No, it didn't.

Q. And it was sufficient last Thursday but it's not sufficient today?

A. No, it was insufficient last Thursday and it's insufficient today and it was insufficient back in May when I testified in the voir dire that it was insufficient.

Q. Well if the sample size was insufficient last Thursday how could you testify in court that if you picked any nine individuals at random through the R.C.M.P. data base you are going to come up with the same thing?

A. Well, in fact I felt and I still do feel that if I took samples of nine individuals from the R.C.M.P. data base I think the results would come out to be very close to this. Maybe not for D17, maybe not for D16, and I wouldn't expect them to be corroborated there, but I just suspect at those two loci that what we're seeing, either a disproportionate increase or a disproportionate decrease, has nothing to do with in fact substructuring in that population. There are many, many alternate explanations as to how those numbers could be statistically different like that. It can happen.

Q. Would you admit, Doctor, that there is at least some degree of more band sharing than what would be expected?

A. Only at the D17 locus.

Q. On page 2 of D-12 --

A. Yes.

Q. -- you state the probability of sharing a band equals 1 minus probability of no bands shared.

A. Right.

Q. And that's just the formula that you're supposed to use for the probability of sharing bands?

A. That's a probability and in fact as I have changed it in the second expression there, it really is the probability of sharing at least one band. It was a shorthand, actually, to be able to fit that line on one line, so in fact the first statement that the probability of sharing should read the probability of sharing at least one band which is the way I've written it on the second line where I have a little more space to write it.

Q. And that is the proper formula for calculating the probabilities of sharing bands?

A. That's correct.

Q. When the frequency calculations were done in Mr. Legere's case as a probability of somebody else sharing the bands that he has that formula wasn't used?

A. That's a different question. You're not asking the same question that this formula answers.

Q. Okay, why is it a different question?

A. It's a different question because this applies to taking two random individuals and then calculating the probability that they would share at least one band, D1, D2, D4, at each individual locus, and that's what that calculates, not a specific band. Not a band that you knew one individual had ahead of time, but that if you didn't know anything about the genetic profile of either of the two individuals this formula would calculate the expected number of shares that you would see if you compared two random individuals.

Q. But we're not doing that.

A. Not in the case of doing the match between Mr. Legere and a forensic specimen, no. We're saying if we have that forensic specimen what's the probability of that as a forensic specimen that we now say we don't know anything about, of in fact sharing a band with something else.

Q. But we are sharing Mr. Legere's DNA profile with an evidence specimen.

A. Right.

Q. So we have our known bands. Everything is known.

A. Right.

Q. The same as when we're comparing Mr. Legere's sharing bands with Donna Daughney or any of the other people from Newcastle?

A. Right.

Q. It's a known factor.

A. Right.

Q. Aren't both set of circumstances the same and the same formula should be used in both processes?

A. No, they aren't at all. Because you had a testing-- I know this sounds like we're getting into statistical subtleties here but the hypothesis that you're testing when you compare a forensic specimen with a known accused is a different question than what you have here. There the hypothesis that you're testing is that they should be identical. This is not asking the question of the probability of these two genotypes being identical. We're asking the question what's the probability that these two specimens could have been generated from two separate individuals versus the hypothesis that they were the product of two samples from the same individual, and that's a completely different question than the one we're attempting to answer when we have separate individuals chosen randomly from the population. Presumably the forensic sample and the Accused, if they match entirely, are matching because they were both products from the same biological individual. We can then test the hypothesis well suppose they came from two different individuals, what's the chance of getting that kind of a perfect match, and the chance of getting that kind of a perfect match is in fact not calculated with this kind of a formula.

Q. Did I understand from your direct testimony when you mentioned the Nichols and Balding formula that that applies to multilocus probes and open bin systems?

A. Well, you can apply it to the fixed bin single locus system as well. It's a way where if you suspect that there was some amount of inbreeding even at a very low level it's an attempt to apply a correction factor to the numbers that you would generate if you used strictly perhaps simplistic assumptions of there being complete random mating, Hardy-Weinberg equilibrium and linkage disequilibrium. So it allows you to correct that formula in a way that would compensate for the amount of inbreeding that you suspect might be present in the actual population. And the net effect is, is that it comes up with a number that is more frequent than the number you get under the non-inbred approach.

Q. And, Doctor, just in brief, when population geneticists are talking about inbreeding they're not necessarily talking about incestuous relationships?

A. No, that's right, and in fact there are people in population genetics that the concept of inbreeding is in fact very much more complicated than a notion that we have of saying that it's equivalent to incest. That you could have inbreeding in a population where there were no brother/sister matings or parent/child matings or uncle/niece matings. You can have what we call inbreeding in a population just by virtue of the fact that if you go back a few generations, enough generations that you've lost track of who your ancestors were, that in fact with a small enough population without any immigration into it stayed the same size, you are necessarily going to get an increased amount of homozygosity, of

genes coming together that have come from a common ancestor that had gone through separate lineages but that now two people who are mating are eighth cousins fourth removed or whatever, which means that they are not strictly unrelated. And so there is a small amount of increased chance that in fact the two genes that have come together could have come from a great, great, great ancestor that way. And if you have a small population that doesn't change, it doesn't get bigger, and you don't have new immigrants into it, that can happen just by virtue of this finite population size. So the concept of inbreeding is used in population genetics in very many subtle ways as just a way of coming up with a number that in fact measures the correlation of two things coming together that both have come from a common ancestor, and is really a statistical concept. So you can have what we call inbreeding in a populations genetic sense without necessarily having any what we would call incestuous matings in the present known population. So the two ideas don't necessarily overlap. If you do have what we would call incestuous matings in the present existent population you would expect to see inbreeding, but if you see inbreeding it doesn't mean that there have to be incestuous matings.

Q. Just like another indication of substructure?

A. That's right, and in fact it can be used and there are ways of referring to it as FST, the inbreeding coefficient from population to total - subpopulation to total population that is a measure of that substructuring. So it's really a rather refined

statistical concept rather than the notion of using that term in general colloquial use. We say there's inbreeding, whatever, we think well, you know, there had been incestuous matings that have produced that. It doesn't necessarily have to be the case strictly that there are incestuous matings in order to have degrees of inbreeding, and indeed if you look at populations - Caucasian populations there are non-zero levels of inbreeding. You can have inbreeding coefficients of .0007 that have been estimated to be the case in certain areas of Quebec. The measures of those are somewhat not that strictly easily calculated and you have to make some assumptions but in virtually every human population there is going to be some amount of what we would call sub-substructuring. It may not be measurable but it would be there.

Q. Okay. Doctor Carmody would you agree that without the knowledge of the frequencies of certain alleles as represented by DNA fragment sizes in a population it is impossible to calculate the likelihood of somebody else out there matching this particular DNA profile?

A. And that's what we have with the bin -- But I would agree that if we don't have those frequencies, unless you make some assumption as is done in the multilocus approach of there being a pragmatic percentage of band sharing of .25 and apply that willy-nilly to every gel and band that you see, you would need a data base to estimate in the case of

single locus probes what the chance of sharing a band is, yes.

Q. And the purpose of forming the data base is to find out what the bin frequencies would be?

A. That's correct.

Q. Now, just to finish off, Doctor, I believe you said that the R.C.M.P. - the fixed bin approach because they have the wider bins, that is a conservative measure?

A. It is a conservative approach where we know the frequencies that we use there are in fact more common and are higher in frequency than the real frequency of what you can detect and distinguish on the gel visually.

Q. Yes. And that is argued by the forensic labs to compensate for maybe the -- I believe you won't agree with the inappropriate use of Hardy-Weinberg formula and Product Rule, but for the shortcomings of nonrandom mating?

A. It should overcome most of - I would say in being careful - I would say most of the effects and most of the reasonably likely effects that are likely to be occurring in human populations in North America.

Q. And is there any statistical way to calculate as to how conservative this is?

A. Not easily that I am aware of.

Q. So although you knew you were conservative you don't know how much?

A. That's right. And there is --

Q. And Doctor -- You have something else?

A. No.

Q. If there is a misuse of the statistics and say there's a misuse of using the Hardy-Weinberg formula and the Product Rule, that could have very serious consequences?

A. Well, I'm not convinced that the consequences are serious. I think they hypothetically could be if you had very, very strong deviations through either substructuring, deviations from Hardy-Weinberg equilibrium and linkage disequilibrium of a relatively strong magnitude. It could change the numbers of let's say 1 in 300 million to perhaps something like 1 in a million as an extreme. Now, going from 300 to 1, that's a big difference. My conclusion, however, would be that that still is telling you, even taking into account that most extreme case, that a genotype - any particular genotype is rare in a population. Now we can quibble over whether 1 in a million is rare or 1 in 300 million is rare and whether there is really any difference between them, any forensically significant difference, and I would say I would rely just on I guess common sense as to whether 1 in a million is rare.

Q. That's if both data bases are reliable?

A. Both data bases are reliable. I mean taking into account all the assumptions, yes.

Q. Taking into account all the assumptions.

A. Oh yes.

Q. Doctor, when you say the R.C.M.P. binning system is conservative but if say, for instance, that the calculation of the frequencies used in the -- it was invalid to use the Hardy-Weinberg formula and

the Product Rule to get your big numbers, that would be much like cheating at cards. If you are going to cheat you can be as conservative as you want with the poor sucker.

A. I don't know whether the metaphor is strictly applicable. I would say that we're taking into account a lot of genetic information at a lot of other loci that have been looked at in human populations and we have some limits. I can place some reasonable limits on what the degree of deviation from Hardy-Weinberg equilibrium and what the degree of deviation from linkage equilibrium can be, and so it's not that they can take the extreme - most extreme values that they're capable of taking but that in fact we're talking about a value that can be off by a few percent perhaps, and that to me, and what I have seen in analyses of those effects, is unlikely to have significant effects on the inference that in fact these genotypes are rare.

Q. But basically the argument of some population geneticists is that the formulation of your bin frequencies and the calculations that the forensic labs are playing with a stacked deck.

A. I don't know playing with a stacked deck, because we don't know ahead of time what --

MR. WALSH: I hope that was a direct quote because that's the way he left the impression.

MR. FURLOTTE: Well, in comparison to the frequencies of --

MR. WALSH: Objection, My Lord. I take it then that wasn't a direct quote. It was Mr. Furlotte saying some scientists say and then he's making up his own words.

MR. FURLOTTE: You're right, My Lord, it's not a direct quote from a scientist. I didn't mean it to sound that way.

A. And the reason that I draw the difference and make the distinction between, to use your term, a stacked deck and the bin frequencies that we have, there is absolutely no information available that would suggest that we are biasing it in one direction or the other direction. In fact it can well be that even if there were certain amounts of linkage disequilibrium or even if there were some deviations from Hardy-Weinberg equilibrium they could go in a direction where the calculations would really show that the genotype is more rare than what we have calculated. In some cases it would be more common, but it could go in the other direction as well. So it's not that you have a stacked deck where you can predict exactly that it's always going to be in your favour. You could have a stacked deck that had been stacked by somebody else and you've been told the wrong information and in fact you could be bamboozled out of your money because you were anticipating another sequence of cards rather than the one that was there and it could go against you. So in fact it could go in favour of the accused if there were deviations as well as it could go in favour of the prosecution.

Q. That's if it's legitimate to use Hardy-Weinberg and the Product Rule?

A. That's right.

Q. And if there is no substructure.

A. Right.

Q. In your paper you have your observed and your expected, okay?

A. Yes.

Q. Why is it that your expecteds do not match your observed?

A. Well, for four of the six loci one would conclude from the statistical analysis that the reason they didn't jive precisely was because the nature of random sampling is exactly what you would expect. You would expect that kind of deviation from what you expected just as the result of the sampling of nine random individuals and it's as though you had flipped a coin ten times and you had seven heads. You're going to get that a significant fraction of the time. You're going to get six heads - five. It's not always going to be exactly five which is what you would predict. You would predict you should get five heads. Well, you know from experience that you're not going to get five heads all the time. And if you got six you wouldn't conclude that in fact that deviation from five was statistically significant. And that's the same case here where when we observe 14 and we predict 9.85 and you do the statistical test it shows that and corroborates in fact that you made the intuition that there's no real difference there. And so those differences at the four and five loci are strictly - we used the term earlier in my testimony - sampling error. Are simply the result of the nature of the sampling

process, that sometimes you're going to get a little bit more, sometimes you're going to get a little bit less, sometimes you're going to get exactly right on.

Q. So you're saying that the best way to prove sub-structuring is to put the issue up on a roulette wheel?

A. No, not at all. Not at all. I'm saying that if one attempts to use data like this to show that there is substructuring I would be very leery of drawing that inference from this kind of small sample of nine individuals. I think it's a case where you might say for unfortunate circumstances we have data on so many individuals from this area. It's in the nature of the process of the nature of the crimes that were committed that the R.C.M.P. had data on four victims and some other alternate suspects as well as an accused. Typically, in a forensic case one does not have this many individuals as random samples from a population and the fact that this has been used in this way I think is rather dubious statistically.

Q. So why is it that the written expecteds do not match the spoken expecteds?

A. The written expecteds don't match the spoken expecteds? I'm sorry if I -- I'm not sure what the distinction is there.

Q. The expecteds that you stated on the stand, do they match the expecteds that you stated in your paper?

A. Well, they don't match the expecteds because there was a revision as I indicated in my earlier testimony where I have now used the expected homozygosity

rather than the observed homozygosity to get my effective number of alleles. And those numbers in some cases cause a slight difference from the expecteds that were written down on this paper to the expecteds that I mentioned in my testimony that I'm reading off of my work notes here. In most cases, in some of the cases they are identical because the expected homozygosity was not really different significantly from the observed homozygosity so the effective number of alleles is basically the same and in those cases the numbers remain the same. So, for example, for D17 16.35 is exactly what I had written down. In the case of D16 I had originally 11.5 which in my revised and oral testimony should really be 18.81 which is a lot higher than that and in fact causes more deviation than the original number it had and it's more statistically significant. In the case of D10 I originally had 2.79 for the expecteds and it really is when you use the expected homozygosity 7.75. In the case of D4 I originally used 14.83. It's actually, now, the appropriate number is 11.8. In the case of D2 it remains unchanged. The 9.85 remains the same. And in the case of D1 where it was formerly 9.85 with using the revised expected homozygosities you really should get 7.75. So there are some changes, not only in the observed numbers which we've spoken about earlier, but in the expected numbers that derive from the fact that I've used the expected homozygosities rather than the observed homozygosities and that generates for some of these loci a different

effective number of alleles that means that you have a different expected value for the number of band shares you should see. And so the numbers in the one submission do not jive for that reason.

Q. So basically what I get, Doctor, is you feel that the size of this nine samples is too small to prove that there is substructure in New Brunswick?

A. That's what I feel, yes.

Q. But then, again, the R.C.M.P. has done nothing to prove that there isn't substructure in New Brunswick.

A. Well, we've done it in the Caucasian data base by looking at the individual samples and comparing them from one population to the next. And other data --

Q. You have never compared New Brunswick population to any other part of Canada?

A. No, we haven't, because we don't have a separate population that we can tag as originating strictly from New Brunswick. The only data base we have that we can strictly say is from people who were living in New Brunswick are these sample of nine. And it's not at all clear that all of these people in the sample of nine actually were born in New Brunswick. I don't even know that.

Q. So the only real evidence that we have which may give us some kind of an indication as to what New Brunswick looks like is the evidence from those nine individuals?

A. Well, we have evidence that we know in our other samples there are individuals from New Brunswick but they're not separately identified and they are

not separately analyzable. That would be an ideal way of seeing whether in fact there was any significant difference in New Brunswick if we had a sample that we could tag and say all of those people are from New Brunswick. Given the limitations of the fact that when you say people are from New Brunswick we hope to mean that is that people who were born here. Now then you can say well certainly not everybody living in New Brunswick was born here and certainly not everybody in the Newcastle/Miramichi region was necessarily born there. From anecdotal evidence that I have heard, I don't want to get into this, but it seems to me that in the Miramichi there are, because of military bases there and because of industry there, there are people coming and going from that region quite often. So what we mean by New Brunswick population has to be refined I think.

Q. So basically Hardy-Weinberg is assumed?

A. Yes.

Q. Linkage equilibrium is assumed?

A. Yes.

Q. Random mating is assumed?

A. Well, that's assumed -- that's subsumed in Hardy-Weinberg equilibrium.

Q. Yes. Substructures are assumed not to exist.

A. That's correct.

Q. And these are the three basic principles upon which you were able to use the 2pq plus the Product Rule to get your numbers?

A. That's correct.

Q. One last question. So the observed -- This is the homozygosity in your paper that you used. So the observed and expected homozygotes differ?

A. Now we're talking about the band sharing or the observed and expected homozygosity?

A. Homozygosity. The observed and expected homozygosity differs?

A. Overall. The problem with doing that test rigorously, statistically, is that the sample is too small. That the only way you can do any rigorous test of that sample is by lumping all the loci together which, as I mentioned in my testimony, has some statistical improprieties in doing that. That you can't rigorously do that. So in fact on a sample of this size you cannot do that test rigorously. But there's no evidence, nevertheless, and one can look at the evidence just without doing a statistical test, there's no evidence when you compare expecteds and observed that there is an increase in the homozygosity at any of those loci.

Q. And the chance that 1 in .8 million that Allan Legere and Donna Daughney would share the particular bands that they do, that's totally irrelevant?

A. That is totally irrelevant because their accidentally sharing bands like that is not as uncommon as this analysis suggests.

Q. It's just by chance.

A. It could be due to chance. It's consistent with it being chance.

MR. FURLOTTE: I have no further questions.

REDIRECT EXAMINATION BY MR. WALSH:

Q. Doctor Carmody you've mentioned - one of the last things you said - you assumed no substructure. Just to clarify that, no substructure affecting these calculations or no substructure, period?

A. No substructure that affect these calculations in any significant way. Statistically significant way.

Q. There could be some substructure?

A. And undoubtedly there is substructure in virtually every human population, not typically detectable though when you look at it genetically.

Q. But not to a degree that would affect these calculations?

A. Not to a degree that it would significantly influence drawing a difference inference from the calculations that we did.

Q. There has been much made of this background band-sharing. Just so that we are clear and the jury understands, we're not talking about the actual matches that the R.C.M.P. declare between two bands; you're talking about sharing one band as opposed to two.

A. It's including all of the potential shares. That you're saying anything that is not a share is a share. That is it could be sharing one band, could be sharing two bands, you can have a situation where you share three bands, that is you have a single band shared with one of the other, or you could have a four band share in fact where you have both like that. So all of those is band sharing.

Q. But this background band sharing is distinct from what the R.C.M.P. are actually calling forensic matches in this particular case?

A. That's right. They are to be distinguished because they are a perfect share through all the bands.

Q. I just wanted to clarify that particular point. Mr. Furlotte had you do some things with 1 in 4500 - Barry Gaudet's 1 in 4500 theory. I believe, Doctor, you had testified previously, I believe it was in cross-examination, that you were consulted by Mr. Gaudet after he had done this - put out this number, is that correct?

A. That's correct.

Q. And in fact that number is disputed?

A. That number is in some dispute and there has been literature that's developed on that topic in fact that I have not been keeping up with.

Q. In fact you didn't necessarily agree with that number as he formulated it, is that correct?

A. Not at all. In fact I would have told him to have done a better experiment, to be honest.

Q. So the numbers that Mr. Furlotte had you doing was on an experiment that you didn't really agree with, is that correct?

A. I was consulted after the fact on that and, as I said a moment ago, I would have told him to use a different experimental design.

Q. Mr. Furlotte brought out the fact that you had developed a formula, you and Doctor Kidd, this particular formula. Who did you consult with in addition to Doctor Kidd with respect to --

A. I consulted with a couple of people at Carleton, Doctor Jussi Helava who works with me, and is my lab associate and teaches in the genetics course, and I consulted with another member of my department who I'm not sure I would say is really supremely qualified in populations genetics but knows quite a bit of statistics and I went through the derivation with him, that's Doctor Hans Damman.

Q. And you have also give it to Doctor Shields as well?

A. And I have given it to Doctor Shields and over discussion over the weekend or since I last testified on Thursday we had two telephone conversations, the first of which I went through the formula and I believe that he concurs that that is the correct approach in terms of the formula. I think we have some differences in terms of what effective numbers of alleles are and so forth, but he is another person that I've consulted on that, and I believe I have consensus on the formula with him.

Q. Doctor, this formula you were talking about formulating it recently, but since Doctor Shields testified have you been giving thought to what he had actually done?

A. Yes, I have. I gave thought during the summer and in fact I --

MR. FURLOTTE: My Lord that was hit on direct examination. He's just rehashing old stories.

MR. WALSH: I don't believe it was. You might be referring to a voir dire Mr. Furlotte.

THE COURT: I don't recall it. There's been so much it's difficult to remember what was covered or not but --

MR. WALSH: Mr. Furlotte has brought this particular point out on cross-examination.

THE COURT: Well, I would -- It's not that great significance that you shouldn't go ahead with it anyway. Go ahead and ask your question.

MR. WALSH: You have been giving this some thought since that time?

A. I have given it some thought. I would be misleading if I said that every day I spent eight hours thinking about it. It is one of these things, as mathematical statistical problems are, that they are like a seed buried under your skin a little bit and sometimes you can't get away from thinking about it but you don't think about it in a concentrated way day after day. You have little episodes where you give it some thought and you come up with some new idea and you try that and it doesn't quite work and then you sleep on it a bit and whatever, ask some people their opinions, and it was only after in fact a little bit of interaction with Doctor Kidd that we were able to derive this ultimate formula.

Q. Is collaboration with other scientists an accepted form of scientific work?

A. Yes, it is. It's, I think, the typical way that science gets done, and in fact I would say that in my discussions with Doctor Shields we approached this very much as colleagues trying to arrive at the truth and there's no particular personal animosity, and I think, I would suspect, that some of his ideas and suggestions may well get incorporated into the way I approach the ultimate publication of this problem.

Q. Doctor Kidd was asked about background band sharing and you were in court when that occurred I believe.

A. Yes.

Q. Is that what you referred to as the birthday problem?

A. Yes, that's correct.

Q. And his opinion was he disagreed with Doctor Shields and his method of arriving at --

A. That's correct. He felt that the calculations were not appropriate in the way that they had been done because they were not answering the question I think as he was suggesting it should be posed and the way I suggested it should be posed.

Q. Let's see if we can cut through this background band sharing. Even assuming the background band sharing revealed high levels of inbreeding, I understand that's where the correction factor would come into play, the Nichols and Balding correction factor, correct?

A. The Nichols and Balding correction factor could be applied in those cases, in that case.

MR. FURLOTTE: My Lord the Nichols and Balding correction factor was brought up in direct examination. I questioned it in cross-examination and now Mr. Walsh is bringing it back up again. This is not a new area that I brought up in cross-examination.

MR. WALSH: It's incidentally mentioned in relation to the background band sharing that Mr. Furlotte - the issues he --

THE COURT: Go ahead with your -- You're going to have just one or --

MR. WALSH: What I want to cut through there, Doctor, is even if there were high levels of inbreeding based on a sample of nine and it showed high background band sharing, and there was high levels of inbreeding, would that turn the rare patterns that the R.C.M.P. have found in this case, would that make them common patterns?

A. It would not make them common patterns in normal collequial use of that term, and I'm just saying roughly you're talking about something changing in the order of going from 1 in a hundred million to perhaps at most something like 1 in 5 million, and my use of the term common is to say that 1 in 5 million, 1 in a million, is not common.

Q. Doctor, with respect to Mr. Furlotte asked you about the term 'inbreeding' and how it's used in population genetics fields, and you said it doesn't necessarily imply incestuous relationships but to have high levels of inbreeding, extremely high levels of inbreeding, does an incestuous type relationship in a community have an effect on putting them up to them levels?

A. Certainly incestuous known relationships within several generations would generate high degrees of inbreeding than we normally see and we'd have to have that over a short period of time. It is theoretically possible if you have a population of 50 people over 300 generations to get fairly high levels of inbreeding where you wouldn't have to have in any one of those generations known incestuous relationships. On the other hand, if you have a population of a 100

individuals, most people are going to know each other and most people are going to realize that they had a great, great, great, great, great-grandmother that was common to both of them.

Q. You had mentioned when you were explaining this part about inbreeding, you mentioned immigration, no immigration. You said that you could have high levels of inbreeding, no real incestuous relationships, but you said there would have to be no immigration. What did you mean by that?

A. That's right. If there were new individuals coming into that population that was getting highly structured like that, they would be bringing in bands in the case of these loci, and bringing in genotypes, bringing in genetic variance, that were not present in that population or that were present in that population, and low frequency, and it would be tending to homogenize that population again so that you would - to expect high levels of inbreeding you would have to have very little immigration into that community.

MR. WALSH: I have no further questions, thank you My Lord.

THE COURT: Thank you very much. Now, have you any further witnesses Mr. Allman?

MR. ALLMAN: No, My Lord, the Crown closes its case. There was one matter of an exhibit which inadvertently we wanted to move to enter as an exhibit. We only have it as an identification. I will check that at lunch. I think I spoke to Mr. Furlotte about it before and he has no problem with that, but in terms of testimonial witnesses we're completed.

THE COURT: As to whether it was marked as an exhibit?

MR. ALLMAN: Well, I spoke to him before and I told him what the identification number was. I understood there was no problem with it being made an exhibit. It was supposed to have been made an exhibit before. It was just a minor oversight. But I will confirm that at lunchtime.

THE COURT: So do I understand the Crown is closing its case?

MR. ALLMAN: The Crown has no more witnesses to call and there's just that one very minor matter that remains to be resolved.

THE COURT: Well, you can resolve that after lunch. There is one minor matter, again. There is a provision in the Evidence Act, I believe, about the number of expert witnesses. I have made no formal order enlarging the number here. I gather that --

MR. ALLMAN: I believe we discussed that earlier, My Lord, and I indicated to you -- Your Lordship made a ruling on this and I said well in that case please consider that I am making this application for all these witnesses, and I think what Your Lordship was saying was you wanted to wait and see so to speak. I would submit that all the witnesses were appropriate and I would ask Your Lordship's leave to have them all called and considered expert witnesses.

THE COURT: Yes. Well, we will deal with that perhaps before the jury comes in, very briefly. It's just a technicality. I felt if any order were required the time to make it would be before the Crown closes its case, and I couldn't recall whether I made an order in the matter or not.

MR. ALLMAN: You hadn't made the order but I had made the application.

THE COURT: All right, we will recess now until perhaps 2 o'clock, if possible, or right shortly after.

(NOON RECESS - 1 - 2:00 P.M.)

COURT RESUMES. (Accused viewing proceedings from holding cell.)

THE COURT: Just before the jury comes in, on the matter of the number of -- The monitor is on Mr. Pugh? Just check that.

MR. CLERK: Yes, My Lord.

THE COURT: At an early stage of the trial the Crown made application to increase beyond five the number of expert witnesses that might be permitted to testify. There was some discussion at the time as to the effect of a judgment of the Court of Appeal some years ago that seemed to imply that the limit of five was for a particular field or type of expertise, but regardless of that I was unaware at the time of just what the whole nature of the case was and I said I would certainly be favorably disposed to increasing the number in the proper circumstance and I would have to gauge the necessity as the trial went along. And in qualifying the experts, as I have done, I have impliedly increased the number as was necessary, and I just wanted to say for the record before the Crown's case closed that I have extended to whatever number of experts there have been that number. And I will do the same, of course, if the need should arise in the case of the defence. Had I felt that

the Crown were exceeding the bounds of propriety and calling expert witnesses whose testimony was overlapping I would have pointed that out and said so at the time, but I don't think that was the case. So I don't think anything more need be said about that. There was nothing else -- Oh, you're --

MR. ALLMAN: The only other matter, and that is a matter that's before the jury, is that item "S" - and I'll repeat this in the presence of the jury, item "S" we would move to enter as an exhibit. That's the back portion of earring P-39. And for some reason we omitted to ask that and I understand there's no objection on Mr. Furlotte's part.

THE COURT: You have gone through your checklist, I gather, for exhibits and --

MR. ALLMAN: That's how we came to find that one.

THE COURT: And matters marked for identification and so on. Well, you'll be saying that when the jury return then. So, could we have the jury back in, please.

(Jury in. Jury called, all present.)

THE COURT: You had a matter, Mr. Allman, about an exhibit?

MR. ALLMAN: There was one minor housekeeping matter, My Lord. We had somehow omitted to ask to have entered as an exhibit item "S" for identification. That's the back of earring number 2 which is P-39. You can mark it whatever number you like. There's no objection on Mr. Furlotte's part. It was just a minor oversight. The back of P-39.

THE COURT: Could you just identify that?

MR. ALLMAN: It's item "S" which is the back of P-39. So if you want to go P-39A to avoid --

THE COURT: Well let's call it P-39A then. Where did that item - or just to better identify the earring, was that found in the Daughney yard or --

MR. ALLMAN: Yes.

MR. CLERK: It was identification "S"?

THE COURT: Yes. So it becomes exhibit P-39A and should be so marked in due course. And have you any other witnesses?

MR. ALLMAN: No other witnesses, no other exhibits, and that's the Crown's case.

THE COURT: Well, now, the Crown having completed its case it becomes my duty to ask the Defence if it wishes to call any evidence or witnesses or evidence in the matter, and if witnesses are called of course it's the privilege of Defence Counsel to deliver an opening address to the jury to review the nature of the evidence that he wishes to adduce. Perhaps I should ask you first if you are going to call witnesses Mr. Furlotte?

MR. FURLOTTE: Yes, My Lord, I will be calling witnesses.

THE COURT: And then I will ask you do you wish to make an opening address to the jury?

MR. FURLOTTE: Ladies and gentlemen, I do wish to make an opening address like Mr. Allman had the opportunity when the trial first opened. I can assure you my opening address will be short and not as long as his. I do not have over 200 witnesses to call.

I think basically before I tell you what my witnesses are being called for and the evidence that I expect them to give is that I would like to remind you that in our criminal justice system, again, an accused person is always innocent until proven guilty, and that means exactly what it says. He's not to be proven guilty until all the evidence is in at trial, until the closing addresses are made by both Mr. Allman and myself, and until, again, the trial Judge charges you on what the law is and how to apply the law to the evidence and the facts as you may find them.

Because a person is innocent until proven guilty the Crown must prove its case beyond a reasonable doubt. That means the onus is on the Crown to prove the accused guilty. There is no onus on the accused through evidence or otherwise to prove himself innocent. Now, that onus on the Crown to prove an accused guilty beyond a reasonable doubt, it's questionable I suppose in some people's minds well what is a reasonable doubt. Well, in some sense of the word it means that if you think Mr. Legere is guilty you would have to bring back a not guilty verdict. If you think Mr. Legere is probably guilty you still have to bring back a verdict of not guilty. It's only once the Crown has proven through evidence and evidence that you accept as fact that if they have shown that beyond a reasonable doubt you feel Mr. Legere is guilty then you must bring back a verdict of guilty. Now, what a reasonable doubt is to one person --

THE COURT: Well, Mr. Furlotte, excuse me for interfering but you are really getting into bounds of law that I will be instructing the jury on. The purpose of your opening address in this situation is to review the evidence that you are going to call in the case and not to instruct the jury on what the law is. I will be doing that. I'm sorry to interrupt you but you do seem to be departing from the traditional role of defence. I know that it's seldom that an address of this type is given because very frequently defence don't call witnesses but -- Okay? You agree with me?

MR. FURLOTTE: Not really, but I believe --

THE COURT: You better, because I'm calling the shots.

MR. FURLOTTE: You're calling the shots, that's why I'm not saying anything.

Let me put it this way then Ladies and Gentlemen.

THE COURT: There's nothing you have said so far that's wrong. It's just that I'm afraid you might make an error.

MR. FURLOTTE: Well, that's quite possible. I'll put it this way Ladies and Gentlemen, because I have elected to call evidence in this case that still does not mean that I have to prove Mr. Legere innocent. I could call a hundred witnesses, or two hundred witnesses if I wanted, and if you chose not to believe a word that any of my witnesses had stated, that still does not take away from the Crown's obligation to prove its case beyond a reasonable doubt. There is no onus on the Defence

to prove a thing.

Now, in this case, as you are probably aware, and you have seen the Crown's case already, it's questionable here as to the weight that might be put on the DNA evidence. Some of you may or may have not thought that the possibility that if the Crown is able to prove its case beyond a reasonable doubt then the Crown must also prove that DNA evidence is reliable. There may or may not be, according to your own assessment of the evidence thus far, that without DNA evidence there's nothing there to prove Mr. Legere guilty. There may be not even enough to prove that Mr. Legere is probably guilty let alone guilty beyond a reasonable doubt. Suspicions will be there always, I would imagine, and that would not be uncommon nor should you feel you're doing yourself - or Mr. Legere I should say, an injustice by being suspicious.

The evidence to be given by Doctor Shields is not evidence that's going to prove Mr. Legere innocent. The type of evidence he has to offer cannot do that, nor is it intended to do that. The evidence to be given by Doctor Shields is basically in dispute of the probabilities - the figures that have come up by the DNA forensic laboratory of the R.C.M.P. Doctor Shields will testify that he analyzed the autorads in which the matches were made across the different probes and in his laboratory he would have also called them matches. So the DNA profile to the evidentiary lanes, the DNA profile of Mr. Legere to the evidentiary lanes, Doctor Shields is not going to dispute that. He

will say that yes, according to the evidence thus far in the DNA typing that that would be consistent with Mr. Legere's DNA profile. What may be in dispute by Doctor Shields is the probabilities that can be drawn from this might not be, and probably are not, as rare as the Crown Prosecutors' witnesses say they are not. He will explain to you, as best he can, as to exactly what substructuring is, exactly how substructuring affects the forensic lab's ability to calculate those frequencies, whether or not substructuring invalidates the ability of the forensic laboratories to use the Hardy-Weinberg formula, 2pq, and then to use the Product Rule to multiply across these multiple loci. If that cannot be done legitimately and validly by the forensic laboratories then you could hardly put any weight on the numbers that they are generating from them.

I believe Doctor Shields, again, will be using this overhead with some of the data he has assessed in this case, some data that he has assessed in other criminal cases by his search of different data bases throughout North America.

Again, you could choose not to believe or not to rely on anything that Doctor Shields tells you. Again, if you choose to do that you still have to find that on the Crown's own witnesses that they were able to present enough evidence to you to convince you that their method is proper and legitimate and that the figures that they generate are real. That the statistics are not misused.

I'll leave you with that and I'll now leave you with Doctor Shields to explain to you and try to help you understand exactly what are substructures, how they can be detected and what effect they have on the ultimate probabilities.

I would call Doctor William Shields.

DOCTOR WILLIAM SHIELDS, called as a witness, having been duly sworn, testified as follows:

DIRECT EXAMINATION BY MR. FURLOTTE:

Q. Would you state your name and address and occupation, please?

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

Q. My Lord if I may lead Doctor Shields through his C.V.

THE COURT: Yes, certainly.

MR. FURLOTTE: Doctor Shields you received your A.B. at Livingston College at Rutgers University, New Brunswick, Ner Jersey, in Biology with Distinction?

A. Yes, I did.

Q. And that was in 1974?

A. Yes.

Q. And you received your Masters of Science at Ohio State University, Columbus, Ohio, in Zoology in June, 1976?

A. Yes.

Q. You received your Ph.D. at Ohio State University, Columbus, Ohio in Zoology in June of 1979?

A. Yes, I did.

Q. And with Dissertation in "Philopatry, Inbreeding and the Adaptive Advantages of Sex."

A. Yes. That's the title of my dissertation.

Q. And your professional experience, you are a Teaching Associate at Ohio State University in General Biology, General Zoology, Ethology, Animal Behavior, Ornithology and Evolution?

A. That sounds like the right list.

Q. And you were an instructor at Wilmington College in Wilmington, Ohio?

A. Yes.

Q. That was in 1976?

A. Yes.

Q. You were a lecturer at Ohio State University, Lima, Ohio, in "General Biology" in 1978?

A. Yes, I was.

Q. You were a professor at the State University of New York, College of Environmental Science and Forestry, Syracuse, New York in "Animal Behavior", "Evolutionary and Systematic Biology", "Topics in Evolution and Behavior", and in "Conservation Biology"?

A. I'm a Professor of Biology and the other things that you listed were some of the courses that I teach.

Q. Some of the courses you teach, okay. And you were also a Director at the Cranberry Lake Biological Station?

A. Cranberry Lake Biological Station which is in the Adirondacks, yes.

Q. And that's from 1987?

A. That's when I have been the Director. I was the Associate Director before that.

Q. In 1986-87 you were a "Distinguished Scholar-In-Residence", Northern Arizona University and Museum of Northern Arizona, Flagstaff, Arizona?

A. That's correct.

Q. Honors and Fellowships, you have received a number of these?

A. Yes.

Q. You received the New York State Regents Scholarship, 1965?

A. Yes.

Q. And rather than read them all off, there is a total of nine honors and fellowships from 1965 until today?

A. I don't have it in front of me so I'll just take your word for it.

Q. Your professional affiliations have been with the "American Ornithologists Union"?

A. I am a member of the "American Ornithologists Union".

Q. The "American Society of Naturalists"?

A. Yes, I am a member of the "American Society of Naturalists".

Q. And affiliation with the "Animal Behavior Society"?

A. Yes.

Q. "Behavioral Ecology Society"?

A. Yes.

Q. "Cooper Ornithological Society"?

A. Correct.

Q. "Ecological Society of America"?

A. Yes.

Q. The "Society for Conservation Biology"?

A. Yes.

Q. "Society for the Study of Evolution"?

A. Yes.

Q. And the "Wilson Ornithological Society"?

A. Yes. I also have been affiliated with other organizations in the past and no longer take the journals so I am no longer -- They're not that important.

Q. You published a book in 1982 titled "Philopatry, Inbreeding, and the Evolution of Sex"?

A. That's correct.

Q. Do you know what use, if any, is being made of this book in universities?

A. I hope it's being read. It's occasionally been used in a course. It hasn't sold a hundred thousand copies. The royalties are small.

Q. But it's being used by other professors?

A. Yes, it has been, and is being.

Q. I see in your C.V. in relation to Published Papers you have a number of - a total of 36?

A. 35 - 36, in that area.

Q. A number of these have to deal with inbreeding - inbred populations?

A. About half of them have to do with general population genetic studies and my specialty in population genetics has been the causes and consequences of inbreeding.

Q. Causes and consequences of inbreeding?

A. Yes.

Q. You received a number of research grants and contracts?

A. Yes, I have.

Q. Ranging anywheres from three thousand to a hundred and twenty thousand, grants for particular studies?

A. Yes.

Q. And what kind of studies would those be in?

A. I and my colleagues and my graduate students have done a variety of different kinds of study. We do everything from studying the behavior and ecology of barn swallows to the conservation genetics of a variety of mammals and birds and reptiles. We also do general evolutionary theoretical studies. Sometimes get money for that.

Q. I see one of them is titled here "The Natural History of Inbreeding and Outbreeding".

A. Yes. That was actually a grant from the National Science Foundation to put on a symposium on inbreeding and outbreeding.

Q. I see you have a number of invited lecturers and participations in lectures?

A. Yes, I have.

Q. Would these be across North America or strictly in the United States?

A. No, I have been in Canada a few times. I've been invited to Queens University, the University of Western Ontario, and across North America including our far western state which was a fun trip to Hawaii. I have also been at the University of Toronto for a different topic.

Q. I see you are a coauthor with J. Yoshimura. How do you pronounce that?

A. Jane Yoshimura.

Q. That's in the "Probabilistic Optimization of Phenotype Distributions"?

A. That's correct.

Q. And you are a coorganizer with N. W. Thornhill on a symposium on "The Natural History of Inbreeding and Outbreeding: Theoretical and Empirical Perspectives on Population Structure"?

A. That's correct.

Q. You have also testified in other courts as an expert witness in population genetics and molecular genetics?

A. Yes, I have.

Q. How many different times would you have testified in court?

A. If we count today it's probably in the neighborhood of 15. 15 or 16.

Q. And have you prepared any articles in relation to forensic DNA analysis for the National Academy of Science?

A. I wouldn't call it an article. What I prepared was in essence a very long letter reporting on what I perceived to be some of the problems with the forensic use of DNA typing at the request of some of the members of the National Academy of Science - that's the United States National Academy of Sciences, a panel that was investigating the use of DNA typing in forensic systems.

MR. FURLOTTE: My Lord I would move to have Doctor Shields declared an expert witness in population genetics and in molecular genetics, in DNA typing analysis.

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

THE COURT: Well, I would declare Doctor Shields an expert for the purpose of this trial in the field of population genetics and molecular genetics.

MR. FURLOTTE: Now, Doctor Shields, in the case of Mr. Allan Legere I believe you analyzed or interpreted the autorads which were prepared by the R.C.M.P. Laboratory in Ottawa?

A. Yes, I did.

Q. And your findings in your reviewing those autorads, what was your interpretation?

A. They were reasonable clean autorads and in my judgment I would have made the same calls that the R.C.M.P. did. In other words where they declared matches I would have declared matches. They declared some inconclusives, I think they were being cautious, but I probably would have done it as well. So I have nothing -- I agree with the R.C.M.P.'s what we call scoring of the autorads.

Q. So you have no objections to the calls made by Doctor John Bowen?

A. No, I do not have any objections.

Q. So, Doctor, in the field of population genetics I wonder if in your own words you could assist the jury in understanding as to what is population genetics in the forensic field and what may be problems within their system as to how they calculated frequencies. I'll leave that up to you as to how you would like to direct them.

A. Okay. Probably the easiest thing to do is to begin with noting what a match might be considered to be.

The kind of match that's done in DNA typing is about the same but with greater sensitivity as coming up with a series of physical measurements about someone. There are physical measurements that vary between individuals. They vary more than most physical measurements do. But in essence what you're doing if you have one probe is you're doing the equivalent of saying that the person is blue-eyed. There is also alleles, genes, for eye color. It's the same sort of analysis. The difference would be that in blue, brown and green eyes with VNTR alleles you can say light blue, dark blue, grey blue, medium blue. You can divide blue up much more or you can divide green up much more so that you get eight or ten or twelve or twenty classes of physical measurement. So that if you get something that matches versus something that doesn't match the next step in the process is to decide how probable that match is, how likely that event is to have occurred. And to do that you have to develop some notion of what the probabilities of events occurring are. The analogy that I use, the example that's used standardly in statistics or probability classes, is to ask a question about an urn, and the urn is closed, and inside the urn there are balls, little colored balls, and if we ask the question what's the probability of drawing a black ball out of that urn you really can't answer the question if that's all the information that you have. If in contrast somebody dumps the urn and we count ten balls and we see that five of them are white and five of them are black we can now develop some notion

of what's the probability of drawing a black ball. The reason why is because we know there are ten possibilities and we know that five of those ten possibilities are black. So that half the time drawing a black ball is likely to occur and half the time drawing something other than a black ball is likely to occur, in the case that we're talking about a white ball. So that in essence is what you need to do and ideally what you would do is you count all of the events that are possible, how many of those events there are, and how many states those events can take, black and white, or black, grey, medium grey, light white, dark white, etc. No matter how you divide it you still have events and in the context of what we've been talking about I guess for the past week a bin is an event. So you say there's 20 bins for this particular locus, what's the probability of drawing something from this particular bin. To do that ideally what you would do is you would count all of the occurrences in each of those bins. You would dump the urn out and take the ten and count five and five. But if I had an urn that had a hundred and fifty thousand balls in it and I asked you the same question we'd spend a long time counting balls. Under those circumstances statistics says that there's a rational way to come up with what we call estimated probabilities, and an estimated probability is nothing more than saying I'm going to sample from that urn. I'm going to take a 100 balls out of the urn and count them and put them in bins and assume that if I did a random sample the frequencies that I get, ten

black, ten white, fifty black, fifty white, says that of the hundred thousand half are black and half are white. And that's a reasonable frequency to use to develop probabilities of drawing a black or a white.

So that's what you really need to do in order to have the kind of system that the R.C.M.P. and the other forensic labs in North America, in particular the FBI and Cellmark in the States, a private company. They all develop a data base in which they attempt to count the number of individuals in different bins, the number of alleles, the number of bands as they're called, or fragments of particular sizes, and in doing so they're making a number of assumptions about how they have sampled.

If I were to ask the question what's the probability of drawing an ace from a deck of cards, most people who play cards would say well there's 52 cards and there's four aces and if they had a calculator they could do it that way. If they remember in their head and they gamble a lot they would say 4 out of 52 is 1 in 13, so the probability of drawing an ace from a particular deck of cards is going to be 1 in 13. That's only true if it's a regular deck of cards. If it's a pinochle deck of cards there's a different set of numbers. For those who don't play pinochle there are 8 aces in a pinochle deck and only 48 cards. There are 8 kings and they go down to 8 nines and there's nothing below nine in a pinochle deck. That is two populations, pinochle decks versus regular decks, and the frequencies between those two populations differ in a way that makes it more

problematic how one goes about getting samples. If you think about it in the context of the black and white balls, let's say that there's actually ten colors rather than five, and over in one of the samples we have two urns instead of one, in one urn there's, in essence, equal frequencies of all ten colors, so one-tenth, one-tenth, one-tenth all the way along, but over in this urn there's less than that, there's a hundredth for five of them and the other five are much, much more frequent, those kinds of frequency differences mean that you'd actually have different probabilities of drawing different colors from those two bins, from those two urns, or from those two decks of cards.

So that's one way of looking at that problem that has been discussed as substructure. You think about it in the context of if you do a, quote, random sample, and you just throw a whole bunch of decks of cards into the middle of a room and shuffle them up, and you have to shuffle them because that's how you get a random sample, if you fail to shuffle them people who open decks of cards know that all of the spades come together and all of the other cards of a different suit come together, if you were to just pick from unshuffled decks you'd get a bias sample. It would not be representative of all of the potential events. So if you shuffle all up those ten thousand cards in the middle of the room and then try and sample them to find out what the frequency of aces, kings, queens, down to deuces is, since we don't know what that frequency is as we would with a deck of

cards, we can't tell whether it's pinochle decks or regular decks except by sampling. If we get a lot more aces than we would expect, 1 in 13, then we may have some reason to believe that we may be dealing with a pinochle deck. If we get way fewer we may have some reason to believe that we're dealing with a regular deck. And the problem with data bases that are taken without regard to potential substructure is in essence you're taking unknown numbers of pinochle decks and regular decks and mixing them together and then sampling from that and coming up with a new probability that in essence is not the probability for either of those original populations. The aces in question, if you take a regular deck and a pinochle deck, and throw them together you get a hundred cards and 12 aces which is a different frequency than either the one in six that it is in a pinochle deck and the one in thirteen that it is in a regular deck of cards.

You can use the same sort of analogy as the little ball analogy to illustrate what we mean by statistical independence and when you can multiply probabilities together. We can ask the question what's the probability of drawing two black balls in a row from that original urn that had five black balls and five white balls. We know that half the time, and you already know the answer because we all know now that when you multiply probabilities together the probability is one-half so it's going to be one-quarter, but let's see how that really comes about.

Half the time you're going to pick the wrong color first, white. So half the time you lose in this little game of pulling two blacks together. Half the time you will pick up a black first and that's a win. That's a partial win. You put that black back in just as you put the white back in in the first chance and you say okay now what's the probability that I'm going to pick a black the second time. Well it's a half again. So half the time on the second draw you're going to lose. You pick a white ball. So the first half you lose half the time; the second draw you lose half of that time which is a quarter which means you lose three-quarters of the time, which leaves the one-quarter that you win.

The reason why independence is important there, and those are statistically independent, that means that there's no influence of white balls on black balls, and I'll show you how that makes a difference. If I were to say that in a particular population the probability of someone with blue eyes is 1 in 10, and I was also to say that in the same population if we go out and independently count the number of individuals with blond hair and we discovered that that was 1 in 10, would the probability of blue-eyed blonds be 1 in 10 times 1 in 10? The answer is no. The reason why is because blue eyes and blond hair are correlated in humans. Individuals with blond hair have a higher probability of having blue eyes than vice versa, than they do other color eyes and other color hair. So that in essence you can't make the

assumption - you can always make the assumption but you can't show that it's going to be the case that these alleles or cards or alleles for eye color are sorting independently until you have somehow demonstrated it.

Now, with that as a background the question becomes how does one develop a probability of matching in the real world using real DNA typing? What people have done is develop data base systems where they go out and sample a certain number of individuals, and that differs, the number of individuals differs between the R.C.M.P. and the Centre for Forensic Sciences in Toronto, and the FBI in the U.S., and you run them on gels and you measure their bands, and once you have that band size measurement you put them into a bin. In essence, a band size measurement is sort of equivalent to height. A bin might be anybody between five foot five and five foot eight, so anybody whose measurements fall between those two numbers goes into that bin which may be bin number four. You do that for enough individuals that you end up with a distribution of allele sizes. The frequency distribution as it's called. And a frequency distribution is nothing more than a count of the number of instances of bands that fall in bin one versus bin two, versus bin three, up to bin 31 if you use all 31, or as is more often the case, a fewer number of bins because you collapsed them. Because individuals less than four foot are rare you say zero to four foot even though there would have been a number of bins there, so you go from 31 bins to 20 bins simply by collapsing - making the sizes

bigger, making the end points of bins bigger. Once you have done that you can do that with other populations.

Now, initially people suggested that there might be this problem with substructure. There might be some problems with lack of independence of alleles across loci which is what we were talking about with blue eyes and blonds. There might be a problem with what's called Hardy-Weinberg equilibrium which is the probability of two alleles at a single locus being reflected well by multiplying those two probabilities together times two. In fact I can illustrate that one using the same analogy, it makes it a little easier I think, using the black and white balls again. There we're asking the question what's the probability of picking one white ball and one black ball, and I think that you can see that if you pick one white ball the first time, okay, then half the time you're going to get a black ball the second time. So one-quarter of the time again. The chance of picking one white ball and one black ball in that order is one-quarter. But that's not the only way you can get a black ball and a white ball. You can do it the other way around. So you end up having one-quarter plus one-quarter which is twice .5 times .5, twice one-half times one-half. Because it doesn't matter whether you get the black ball first or the white ball first you still have - you have twice as many chances of getting one white and one black as you do with getting two black or two white.

That may also not be true. That assumption may also not be true and that will influence the likelihood of different events happening. Well rather than simply making all of those assumptions some people, myself included, suggested that it might be better to test for some of those assumptions, to actually look at the data and see whether these three assumptions hold or not in the real world, and the one that I would like to focus on here simply because I believe the other two are harder to test, as was testified to today, and are less critical as far as I'm concerned in doing these sorts of analyses is whether there is substructure or not. Substructure here is very simply the question of whether there are allele frequency differences between different subpopulations within a single population. And let me begin by noting that as far as I'm concerned the human race is a single population. All humans are one species. So the fact that forensic laboratories regularly make racial data bases already indicates that everybody recognizes that there are potential problems if there are genetic differences between humans, that in order to come up with a reliable and accurate probability you have to have the right data base. You don't want to test someone who comes out of a pinochle deck using the frequencies that you'd get from a regular deck of cards, and vice versa.

If you're going to have an unbiased and reliable estimate of probabilities of these kinds of matches you need to know what population you should be using, or you should come up with ways of correcting for any potential biases that would result for whatever reasons.

To look at whether there are potential biases one of the things that you can do is simply look at comparisons of different populations. You can ask the question do populations differ in allele frequencies. And I would like to start using the overhead if I might, My Lord.

THE COURT: Yes.

DOCTOR SHIELDS: The kinds of data that I am going to show you will include data from the R.C.M.P., the Royal Canadian Mounted Police, as well as the Centre for Forensic Sciences in Toronto, as well as the FBI which has their own set of data bases, as well as a place called Orange County Crime Labs. That's Orange County, California which includes San Diego and that part of California. There are lots of laboratories now that are developing data bases using in essence the same technique as it was originally designed jointly by the R.C.M.P. and the FBI. So what we're looking at here is a comparison between races. Between races and the two races are Black and Caucasian in the FBI data base. Almost all of the ones I'm going to show you, I'm going to go through them pretty fast after this one, have the same sort of structure, if you will, in terms of the graph. And you're looking at down here are the bin numbers that are used by forensic laboratories, bin 1, 2, 3, 4, etc., and in essence these are equivalent to a certain number of base pairs, from zero base pairs to often if it's the real bin 1 it will be to six forty base pairs but it may be as high as thirteen eighty-two, it may be as high as two thousand.

Depends on how many individuals occur in that part of the distribution of alleles and the distribution of allele sizes.

What you are looking at on this axis is the frequency, the proportion of the total number of alleles that are found in bins. So in bin number 1 here somewhere slightly less than .01, or less than 1% of all the alleles are found in bin 1 for Caucasians. In contrast, in this same bin, over 8% of the alleles are found in that bin for Blacks.

Now, just looking at this particular graph one can visually see differences especially if one is attuned to looking at graphs. One can also see similarities in this particular graph. Okay? The question becomes how do we decide objectively what's going on with these kinds of analyses. How do we decide objectively? Because I can see that this .08 is bigger than the .008, and I can see here there's a big difference. I can see here that there's almost no difference and here there's almost no difference, and here there's almost no difference. I can see that out here at this end of the spectrum, the very large alleles, that Caucasians have many more of those than Blacks do except for the last bin. So I can see that there are differences and there are non-differences in different bins. So is there a way that scientists have of deciding whether this is a real difference or not a real difference. Well, you have heard about the way we do that and it's called statistics. We can do a statistical analysis to decide whether the distributions of alleles in the

Caucasian data base for the FBI differs from the distribution of alleles in the Black data base from the FBI. We can see whether those two distributions are statistically the same, or at least that you can't tell them apart statistically, or whether you can say reasonably, unequivocably that they are different with some reasonable degree of sureness.

So what we do is we do -- There are a variety of different kinds of statistical analyses that allow you to do these sorts of things but they all have one and the same sorts of properties. They have a similar property. And those properties are that you develop using mathematical formula which I will not bore you with, a number, a statistic, and that number when associated with other numbers that go with it, which in this particular case there's 16 degrees of freedom which is what DF means, means that we have 17 bins so we're measuring the difference between 17 bins but we only have 16 to tell us the differences. Now, the reason for that is because once you've put in numbers for 16 when you're dealing with numbers that range between zero and one and add up to one is that the 17th bin is always known when you get to the 16th.

You have a statistic and the degrees of freedom that go with the statistics, you can develop what's called an alpha probability level, or P. That P stands for the probability that you would be wrong if you concluded that those two distributions were different. I'll repeat that again. It means that you have less than one chance in a hundred thousand of being

incorrect if you conclude that the differences between these two distributions are real. That they are real significant differences. Okay?

So that particular level means that it's extremely unlikely that those are similar. One time out of one hundred thousand where you ran this particular test you would find differences that big and you would be wrong in concluding that they were different. In other words one time out of a hundred thousand would you find differences that big by chance.

So that's the way that probability works. That probability, whenever it appears, is the probability of making what we call a type one error, a probability of concluding - of falsely concluding that they are different.

I'm just going to briefly show you one other thing and then tell you how we use these probabilities.

This is what people call the normal curve. It's the normal distribution curve. If we go out and we measure everybody in here height, okay, most of the time when we measure height for one sex, actually, so I'll just do it for one sex, if we measure all of the females or all of the males in here, their height, we would find a distribution that looks something like this, and the mean or median would be here in the middle. That would be the average height of all of the males in this room. In addition to the mean there are going to be individuals who measure different distances away from that mean which is why we call it a distribution. Okay?

What we know from standard statistical practices and theory, as well as lots of empirical analyses, is that for things that are distributed normally one can be 95% sure that all of the values for a real distribution will fall within plus or minus 1.96 of the standard deviation of that mean. This has been translated into sciences - empirical sciences' reliance on what's called the .05 alpha level. Most scientists are willing to reject the no hypothesis that two distributions or two statistics are the same if the probability of making an error in rejecting the no hypothesis is less than .05. In other words if that P that we have looked at before is less than .05 scientists tend generally to accept the rejection of the no hypothesis. They accept that there's a statistical significant difference between two distributions or two values.

Almost invariably scientists suggest that anything greater than .1 at the alpha level is not statistically significant, and then there's always those arguments that scientists have of what happens between .05 and .1. So things between .05 and .1 some people would say are significant, other people would say they're not. But if it's greater than .1 it's not significant. If it's less than .05 it is.

This is just to reiterate now using more of the FBI's data bases for this particular locus, locus D17S79, which is one of the loci that was used in this case, what kind of frequency differences there are between Caucasians, Blacks, Hispanics from Miami, and Hispanics from Texas. There are a couple of

things to notice here. The Hispanics from Miami are likely to be Cuban ancestry. Most of the Spanish-speaking people in Miami are Cuban or otherwise Caribbean. Most of the Spanish-speaking people in Texas, however, are Mexican descent, so they actually have a different ancestry. Hispanic people from the Caribbean are often mixed Caucasian/Black. Hispanic people from the Southwest and particularly from Mexico are often mixed Caucasian, some Black, but not merely as much as Caribbean, and a lot of native American Indians. Look at the differences in frequencies between these. Look at the total analysis and you can see that indeed in this case you have less than 1 chance in a million of being wrong if you conclude that those frequencies are different between those races and between the two ethnic groups within the single Hispanic group. The same sort of analysis now looking at just those two Hispanic groups. Looking at the significance or absence of significance for this particular locus, the locus D2S44, in a comparison of Hispanic Florida and Hispanic Texas data base from the FBI's Hispanic data base, subpopulations within a single data base, and again the differences are highly significantly different.

You are very, very safe in concluding that the frequencies differ between Hispanics in the southeast of the U.S. and Hispanics in Texas of the southwest.

Whether those have important forensic impacts can perhaps be illustrated for now by noting that in one particular case that I was involved in these two data bases gave frequency differences, bottom line match probability differences, of the difference

between one in about 17 million and one in about 78 million. Both small numbers but one is much, much, much smaller than the other. Just as a first approximation.

This is data from that Orange County data base that I talked about a little earlier from California. So locus D1S7 and it's a comparison of the allele or bin frequencies between Japanese Americans, Chinese Americans, Korean Americans and Vietnamese Americans. Now, the Vietnamese Americans in California are American citizens but mostly were born in Vietnam. They arrived after 1975 after the end of that war. The Koreans, Chinese and Japanese include a mixture of people who have recently arrived from those shores and people who had been around in Southern California for a long period of time. The bottom line, however, is that we're talking about four different groups, ethnic groups, within the Mongoloid race. A single race, four ethnic groups. There are statistically significant differences in allele frequencies between those ethnic groups.

The first analysis where I discovered what I thought was reasonable evidence of substructure was the first comparison done between the FBI's Caucasian data base and the Royal Canadian Mounted Police's data base. For locus or probe D2S44 when you compare those two you find statistically significant differences in allele frequencies. Canadians in the Royal Canadian Mounted Police data base have different allele frequencies than U.S. citizens in the FBI data base. These are Caucasians on the same continent with

slightly different patterns of ancestry, however, which I think you've already heard about. Canadians, the vast majority of citizens of this country, descend from two major ethnic groups, the British and the French. In the United States we also have lots of British and French ethnic background, people, but they make a much smaller proportion of our total population. So the United States is more of an aggregate of many, many ethnic groups than Canada is, and that may be part of the explanation for the difference between the R.C.M.P. and the FBI data base. That is true with this particular probe, locus D2S44. There are no significant differences at these two probes between the R.C.M.P. and the FBI. Probe D4S139 you see the probability is .116. You would say those are not significantly different. And in looking at that graph you can see that all of them in essence are very, very close together. The same with probe D1S7 there are no statistically significant differences between those two distributions. There are, however, significant differences in the last two probes in common between the two. Probe D17S79 where the probability is less than 1 in a thousand that you would be wrong in concluding that the frequency of alleles are different between the FBI and the R.C.M.P. data bases for this probe, and the same is also true, five chances out of a hundred you'd be wrong, in comparing the frequency distributions at D10S28 versus the FBI and the R.C.M.P.

Much to my surprise I recently became involved in a case in Toronto and was given the Centre for Forensic Sciences' data base. They have their own Caucasian data base in Toronto which is different from the R.C.M.P. data base, different in terms of the individuals that are in it, but just as importantly to my way of thinking, different statistically. For locus D2S44 there are statistically significant differences in allele frequencies between the R.C.M.P. composite data base representing all Caucasians in Canada and the Centre for Forensic Sciences' data base representing Caucasians in Toronto. There are also statistically significant differences at D10S28, one of the loci used in this case, that P is less than .05.

THE COURT: May I just ask there, Doctor, the Centre for Forensic Science, is that the Ontario Provincial Laboratory?

A. I think it's the Toronto Metropolitan area's crime laboratory. I don't think it's an Ontario Provincial but I could be wrong, I don't know. I know it operates in the Toronto Metropolitan area.

There is no difference at locus D1S7. It's not that simply these differences occur as an artifact of doing the analysis. You can show that at some loci there are no differences which says that when you find differences they're likely to be real, and in fact the statistics say that they are real. They even give you the probability at which you can weight the fact that they are real.

Here's probe D17S79. It's one of those probes, again, highly significantly different. You can see these differences and, again, if you want to look at these sorts of graphs just note that here the probability of this particular bin in the R.C.M.P. is about .13, and in the C.F.S. it's about .26. Twice the frequency, which is the equivalent of the difference between a pinochle deck and a regular deck of playing cards, four aces versus eight.

The final analysis - I'll show you the four of them together. This is the FBI's C2 data base, and the FBI's C3 data base, two incarnations of its data base, the R.C.M.P. and the C.F.S. Here is the R.C.M.P. This particular one it doesn't really resemble the other three very much. This particular one resembles the FBI's C2 better than it resembles the C.F.S. which is Toronto's Canadians. Okay? That's all I want to do with here for a little bit.

THE COURT: I'm just wondering about marking these as exhibits Mr. Furlotte. What did you propose there?

MR. FURLOTTE: I'll allow Mr. Walsh to see them here and if he has no objections I think they should be put into --

MR. WALSH: Well I have no objection. I'd like to have a copy of it though just for my own --

MR. FURLOTTE: Yes. We could get the clerk to make copies because I don't have copies for myself either.

THE COURT: These are black and white?

MR. FURLOTTE: These are black and white.

MR. WALSH: Black and white. Well I certainly have no objections.

THE COURT: Well, why don't we do this. Why don't we have a recess at this point. How long are your lectures regularly?

A. 45 minutes or I fall down.

THE COURT: Well, you've earned a five minute recess. During the recess the Clerk could run off copies of these. You are satisfied with the authenticity of them as compared to the slides?

MR. WALSH: Oh yes, I have no problem. I think some of them - the Doctor can go through them there - some of them he didn't bother putting on there for obvious reasons so I think we could go through them and just select whichever ones he wants to use. Whichever one he has used we could mark as an exhibit.

THE COURT: Well, could you, Doctor, pick out from those the ones you have used.

MR. WALSH: Or intend to use.

THE COURT: Or intend to use. And we will have copies run off. And perhaps you would make a half dozen extra copies in case the jurors later want to look at them. So, would the jury go out, please.

(RECESS - 3:15 - 3:40 P.M.)

COURT RESUMES. (Jury called, all present.)

(Mr. Legere viewing proceedings from cell.)

THE COURT: I believe the slides - or at least printouts of the slides are being tendered in evidence Mr. Furlotte?

MR. FURLOTTE: Yes, My Lord.

THE COURT: And copies have been provided the clerk. He tells me he hasn't had an opportunity to run off copies yet because the photocopy machine here was being otherwise used, but can we give them numbers now.

The slides would be D-14, 1, 2 and 3 and so on. How many are there all together?

MR. FURLOTTE: We will be putting in more also.

MR. CLERK: I have 14.

THE COURT: So those are ones that have been used so far?

MR. FURLOTTE: Those are the ones that have been used so far.

THE COURT: So they would be 1 to 14. 1 in brackets down to 14 in brackets. The others could be added on, 15 and so on. 15 in brackets that is. Are they in the same order I wonder?

MR. FURLOTTE: I think those are more for teaching purposes so maybe we could even renumber the rest of them D-15.

THE COURT: Okay. No objection.

MR. FURLOTTE: The others will have more to do with specific case evidence.

THE COURT: All right.

(Clerk marks slides D-14(1) to D-14(14).)

THE COURT: So, Mr. Furlotte, do you want to get your --

MR. FURLOTTE: Yes. Doctor Shields maybe you could continue on with your explanation of substructures within general populations.

A. The data that I showed would just illustrate that substructure does exist. It's statistically demonstrable and one of the questions that people would have is how does that come about. The easiest way to do that is to just talk a little bit about how VNTR's or any other genetic alleles are transmitted. They're transmitted from parents to progeny. There's a connection, an ancestral descendent connection, for what kind of alleles that you're going to have. You

get half of your VNTR alleles or any other kind of alleles from your mother and half from your father, and if you do the calculations which you then discover is that, for example, siblings within a family are a subpopulation of the general population that they live in. The actual probability, for example, of a five band match, a five locus match, ten bands, for a full sibling is not the hundreds of millions that you've heard, and I think you actually may have heard the number, it's one in one thousand and twenty-four. So that the probability is much, much, much higher for relatives and relatives don't just come in terms of first degree kin, parents and progeny. They come as cousins, and as was suggested earlier, they also come insofar as human populations are not random mating, in larger kin groups some of which we call races, some of which we call ethnic groups, some of which we call religions. The strict definition of random mating is very simple and it's immediately apparent why humans aren't random mating. Random mating means that any individual of one sex has an equal probability of mating with any other individual of the opposite sex, everywhere there are humans. We know that's not true. At the very least people on different continents have higher probabilities of mating with each other than they do with people on other continents. With the advent of the jet age that we have now that's less true but it is not untrue. It is also not untrue that people tend to marry people with similar religions, with similar ethnic backgrounds, similar races. Under those circumstances one can get

subpopulations within larger populations, across races and within races and across geographic areas. So what you are looking at when you see statistically significant differences in allele frequencies between two subgroups is an indication that the members of each of those groups are slightly more related to each other than they are to members of the other group, and in that sense they have a higher probability of carrying the particular set of alleles in common than they do with members of the other group. Pinochle decks and regular decks. The cards in a pinochle deck are more related to each other than they are to the cards in a regular deck and vice versa. And that really works because relatedness in this case simply means the probability that they're going to look alike. That they're going to carry the same information. That you're going to be an ace versus that you are going to have a deuce. The probability of a deuce in a pinochle deck is zero. The probability of a deuce in a regular deck is one out of thirteen. So there's a different probability depending upon which family of cards you're looking at in the extended family sense.

We have known for a long time that genetic elements vary among ethnic groups. They vary geographically. They vary among populations and within populations of humans. We know that for a lot of different kinds of alleles. Under those circumstances it becomes a question of whether one can use a small data base, which is what 900 or 700 individuals is, and in some cases some of the data

bases that are used are 200 individuals, whether you can use a small data base to effectively estimate the frequency of alleles at these VNTR loci because they have as many as 26 bins. So even though they have bins, they still have 26 of them and you've got to get the frequency of all of those 26 fragment size types.

If there were 25 different colors of balls in this giant urn that we have with the hundreds of thousands of balls and I told you there were 25 different kinds and I asked you what would be the probability that you would come up with a good estimate of those frequencies of those colors, and I said that you were going to do it with a sample of 20, I think everybody would immediately say that you can't even estimate 25 colors with 20 samples. The more colors, the more flavours, the more VNTR alleles, the bigger the sample has to be to effectively estimate the frequencies in those bins. So that when you have 25, and you need samples of 5, 6, 700, a 1000, and the R.C.M.P. has the biggest sample size of all of these data bases, so in that sense no problem, when you look at that and compare it to another data base and you find that the frequencies differ between those two data bases, you then have the question can those differences affect the probability that you produce to weight the match. What kind of effect will they have? We know that there are statistically significant differences in frequencies. Are the frequency differences that would result or are the frequency differences that could result in any particular case be big enough to worry

about it, and that's where there seems to be some difference of opinion.

I would note that in one case that I was involved in in a case that Cellmark had put together -- Cellmark is a private company in the United States, in which they were trying to do a forensic match on a person in Guam which is an American territory or a territorial protectorate in the South Pacific south of Japan. The native people of Guam, the Guamanians, are members of the Micronesian race. There is no data base for Micronesians anywhere on earth for VNTR's. Andwhat Cellmark did was reported the probability of a match on the basis of their Black, White and Hispanic data bases. They reported those probabilities as one in a million, one in fifty-two thousand, one in twenty-nine thousand. After having done that they went back and said well this isn't the best way to do this. We're going to get a sample of Guamanians to find out if what we've done is reasonable. Is there enough variability there. Are we biasing against this particular defendant by using the inappropriate data bases to come up with these probabilities. They did argue that one in a million, one in fifty-two thousand, one in twenty-nine thousand are not forensically significantly different. They argued that those are forensically small. All three of them are small. Therefore, it doesn't matter what data base you use.

When they developed their data base with 15 Guamanian policemen who volunteered their blood and they ran it, and you added the two adults, accused and victim in the particular case, they had 17

individuals, and you use their standard technique to develop the probability of a forensic match by a random individual in the Guamanian population the probability was one in one hundred and seventy-eight. And I don't think very many people commonsensically would say that that's not a different probability than any of the three that were originally offered.

So the problem that some people have, and myself, in my opinion this is my major problem, is that in some circumstances there is evidence that suggests that it may be a problem to use the simple Product Rule and the simple multiplication, what we call the binomial expansion 2pq to develop these probabilities. That in fact if you've got the wrong data base you may be coming up with really wild numbers that have no bearing on reality.

That's sort of the general stuff and if you want I could move on to this specific case.

Q. Whatever you like, Doctor.

A. Back in May when I first saw the autorads in this particular case I noticed what I thought to be extra band sharing. More band sharing than you would expect by chance. If I could step down Your Lord.

THE COURT: Yes.

A. This particular overhead I put together back at that time to illustrate what I thought was potentially a problem with using the R.C.M.P. data base to generate a probability for Mr. Legere. I noticed that if you look at the five individuals that I had available at that particular time there was an extraordinary amount of band sharing such that Murphy shared four bands

with Linda. The probability of sharing those four bands with Linda using the standard forensic laboratory technique of multiplying those probabilities together was 1 in 10,800. Now, in a separate and therefore independent comparison you compare Legere with Murphy and they also shared four bands. And the probability of that based on the frequency of those four bands in the R.C.M.P. data base was 1 in 2,749. The probability of sharing four bands for Legere with Donna, and this is not an entirely independent analysis because Linda and Donna are sisters, the Daughney sisters, the probability comes out 1 in 5,616. And Legere with Nina the probability here is 1 in 9.

Now, the probability of all of these events together is 1 chance in a gargantuan number. In other words the actual band-sharing patterns seen in these 5 individuals tended to indicate that the 5 individuals had more bands in common than you might expect by chance. It was also found when you looked at the probability of 3 unrelated individuals sharing the same band, which in this case I noted was Legere, Murphy and Donna or Linda, this is separate, I didn't go into this because it's not independent of this, because these 0 nine sevens are also in this analysis, and that probability is 1 in a 1000. These are all, quote, small probabilities. With the addition of the other individuals the same analysis shows a similar pattern.

At locus D1S7 Legere and Donna matched exactly in the genotype. Okay. They matched exactly. Both bands at that particular locus matched both visually and in terms of the band sizes using the plus or minus 2.6% percent that the R.C.M.P. uses. The probability of that happening is 1 in 6,283 if you use the standard logic of the R.C.M.P. data base. For locus D17S79 six different individuals out of the ten shared one allele, Murphy, Linda Daughney and four individuals whose names I do not know. What's the probability of that? 1 in 1,613. Four different individuals shared a different allele at the same locus, Legere, Donna, Nina and 188B. The probability of that is 1 in 279. The probability of both of those two events together if one uses the underlying logic of the R.C.M.P.'s analysis is that number times that number which is an exceedingly small number. If you keep on doing this for each of the loci then you discover that there's at least to my way of thinking some evidence that there is a greater degree of band sharing in the New Brunswick population represented by the 10 individuals in this case then you find in the R.C.M.P. data base by itself.

I guess it was either Thursday night or Friday that I was faxed the particular analysis that Doctor Carmody produced, and as I told him on the phone I thought it was an elegant treatment. The formula that he produced in collaboration with Ken Kidd and who else is a legitimate formula. It's the right formula in my opinion. The difference that he and I would have about it is which assumptions one uses

to plug data into that formula. And all I would do is note that it is in evidence and I did the same analysis that he did, I used the chi-square goodness of fit test, I did the analysis after coming up with my estimate of the number of band shares and discovering that his original estimate of the number of band shares was incorrect and was changed during the second fax which happened on Saturday. When I got the second fax I had their number of band shares that they estimated in the observed sense, their expected number of band shares which they estimated from, as he put it, the effective alleles based on the observed homozygosity, and I ran a statistical analysis. With that statistical analysis the results were very, very simple, and I will show you that statistical analysis so that you can see what it looks like.

First, let me note that this will also, I hope, be put into evidence and if anybody wants to can do this themselves.

This is the way you decide whether bands are shared between individuals. What you are looking at is each of the loci, locus D1S7, D2S44, D4S139, and for each of the loci the two bands for each of the individuals involved in this case. Okay?

If you remember Doctor Carmody talked about the fact that there were a couple of cases where you could only do twenty-eight comparisons and that's because there are no measurements for these two loci for this individual. They do not show up in the gel. It's not a problem; it's just a fact of life that you deal with in doing the analysis. What I

have got here is the measurement as it's presented on the sizing sheet from the R.C.M.P. plus 2.6% and minus 2.6% in base pairs. So that Mr. Legere at locus D1S7 has a band at 7301 base pairs, that's what it's measured at, and therefore its matching window is, according to the R.C.M.P.'s protocol, is 7,111 base pairs to 7,491 base pairs. So if we want to decide if anything matches that what you do is you go across the same row and you see if there's any individuals anywhere, and there are, Donna, who have a band that overlaps this interval. And what you can see here is that 7,578 is up here but the 7,491 falls in between these two, and the 7194 falls in between these two. So these two are a match, the 7,301 and 7,386. In addition, that's the actual locus where they match at both. Forty-six eighty-eight matches forty-five fifty. And you literally just count. You say where does number 1 match? Does it match number 2, number 3, number 4, number 5, number 6, and you add them all up. When you add them all up you come up with your observed number of matches. When you come up with that observed number of matches you can then take the expected number of matches and do what's called the chi-squared analysis.

THE COURT: Excuse me just a minute, Doctor. I understand the screen can't be seen in the holding cell. I'm just wondering how we might remedy this. Well, you have copies of these slides Mr. Furlotte?

MR. FURLOTTE: Yes, I have. These slides here yes I have copies of.

THE COURT: I wonder if we couldn't have copies of those run off straight away, Mr. Pugh, and Mr. Furlotte you then provide Mr. Legere with copies of those.

MR. FURLOTTE: Yes.

THE COURT: So that he could follow those on. I'm not sure how much of it is, but where Doctor Shields is standing must surely be seen on the monitor because the bench here is seen and you're in line with the bench so you must be safe. Run off a number of copies Mr. Pugh, please. (Clerk making photocopies.)

MR. CLERK: Here's the first copy.

THE COURT: Give those to Mr. Furlotte and, Mr. Furlotte, you take them into Mr. Legere, please.

MR. FURLOTTE: Even if the monitor was able to show the screen you wouldn't be able to recognize it off the television.

THE COURT: But this is a reasonably satisfactory way of doing it?

MR. FURLOTTE: It's the best we can come up with.

THE COURT: Well, I can come up with a better one and that is to bring the Accused into the courtroom and let him resume his place there. Why don't we do that. Have him brought in.

(Mr. Legere returned to courtroom 4:10 P.M.)

THE COURT: All right, Doctor Shields, carry on if you would, please.

DR. SHIELDS: Thank you. What I have done here is to literally just provide for you the explicit statistical analysis that you do, the chi-squared goodness of fit test, and I will tell you a little bit about it so that you can see what it's about.

You may remember the testimony that when you looked at, for example, locus D1S7 you found that there were three matches and the expectation initially was that there were 9.85 matches. Okay. So what you've got is these three matches observed and 9.85 expected. Since you have 36 comparisons that means that you have 33 no matches when you only expected 26.15.

Now, this analysis, like any other statistical analysis, takes into account the sample size. This is 36 comparisons. It's not a sample size of 9. It's a 36 comparison sample size. When you have that much of a sample this particular analysis will tell you whether you have statistical significance or not. It will take into account the sample size. The bigger the sample size the less the difference needs to be to be declared statistically significant. The smaller the sample size the bigger the difference has to be to be declared statistically significant. The critical value for all of these chi squares is 3.8 and a little change. If a chi square is greater than 3.8 it means that you can with little chance of being incorrect, with less than 5 chances in a 100 of being incorrect, conclude that the observed and the expected are different, and because you can look here and see which way you can see that as noted in this particular case, D1S7, there are fewer matches than you would expect by chance. In locus D2S44 there are more than you would expect by chance. This is the expected. D4S139 there are fewer. D10S28 there are more. D16S85 there are fewer. D17S79 there are more

than you would expect by chance. If you then look at these as individual loci this is a significant difference. There are significantly fewer than you'd expect by chance. This is not a significant difference. What this is saying, that it's right on to use - or bang on, to use Doctor Carmody's term. D4S139 is bang on. It is not statistically different. D10S28 is statistically significant and there are more shares in the New Brunswick population than you would expect by chance based on the data that's presented in the R.C.M.P. data base. D16 is, at best, marginally significant and it is less with this particular analysis.

The D17S79 is significantly different and there are more shares than you would expect by chance using Doctor Carmody's equation.

The bottom line conclusion: three of them show significant differences from expectation, three of the loci, and three don't. Two of the loci show more shares than you would expect by chance and one shows fewer shares than you'd expect by chance. Let me tell you what that may mean. If there are fewer shares than you would expect by chance what it's saying is that there is a greater degree of band sharing at that locus in the R.C.M.P. data base than there is in the New Brunswick data base. The same that the New Brunswick data base has more variation at that locus than the R.C.M.P. data base. But it means they're different. What do the other two mean that are statistically significant? The other two mean literally the opposite. There's a greater degree

of band sharing in the New Brunswick data base within it than there is between it and the R.C.M.P. Well than there is within the R.C.M.P. And it's saying that from this evidence which is nothing more than a comparison of the observed and the expecteds generated by the R.C.M.P. and faxed to me this weekend that 3 loci are statistically significant and two of them have a greater number of band shares than you would expect by chance.

That's using all of Doctor Carmody's assumptions. One of those assumptions is that a reasonable way to determine the number of alleles is to use what he called the effective allele number. It is used in very standard ways in population genetics. It is used in population genetics when you have what we call discrete alleles, the alleles where you know that this one is one allele and that one is a different one. VNTR systems don't work that way. They're continuously variable in size. What we do to develop a system that we can do the analyses on is we bin them. We know how many bins the R.C.M.P. and other forensic labs use because it's provided in their own data. That to me is a more defensible and a more logical way of determining how many alleles we're dealing with. We both agree that the really appropriate way to do this is to use the observed allele frequencies in all of the bins. There are other ways of doing it, however, as he noted that may be reasonable approximations. One reasonable approximation is to say well let's assume we have a certain number of bins and there's an equal frequency

in all of those bins.

When you use the observed number of bins to generate the expected band sharing, that's what I did over here, the analysis changes but not in a very significant way. What happens is that the expected number of matches goes down, and the reason why is because there are more bins than there are effective alleles and by having more bins you have a lower probability of matching. So the expected number of matches goes down. When those expected number of matches goes down and you use the actual one that I used which was with Linda rather than Donna, and it doesn't matter which one you use, you can also use this set of observes, what happens is that now there are only two that are statistically significant as individual loci. The D17S79 is very significant, okay, and the D2S44 is significant. What changes between Doctor Carmody's and my set of assumptions is not how many significant differences we see but, one, where the significant differences are. Whether it's at the D2S44 locus that there's a significant excess of observed shares or whether it's at the D10, right here.

The other thing that changes, however, is that if you look at the observed and the expected under these sets of circumstances where you conservatively assume that the number of bins actually used is an appropriate estimate of the number of alleles that you should use for this analysis, the observed exceed the expected for every locus. The observed is always greater than the expected. To me that is significant

evidence for increased band sharing in New Brunswick relative to what you would expect from the R.C.M.P.

The final analysis which was discussed earlier then allows one to say that even more conclusively is what's called a heterogenating chi-square. This is the statistic that Doctor Carmody mentioned. You can just pool all of the observes and all of the expecteds together and you come down to the bottom with a particular number. 65 and 65 is what it is right here. Okay. The same. Obviously there's no statistical difference between the observed and expected when you pool all the loci. But let me just point out that if you pool a locus where there's greater than the observed -- the observed is greater than the expected, and you pool a second locus where there is less than the expected, that's what happens, and there's a statistical test that allows you to determine whether you can legitimately pool across loci. That's a heterogenating chi-square and that's the number that results from that. And that is highly significant and what it says as a bottom line is that you cannot defensibly pool loci. You have to look at each of these loci individually. You do it with the other set of assumptions and in fact the heterogenating chi-square is below the critical value. Okay. Not the 3.8 I mentioned before but because this has five degrees of freedom rather than one the critical value is higher. And what it says is that when you pool over here you're pooling things that look alike and that's legitimate. You only can't pool if you have opposite effects in different ones.

The bottom line is the same in either case. There is reasonable evidence that the degree of band sharing in the New Brunswick population is greater than you would expect given the frequencies reported for all of these loci in the R.C.M.P. data base and the two different ways of analyzing whether there's increased band sharing, the way that I agree is a good statistical way to do it, Doctor Carmody's and Doctor Kidd's, or the way that I did it which is simply to look empirically and say what happens if we just multiply the frequencies together the way that you develop the match probability that's presented in case work. Does that provide us with numbers that we know are not likely to be true and therefore tell us that there's a problem with the analysis.

Finally, there's a third thing you can do. You can take each individual and ask how many total bands does it share with each other individual. That number comes out to be 2, 3, 4, 1, 0. I don't think there's anybody who shared five or more. But you do that for each individual. You end up with 36 numbers again. You can average those numbers and you come up with what's called the background band sharing. And this is not novel statistics with me. Alex Jeffries, the gentleman who developed these kinds of DNA finger-printing probes, is the one who pointed out that in order to do these kinds of analyses it is imperative that you know what's the probability that somebody at random is going to share a band with you, if you're then going to develop a probability of what's the likelihood of sharing a whole bunch of bands with you, because it makes a difference. The reason that

brothers or sisters, or brothers and sisters together have a probability of being identical at ten alleles across five loci is because they have a background band sharing of 50%. That's where it comes from. It's .5 to the 10th power. One-half times one-half ten times. The reason why that number is so much bigger than all the other numbers is because siblings on average share 50% of their bands. So if it turns out that individuals in a general population while not being as related as sibling are more related than the zero that's assumed by simply using 2pq and multiplying the probabilities across loci, then that correction factor has to be used to come up with a reasonable estimate of probabilities.

To show that this is not, again, simply theoretical or simply statistical but may have some forensic implication as well, the last thing I want to do is show these probabilities for this particular case which depends on the data base and the other assumptions that you use.

Doctor Carmody presented data which is similar to data that I have orally presented comparing the probabilities that result for Mr. Legere depending upon whether one uses the R.C.M.P. or the FBI data base. He added the new Montreal data base and the Minnesota data base as well. Now, I have some other data bases to look at.

Here's the probabilities of a single locus match using the R.C.M.P. data base for Mr. Legere. Those numbers may look familiar. Here are those probabilities using the Centre for Forensic Sciences' data base.

Here's those probabilities using a Chinese data base, and here's the probabilities using the East Indian data base generated by the R.C.M.P. So it can range from a 1 in 66 to 1 in 522 for D10S28 for the same two bands. Those are the probabilities at that particular genotype.

For a four locus evidence match with LJ it ranges from 1 in 5.2 million to a lower number 1 in 3.9 million if you were in the C.F.S. data base, to not possible in the Chinese data base because they don't have D17S79, to 1 in 16.4 million if you use the East Indian data base. Okay.

Five locus evidence match, 1 in 310 million versus 1 in 341 million, versus 1 in 2 billion.

Now, a four locus match between the R.C.M.P., the C.F.S., the Chinese or the East Indian, the four locus match at D1, D2, D4 and D10, would range somewhere between 1 in 35 million if you use the R.C.M.P. to 1 in 469 million if you use the Chinese data base.

Using those forensic probabilities alone I also think that common sense can enter into the analysis. The way I look at it is I ask whether someone entering a lottery would pay no attention to the differences and odds of it. Whether I said you had a dollar to spend in a lottery and you could go into a lottery with odds of 1 in 31 million versus 1 in 469 million would you make a choice? Would you pick the one with the bigger odds, and if you would I think that's a rational decision and I think it's therefore a meaningful decision. So if those numbers are different --

I don't think they're equivalent. I think they have different messages for the people who are hearing them, and you have to know which is the most accurate in a particular case. To do that one can take other kinds of evidence from a particular case and develop what probabilities would likely occur using that kind of evidence.

So the last thing that I did for this particular case was to take the new background band sharing. I added all the nine individuals - you always leave out one of the sisters because you don't use related individuals, and the background band sharing if you go through and do everybody against everybody else is .197. It is not zero, it is not .25 which is what is standardly used as a conservative estimate in other forensic analyses as Doctor Carmody testified to earlier, over in Great Britain in particular. So that .197, okay, if you use it to develop a probability and a probability of a five locus ten band match results in a different probability than any you've heard before, it says that that probability would be 1 in 11 million versus the 1 in 310 million that you heard from the R.C.M.P. Well 1 in 310 million in essence to most people means that's it. There aren't 310 million people in this country. And that's one of the things you can do with probabilities is you multiply a probability times the number of potential events to come up with the likelihood that it'll happen. At 1 in 11 million maybe there's two in Canada that match. And if we were to go to a different city or a different place we might

say that there's four or five. It is not the individual. It has a different meaning. Okay. That assumes that all of the potential contributors are not related. If there are potential contributors that are related that probability changes and it changes in a very standard predictable way. What you do is you take the background band sharing and add it to the background band sharing that you know would be true for a particular class of relatives. For example if there were half-sibs involved in a particular case, in a case where the background band sharing was similar to what's available here, you would take .25 which is the relatedness between half-sibs versus the .5 between full sibs, you would add it to the .197 and you'd take that to the 10th power to come up with the probability of a random, in quotes, five locus ten band match with a half sib, in a population with that much background band sharing. That probability is 1 in 3.139. That probability is true if there are half-sibs, nephews, uncles. All three of those classes of relatives would be potential contributors and could match with that probability at five loci and ten bands.

Under those circumstances I don't think we're talking about forensically uninteresting or forensically not different probabilities.

MR. FURLOTTE: Doctor, did you do anything else in relation to this particular case?

A. I don't remember. I must have but I don't remember.

Q. Now, if substructure does exist within the Caucasians or within Canada in particular, what does that do for your ability to use the Hardy-Weinberg formula, 2pq, and to use the Product Rule?

A. It influences the way you would go about using them. It influences the way you would go about developing probabilities. Okay. If you actually had a good estimate of the background level of band sharing you could still use the Hardy-Weinberg. You wouldn't need to but you could. Background level of band sharing doesn't need you to make assumptions, you just use it.

Q. Now, the background level of band sharing that you found in this case here, is there any way to tell how accurate that might be?

A. It's totally accurate for the nine individuals. Are you asking is it accurate for --

Q. For New Brunswick.

A. Only by adding more data.

Q. Now, you have the possibility taking in half-siblings, uncles, nephews, that the probability from 1 in 310 million drops down to 1 in 3,139. I notice Doctor Carmody put upper confidence intervals on the 310 million. Would you also put upper confidence intervals on the 1 in 3,139?

A. If that's based on background band sharing you don't have to. If it's based on an estimate -- The reason there are confidence limits on the original is because it's based on a frequency estimate and the frequency estimate itself has a confidence limit around it. When we measure, when we count the number

of individuals that's an estimate of the frequency rather than the known frequency, and when you do that you have to say well this is what our estimate is but the sample size says that it could be anywhere from a much smaller number to a much larger number of alleles in this bin, and that's not true with background band sharing. You don't put confidence limits on the average relatedness between sibs for example.

Q. Okay. Now, the R.C.M.P. uses a data base and there's is somewhere around 900 there now, but some forensic labs use data bases just over a 100, or what size?

A. I have seen some loci being used in a particular case with data bases that are just over a hundred. More standardly they seem to use 200 individuals as their cut-off.

Q. How big a data base would be needed say for New Brunswick or the Newcastle region if you wanted to do an unquestionable test as to unrelated band sharing?

A. The way it stands right now that the sample size is already factored into the analysis and the analysis says that there are statistically significant differences in the number of expected and observed band shares.

Q. Which could reduce the figure down to 1 in 3,139?

A. If you're talking about for half-sibs, nephews and uncles. Then reduce it down to 1 in 11 million if you're talking about unrelated individuals.

Q. If it's unrelated it's 1 in 11 million. If you take into consideration related individuals, half-siblings, uncles and nephews, it drops it down to 1 in 3,139?

A. That's correct.

Q. And for full siblings it would drop it down again?

A. Yes. Do you want to know?

Q. Yes.

A. 1 in 37.

Q. With that kind of background band sharing?

A. Correct.

MR. PURLOTTE: My Lord I think it might be an appropriate time for a break at this time. I will not be all that much longer with Doctor Shields and I would like overnight to --

THE COURT: Well, that would be fair enough I think. It's 20 to 5 now. I take it that you would be finishing fairly --

MR. FURLOTTE: I don't expect to be any more than 15 minutes.

THE COURT: Do you have any estimate of your cross-examination? Well, I --

MR. WALSH: Do you want me to put confidence intervals around those, My Lord? I would think that I should -- Again, I don't want to be out on a limb but I should be done in the morning. Just depends how well Doctor Shields and I get along.

THE COURT: Well, rather than make liars out of both of you let's leave it right at that. Well, you shouldn't discuss the case with anyone until all of your evidence is completed, Doctor, according to the rules of the game. So we will come back in the morning then. I don't want to press this unduly but did I understand from what you said, Mr. Furlotte, earlier, that you would have just the one witness? I thought you used the expression "my witness" will say so and so in your -- I don't want to bind you to it but

I'm wondering what we can tell the jury about --

MR. FURLOTTE: I'd rather not tell them anything.

THE COURT: All right, that's fair enough, I'm not going to press you. We will see you at 9:30 in the morning then, jury, please.

(ADJOURNED 4:45 P.M. TO OCTOBER 29, 1991 @ 9:30 A.M.)

OCTOBER 29, 1991

COURT RESUMES. (Accused present.)

(Jury called, all present.)

THE COURT: Now, Mr. Furlotte, you have some more direct examination.

DIRECT EXAMINATION CONTINUED BY MR. FURLOTTE:

Q. Doctor Shields you have been declared an expert witness in population genetics and I see from you C.V. from the time you obtained your Ph.D. in 1979 you had a dissertation in inbreeding. That's correct?

A. It's about inbreeding, population structure and the evolution of sex, yes.

Q. And as I go through your C.V. you have carried a special interest in inbreeding and inbred populations throughout that time?

A. Inbreeding, inbred populations, population structure in general.

Q. And from the evidence that you have given in court you have testified that you have identified statistical significant differences within Caucasian populations across Canada.

A. That's correct.

Q. And as a result of your findings what is your opinion as to the R.C.M.P.'s ability to use the Hardy-Weinberg formula, the 2pq, and the Product Rule to gain the numbers that they do in probabilities?

A. Without correction factors I think there's enough evidence to suggest that the assumptions are at least at best untested and unproven and may be wrong, therefore, I don't think that you should be using it without correction factors.

Q. I believe you mentioned there was other people who shared your opinion?

A. Yes, there are.

Q. And the National Academy of Science had a special project to look into the dispute between people with your opinion and people supporting the opinion of the forensic fields?

A. The U.S. National Academy of Science has put together a panel to examine all of the issues involved in the forensic use of DNA typing. Part of what they were looking at is differences of opinion among experts in a variety of different fields.

Q. And had they concluded their analysis?

A. The panel has finished its deliberations and discussions and produced a draft report which is what we call in review.

Q. And has that draft report ever been presented in other courts?

A. Pieces of that draft report were presented in a case in either Maryland or Virginia and those pieces then became part of the public record in the U.S. and were disseminated around the U.S. and at least one of those pieces was also presented in a case in Oregon.

Q. And does the National Academy of Science support your position or support the forensic field's position?

MR. WALSH: Well, My Lord, I don't think that that's a proper question. I mean we don't have a final report. That evidence is clear. We would have to get into the whole aspects of the National Academy report and I don't have any -- there's no witnesses here from the Academy that can actually present their findings with respect to that report. Mr. Furlotte is attempting to do the same thing again. And if we want to get into this I think --

THE COURT: Well, this matter came up with earlier witnesses for the Crown, of course, and I think there was a suggestion, and perhaps Doctor Shields would agree, I don't know, I mean he's not volunteering information on this, I recognize that, but there has been a suggestion that it would be highly unethical for anyone to have used or to have disclosed that report before it were vetted and formally released. Do you agree with that Doctor Shields?

A. I do and I don't Your Lordship. I always want to say Your Honour, I apologize for that.

THE COURT: That's all right. Some say god.

A. The case in either Maryland or Virginia one of the members of that panel testified about what that said, and then the jurist in that case, the judge, agreed with the Defence objection to that that if he's going to testify about it he'd better show it, so he brought in pieces of the report. In the U.S. once those pieces of the report become part of the public record they are public record and therefore other people now had access to those. It is a -- I agree that it is

a preliminary report. I agree with what the prosecutor was saying. It is not the final report and I don't think it's unethical to say what's in the draft as long as everybody understands that it's a draft and it may change.

THE COURT: Well, how far do you intend to go with this Mr. Furlotte? I mean have you got copies of portions that are going to be read?

MR. FURLOTTE: No, I do not. I do not have copies. My Lord it's just that Doctor Carmody --

MR. WALSH: Well, if we are going to discuss it, like as far as the National Academy report, when the final report comes out that's certainly going to be something that we wouldn't have any objection to, but at this particular point it could be misleading. We don't know all the context, all the aspects, and I think that what we should do, My Lord, if he wants to pursue that is have a discussion on it unfortunately in the absence of the jury.

THE COURT: Well, I think I can say flatly that it offends the best evidence rule. If a report is going to be - or the contents of a report are going to be put into evidence then the report should be produced and put into evidence, and if it's not produced questions can't be asked about its contents. I think it simply offends the best evidence rule.

MR. FURLOTTE: My Lord I believe this case is analogous to Doctor Carmody testifying that the formula that he prepared last Thursday, that he consulted with Doctor Kidd and he consulted with a couple other --

THE COURT: That's not that type of thing at all. It's completely different. That doesn't offend the best evidence rule and this does. I won't permit questioning along that line.

MR. FURLOTTE: Doctor, as a result of your findings that there is substructure and statistical significant substructure in Canada amongst the Caucasian population does that support the use of the probability figures generated by the R.C.M.P. data base or is that a misuse of statistics?

MR. WALSH: That's a leading question, My Lord, of the utmost. He's not on cross-examination now.

THE COURT: Well, it is leading but let's have it answered anyway.

A. I don't believe it's a misuse of statistics. What I believe is that the assumptions that you use to make those probability calculations without corrections are shown by the evidence to be iffy, or wrong, depending upon which analysis you're talking about. Under those circumstances they produce a number that is not likely to be true. I don't think that's a misuse, I think it's a mistake.

MR. FURLOTTE: Is there a proper way to do it? A known proper way to do it?

A. There have been a number of suggested proper ways of doing it. The one that everybody agrees would be the least what we call assumption laden where if those assumptions were violated it wouldn't matter because the final probability would be robust to any violations of the assumptions is what we call the empirical

probability where you look at the entire multi locus genotype, all five loci, in a particular case like this, and you ask the question in the entire data base do I ever see all five of these loci with these two bands at each of these loci matched by anybody else in the data base besides the particular person in a case. If the answer is no then you can say that it occurs with a frequency of at most 1 divided by the total number of the data base. It's a simple counting of the probabilities. And that would be 1 in 732 or 34 or whatever it is in terms of the R.C.M.P. data base that was used in this case.

Q. What the R.C.M.P. data base was at the time you did these calculations.

A. That's one way. The second way is that there are ways to correct for biases that result from violation of the assumptions. Some of those ways are what I suggested yesterday. If you come up with a measurement of the background band sharing you can generate a new probability that's based on that. That probability will be less likely to be biased by the changes in allele frequencies from one portion of a Caucasian population to another. There have been similar correction factors suggested by others. One that we have actually heard about is Nichols and Balding.

Q. So in the scientific field everything is still, as you said, iffy?

MR. WALSH: That's another leading question, My Lord, of the utmost.

MR. FURLOTTE: Well I believe that's what he stated. I'm just asking him to repeat it.

THE COURT: Well, it was something else that was described as being iffy. Well, why don't you rephrase your question Mr. Furlotte.

MR. FURLOTTE: In other words, Doctor, I believe what you're saying is that in the scientific field there has not yet been declared a valid way to calculate the probabilities?

A. The ways that are currently being used to calculate probabilities are considered to be controversial is the way I would answer that question.

MR. FURLOTTE: I have no further questions.

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

MR. WALSH: Yes, My Lord, thank you.

MR. FURLOTTE: My Lord I believe we still have to put into exhibits those transparencies that were shown yesterday.

THE COURT: Oh yes, you're quite right. Yes. We were going to call those numbers D-15(1) to whatever. I forget how many there were. Perhaps Doctor Shields would put those in the order in which they were presented.

MR. FURLOTTE: I have here for the first one the bands matching in the Legere case.

THE COURT: That would be D-15(1).

MR. FURLOTTE: Additional matching in the Legere case.

THE COURT: D-15(2).

MR. FURLOTTE: Band sharing in New Brunswick, Canada from Legere case.

THE COURT: D-15(3).

MR. FURLOTTE: And the Goodness of Fit Test.

THE COURT: That will be sub (4).

MR. FURLOTTE: And the comparison of match probabilities.

THE COURT: (5).

(Clerk marked transparencies exhibits D-15(1) to (5).)

THE COURT: Yes. Well now, Mr. Walsh.

MR. WALSH: Yes, My Lord.

THE COURT: Just on those last exhibits, do you have spare copies of those Mr. Pugh?

MR. CLERK: Yes, My Lord.

THE COURT: Are there enough for the jury later?

MR. CLERK: I have six.

THE COURT: 6 for the jury. Well, we won't distribute them just yet but perhaps during a recess they could be sent out with the jury and they could examine them. And the other ones, we hadn't distributed those, had we?

MR. CLERK: No, I have those as well.

THE COURT: Well, the same with those. Okay.

MR. WALSH: Yes, My Lord, thank you.

CROSS-EXAMINATION BY MR. WALSH:

Q. Doctor Shields it is my understanding of your testimony yesterday what we have is an agreement between all of the experts, yourself and all the Crown experts, that there is a four and five probe match at these highly polymorphic areas of the human DNA, is that correct?

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A. That's correct.

Q. And this would mean that, assuming for a moment that the substances that are matching are semen and hair, this would mean that the semen left in Nina Flam and on the Daughney sisters is consistent with having come from the same person, that person whoever belongs to 56A-69A, that hair sample, is that correct?

A. It's consistent with that, yes.

Q. And if the jury accept that that hair was in fact taken from Mr. Legere then we have agreement, Doctor, that the semen is consistent with having come from Mr. Legere, correct?

A. That is correct.

Q. The only two possible conclusions then that could be drawn from that is that the semen was in fact left by Mr. Legere or it was just a coincidence and someone else with the identical DNA pattern left that semen, is that correct.

A. Those are the two conclusions one would draw if there were no laboratory mixups which I see no evidence of. So in the absence of laboratory mixups, yes, those are the two conclusions one would draw.

Q. In the absence of that, and if we agree that these are matches, that's the two conclusions that you could draw?

A. That's correct.

Q. And I understand, Doctor, that you would also agree that a four or five probe match at these highly polymorphic areas of human DNA, without even developing probabilities you would consider such a match a rare or an exceedingly rare event?

A. That's correct. It would depend on whether we're talking four, five, six, seven, eight loci whether I would call it rare or exceedingly rare.

Q. But four or five probe match you would consider that rare or exceedingly rare?

A. Rare in most populations, yes.

Q. Therefore, Doctor, without even developing probabilities, talking about numbers, you would agree that it would be a rare or an exceedingly rare coincidence for someone other than Mr. Legere to have left that semen?

A. That's correct.

Q. So the jury can take that into the room with them when they go.

A. Yes, they can.

Q. Now, Doctor, apart from being qualified on the actual testing, the molecular biology, the RFLP technique, you were qualified in this court as a population geneticist, is that correct?

A. That's correct.

Q. And your testimony was essentially yesterday since you agreed on the matches, your testimony dealt with the area of population genetics?

A. That's correct.

Q. Now, just so that we can reduce it for both myself and the jury's purposes to an understandable aspect, my understanding, and correct me if I'm wrong, that there are two general aspects associated with population genetics. One is the theoretical or mathematical aspect and the other is the empirical aspect. Is that a general category?

A. That is a general category. Just let me expand on one half of that to make it clear. The empirical aspect is often also called ecological genetics or field genetics. In some cases it's general genetics. If you gather data that is used in population analyses that's the empirical side of population genetics.

Q. So the methods that you would use like you used yesterday are the statistical aspect of population genetics?

A. Yes.

Q. In that respect population genetics is almost like a single discipline in the sense that all population geneticists use statistics in their work, is that right?

A. That's correct.

Q. Now, when we talk about the empirical observations, empirically looking at populations, from a layman's point of view I understand that to be looking at a particular type of population to see how these statistics or the theory applies, is that fair?

A. It's that aspect and it's also using data from particular populations to test and refine and generate theory. So it goes both ways.

Q. I believe one of the ways you have described that is you use a particular empirical system to test the theory and to inform the theory and to generate new theories?

A. Yes.

Q. You want to go out into the population you are looking at and see what's going on there, is that correct?

A. That's correct.

Q. To see what your statistics - whether the statistics are right.

A. Of course.

Q. You do empirical study of populations, Doctor?

A. Yes, I do.

Q. And I was looking at your C.V. and it would be fair to say that your professional experience, publications and interests primarily lies with respect to animal populations as opposed to human populations.

A. That's correct.

Q. And your empirical study, Doctor, in fact is done with many kinds of animals. You deal with swallows, chipmunks, beavers. You have an expertise with respect to Mexican wolves. You deal with certain types of insects. Things of that nature. Is that correct?

A. That's correct.

Q. And in fact you're the Director of the Cranberry Lake Biological Station and there you do important work associated with rare species trying to preserve the wildlife. Is that a fair assessment?

A. That's correct.

Q. On the other hand, Doctor, if a person works exclusively or let's say 95% of their time on humans, particularly someone who had done postdoctoral work in human population genetics and has studied human populations worldwide, you would consider him a human population geneticist, would you not, under that definition?

A. You could, yes.

Q. And based on that you would consider Doctor Kenneth Kidd to be a human population geneticist, would you not?

A. Yes, I would.

Q. You do not consider yourself to be a human population geneticist, do you?

A. No, I do not in the sense that you mean it, right.

Q. I will move on to another topic Doctor. I believe you said yesterday at the beginning of your presentation that you wanted to address - the most important question you wanted to address for the jury here was this whole question of substructure. Is that fair?

A. Yes, it is.

Q. This for you was the important issue?

A. Yes, it was, and it is.

Q. And then you proceeded on the overhead to demonstrate allele bin frequency differences across races and within races, is that right?

A. That's correct.

Q. And this is something that you have been doing in other cases that you testify in. You are demonstrating that there are allele bin frequency differences within races and across racial groups. Sometimes your data

changes in terms of what you are using for illustrative purposes but that's essentially the point you are trying to get across, is that right?

A. I think it's probably fairer to say that when I started I said in court, and I think you know this from another case in Canada, that I was worried that there was substructure and there wasn't enough data to say, and since then there are data coming in that say there is substructure.

Q. And that's what the allele bin frequencies, comparisions, all those Texas and Florida --

A. That's correct.

Q. -- and Guam and all these things that you were demonstrating yesterday that's the point. They were simply illustrative of the point that you are trying to make?

A. That's correct.

Q. And you have been giving this message on numerous occasions?

A. That's correct.

Q. You have given it previously at this hearing in the spring, is that right?

A. That's correct.

Q. And I remember seeing an affidavit that you filed in a case in New Hampshire called Vanderbogart and you did the same kinds of things, you were getting this message across about substructure, is that right?

A. Yes.

Q. Anyone who, for example, read the transcript of your hearing in the spring, or read that affidavit, say for example a population geneticist who read that, would understand the message that you were trying to get across?

A. I would hope so.
Q. And the basis for your message.
A. Um-hmm.
Q. As you say, the data changes somewhat but the points are the same?
A. That's correct.
Q. And someone like Doctor Kidd who looked at - read your transcript of your testimony in the spring or read that affidavit you would hope that he understood the message that you're trying to get across.
A. Sure.
Q. In fact, Doctor, one of the - you didn't do it here, this trial, but previously you wanted the sets of data that you used to demonstrate that there are allele frequency - bin allele frequency differences in the world was the - part of it was the Karitiana.
A. Doctor Kidd's data.
Q. Doctor Kidd's own data. So he'd pretty well understand what you were meaning?
A. Yes.
Q. And you would expect that he would understand the points that you're making, the message on substructure?
A. Absolutely.
Q. You are aware, Doctor, that Doctor Kidd doesn't agree with your conclusions that you have drawn from this data with respect to the forensic implications of substructure for human populations?
A. I have read testimony that says that the differences while real, as they have turned out to be, he believes are not forensically important I guess.

Q. And he doesn't agree - you two do not agree on that?
A. That's correct.
Q. Thank you. I would like to move on to another topic Doctor. You used yesterday, and at the risk of beating this to death, the term 'statistically significant difference' has come up time and time again and I take it - and you used it yesterday. In fact what you were showing are statistically significant allele frequency - or allele bin frequency differences, is that right?
A. That's correct.
Q. So I take it that the term 'statistically significant difference' is a recognized concept in statistics?
A. Yes, it is.
Q. If two figures are not statistically significantly different, not statistically significant different, what does that mean from a population geneticist's point of view?
A. From a population geneticist's or a statistical point of view it means exactly what I was talking about yesterday. The probability that is produced by a statistical analysis is going to be greater than .05. That means that you are going to have more than a 5% chance of making an error if you conclude that there is a difference. That's explicitly what not statistically significant means. It means that you have a higher than a 5% error rate when you conclude - if you conclude they are different.
Q. But what if you conclude that they're not -- Maybe I misunderstood. What if you conclude that they're not statistically significantly different?

A. That's exactly. I think you did misunderstand. If you conclude they're not what you're saying is literally when you use statistics that you have a higher error rate than you are willing to accept. If you conclude they were different that's what not statistically significant means. It also means, again, maybe for a layman to think about that way --

Q. That would be the easiest way.

A. It also means that there is not enough evidence to decide they're different and therefore I'm willing to accept now that they are not different.

Q. From a layman's point of view if there's a finding that they're not statistically significantly different there's really no difference between those - the two numbers?

A. Correct. The two distributions or the two means. Whatever it is you were testing.

Q. Okay. So if I tested one sample population, came up with one number and I tested another sample population and came up with another number, and by your calculations and depending on sample size you came up with two numbers and if they were not statistically significantly different from a layman's point of view that would mean that there's really no difference in those numbers.

A. It means that you can't distinguish which of them is - that they're the same numbers.

Q. They're the same numbers.

A. Yes.

Q. Even though they look different from a statistician's point of view they're the same numbers.

A. You can't distinguish between them, yes.

Q. Okay. And that's a recognized concept in statistics as you have pointed out.

A. Absolutely.

Q. We have also been introduced to the word 'confidence interval' at this trial, and I take it that is also a recognized concept in statistics.

A. Confidence intervals are a recognized concept, yes.

Q. And what is the purpose behind the confidence interval in your mind?

A. Confidence intervals are a way of looking at variations around something. They are a way of coming up with a level of confidence to believe that you have done a reasonable job estimating something. Confidence intervals go around means or they go around frequency estimates. They go around what we call point estimates.

Q. Like these numbers here on this summary chart here?

A. No. The numbers that they would go around -- Yes, this one, that's a point estimate. This is not. Okay?

Q. Yes. Continue.

A. Point estimates they go around. And what they do is they say that given a particular sample size, and given that this is the number that I estimate, we can use frequencies since that's what we're talking about, I come up with one in ten as the frequency of a particular allele. 10%. We know that sampling theories suggest that if we took this - we did this with a small sample, for example ten, that we don't have much confidence that it really is 1 in 10, so we can take different levels of confidence and say

well we want to know with a 99% confidence, okay, what the real value of this 1 in 10 that we have estimated is, and if we do that then we're going to come up with a 99% confidence limit which means that 99% of the time if we get a 1 in 10 in a sample of the size that we're talking about the real value, the true value, the accurate value, will fall somewhere between the two ends of that confidence limit, and if it was 1 over 10, for example, it might be somewhere between .005 and .015, so between 5 and 15 rather than the 10. So what it would be saying is that 99% of the time we would be reasonably certain that it's going to fall between .005 and .015, but we don't know that it's .01.

Q. From, again, a layman's point of view like my own, because you are making projections on a larger population based on a smaller sample of that population you can't give an exact figure when you are projecting frequencies. Is that from a layman's point of view? So you are giving an estimate and the confidence interval gives you a way of weighing that particular estimate.

A. It tells you where the actual value should lie.

Q. It tells you where --

A. It doesn't weigh it. It says it's somewhere between those two numbers.

Q. Between those two numbers.

A. And the most likely place it is is in the middle which is the estimate.

A. In the middle is the best estimate. You use confidence intervals in your own work, Doctor?

A. Sure.

Q. In fact I read something a long time ago in one of your publications on one of your animal populations that you actually gave confidence intervals when you were giving your frequencies. You used confidence intervals in part of your work.

A. Absolutely.

Q. And that's to show the expected variation, that the number you are giving is not exact and it's probably within this particular frame.

A. Right.

Q. 99 - say, for example, 99.7% confidence that the number will be somewhere in there and this is our best estimate somewhere in the middle.

A. Yes. That 99.97 is not very different from the 100% confidence limit, and a 100% confidence limit is very simple, it's going to fall between 0 and 1.

Q. Yes, I agree.

A. Okay.

Q. I understand. A 100% confidence, Doctor, if we went out, for example, and sampled the whole population of Canada we would have a 100% confidence then in the number that we generated?

A. No, you only have to sample one individual because the 100% confidence limit means that the frequency falls between 0 and 1.

Q. Okay, but that wouldn't be very informative would it?

A. No.

Q. No. So the confidence interval is a recognized concept in statistics?

A. Yes, it is.

Q. Whether something is statistically significantly different is a recognized concept in statistics.

A. It is.

Q. And to the layman you wouldn't expect the layman to have that kind of knowledge about statistically significant confidence intervals, would you?

A. No, I wouldn't.

Q. No. And statisticians need to use those kinds of concepts so they can actually put meaning to the numbers that they generate, is that right? Have a way of looking at the numbers and derive some meaning from them.

A. I believe so, yes.

Q. Correct me, you filed an affidavit in a case, as I pointed out earlier, in New Hampshire called Vanderbogart. Do you remember that Doctor?

A. Yes, I do.

Q. And what I understand happened there is under their system the FBI's chief scientist, Doctor Bedowle, had refuted some testimony that you had given in that case and you had filed an affidavit in support of why you should get back on the stand and testify again. Is that a pretty basic understanding?

A. No, the affidavit was in lieu of testifying again. It was allowed as re-rebuttal and it may be the law is different in the States, I don't know.

Q. So you were going to -- The affidavit was filed as evidence that you were presenting to a court in this particular case in New Hampshire to rebut what Doctor Bedowle had said about your testimony?

A. That's correct.

Q. And part of what you did in that affidavit, Doctor, is pretty well what Doctor Carmody did is you had got some data from Mr. Furlotte about that time on this case --

A. That's correct.

Q. For want of a better term, the Legere data, and you took that data and you ran it through the FBI data base.

A. I took the bands - the matching bands and ran it through.

Q. Yes, well the Legere data.

A. That's correct.

Q. That's a quick way of saying it. And you took those matches, run them through the FBI Caucasian data base, and you came up with a - just on a four probe match you used that as illustrative only, and you came up with 9.6 million, something like that.

A. Yes.

Q. And the R.C.M.P. had generated a four locus - a four probe match at 5.2 million, is that correct?

A. That's correct.

Q. And what you were doing - and Doctor Carmody did the same thing, he compared the FBI with the R.C.M.P.?

A. That's correct.

Q. So in this affidavit which constituted evidence that you were offering to the court part of what you did in that affidavit was show the Judge that look, if we go through the FBI it's 9.6 million and if we went through the R.C.M.P. it would be 5.2 million, look at the difference, is that right?

A. That's correct.

Q. Tell me, Doctor, why you didn't mention to the Judge that those numbers are not statistically significantly different?

A. Who says they're not?

Q. You agreed that they weren't.

A. No.

Q. On the voir dire you agreed that they were not statistically significantly different based on the sample sizes that you were using.

A. What I probably said in the voir dire is that I would not conclude they were different. That's not the same as saying they are not statistically significant.

Q. You would conclude that those numbers were not different?

A. I would conclude that one couldn't demonstate. You can't do a statistical test on those.

Q. So you would conclude that those two numbers were not different?

A. I would conclude that they are not necessarily different, yes.

Q. Okay. Did you tell the court that in the affidavit?

A. Of course I did.

Q. Where?

A. In the affidavit.

Q. In the affidavit.

A. I just said those are the numbers you get if you do that.

Q. But what was the purpose by holding up those two numbers?

A. To show that you get different numbers if you run the same things through a different data base.

Q. But you just told me, Doctor, that you didn't - that they weren't different. That those numbers were not different.

A. Let's do it -- May I answer your question?

Q. Sure, that's what I'm asking.

A. We will show you exactly why. Fine. Prior to the Legere case and prior to the suggestion of putting this together Doctor Carmody didn't do 95% confidence limits, neither do 99% confidence limits. I think you know that his affidavit that you're talking about from that Legere hearing was done in response to my affidavit.

Q. Oh, I -- Doctor, well, that's a statement of yours, is it? Is that your belief Doctor?

A. Yes, that is my belief.

Q. I see. And do you know when we received that affidavit Doctor? When we became aware of that affidavit. Do you know that?

A. No.

Q. So if, Doctor, the calculations were generated before we even became aware of that affidavit what would your conclusion be then? You are suggesting that Doctor-- You have just suggested that Doctor Carmody did those statistics because of your affidavit filed in some court in New Hampshire, is that right?

A. That's correct.

Q. Do you know when we received that particular affidavit?

A. No, I only know that Doctor Carmody and Doctor Kidd testified about the affidavit at the hearing.

Q. Yes. Do you know when we received it?

A. No, I don't.

Q. So, Doctor, if Doctor Carmody had generated those numbers prior to receiving that affidavit your statement would be incorrect, would it not?

A. Yes, it would.

Q. Thank you. Now, let's continue with your answer Doctor.

A. All right. In any case nobody had ever done that 95% confidence limits. The FBI presents their data as one - and in fact this is presented as 1.52 million. I don't see any confidence limits around it, never have, until the first time we did this Legere hearing. Okay? Under those circumstances all I'm doing is pointing out that you get different numbers if you run the same individual through different data bases, and I did the same thing here without providing confidence limits on them. I'm not saying - I've never said that I thought the numbers are the same or different or anything else. They are different in fact and maybe not statistically. You can't know whether they are different statistically.

Q. They're maybe not statistically different. What do you mean by that?

A. You would have to be able to do a test and the only way you can do the test is what we call bootstrapping.

Q. And you mentioned confidence intervals in that affidavit?

A. I probably did. I may --

Q. Well, Doctor, perhaps if you --

A. I don't remember.

Q. Would you like to see the affidavit, Doctor?

A. Sure. Oh, I know, wait. There's another piece. My report to the National Academy.

Q. Oh no, no, no, no, no, no. I'm talking about this --

A. They went together in that trial.

Q. Oh, I see, but in your affidavit did you mention confidence intervals?

A. No, I did not.

Q. No. Thank you. I didn't think so.

A. I didn't have to. I mentioned it in the other piece that was presented as evidence.

Q. With respect to --

MR. FURLOTTE: My Lord I am going to suggest that if the Crown Prosecutor is going to cross-examine this witness on affidavits and evidence that he produced at another trial then let him present all of the evidence to this witness, not just the affidavit but the part that was attached and all the evidence he put in at that trial so the jury can get a proper context of this evidence.

MR. WALSH: I have finished on that aspect My Lord. I was just trying to clarify a point. I'm moving on.

MR. FURLOTTE: I would suggest trying to mislead.

THE COURT: Well, you are stopping there at that in any event.

MR. WALSH: Yes. I may go back to it, My Lord, just as soon as I can find my spot in the voir dire and we'll just maybe touch back on that. But I don't have to accept the statement from Mr. Furlotte but I won't say anything further.

MR. LEGERE: Your Honour can I be excused again before I get sick here.

THE COURT: What do you have to say Mr. Furlotte? Do you concur in that -- All right. Would you remove the Accused, please, Sheriff.

MR. LEGERE: Don't worry, Mr. Shields, you were in Bagdad when he was still in his dad's bag.

(Accused removed from courtroom and views proceedings from holding cell.)

THE COURT: I'm not sure what that was meant to represent, that remark, but Doctor Shields pay no attention to it.

MR. WALSH: Doctor Shields let's move on to something that's maybe a little clearer then. What do you think the probability is, Doctor, this morning of me being able to convince you that the calculations you did on background band sharing are incorrect, in the next half hour? Not very likely, would you agree Doctor?

A. On the basis of the analysis done with Doctor Carmody's pretty close to zero.

Q. Okay, I didn't think so. It would be wiser for me to simply note that Doctor Carmody and Doctor Kidd don't agree with you with respect to this background band sharing and the high levels?

A. They agree that there is - at least Carmody agrees on the stand that there are statistically significant differences, yes.

Q. Yes, but in terms of the final conclusions that you have drawn they disagree with you.

A. They disagree, yes.

Q. That would be the wisest thing for me to do is simply note that they disagree and go on to something else, is that right? Okay. I'm going to do that and what I would like to do is perhaps approach it from hopefully a little bit more practical perspective so we can put this whole thing in context. The numbers get

confusing, pi squared tests, things of that nature. At the outset of the cross-examination here just a little while ago we had discussed the various aspects of population genetics, the statistical versus the empirical. The method you arrived at to conclude that there were high levels of background band sharing in the area from which these nine people came from is statistical.

A. The first method I arrived at is actually empirical. I counted the bands shared.

Q. On that particular -- on those autorads.

A. That's correct.

Q. But the final conclusion that you were demonstrating here yesterday with the calculations is statistical, am I right?

A. It's statistical and it's based on a whole set of assumptions that Doctor Carmody and Doctor Kidd came up with.

Q. And to paraphrase your own words, Doctor, from one time before, both the theoretical and the empirical aspects together are important in understanding any particular scientific discipline.

A. Yes.

Q. Statistically you claim you have shown high levels of background band sharing?

A. Statistically I've claimed that there are higher levels of background band sharing than one would expect by chance, using a variety of tests.

Q. So I'll use high levels of background band sharing to mean higher than what you would expect.

A. By chance.

Q. By chance. Now, empirically, now I'm talking my eyes, what kind of forces would have to be at work in a population to arrive at those levels that are high levels of background band sharing as high as you have seen here? What kind of forces would have to be at work to generate that kind of relatedness?

A. There are three forces that could generate it. One is the general background level of inbreeding which means population structure. High mutation rates could also generate it. And then selection on particular alleles or alleles that are linked to the alleles that you are looking at.

Q. Okay. Now, background band sharing is indicative of inbreeding, is that not correct?

A. It's indicative of the generic meaning of inbreeding which means shared bands. So yes.

Q. Shared bands. And what kind of things create inbreeding, high levels of inbreeding?

A. There are lots of different things.

Q. Okay, let's take it from the most basic understanding that we have. Would you agree, Doctor, that incestuous type relationships as being a norm in a small community would that generate high levels of --

A. Absolutely.

Q. Yes.

A. If you want I can answer it. I'll give you a whole list of them.

Q. Okay, please. That's what I want to know.

A. Yes, I'll give you a whole list. For example there are certain human societies that are polygamous. Polygamy generates high levels of inbreeding.

Q. Again, for the layman?

A. Polygamy is where there is one male and many females as part of the marriage system. It still happens, for example, in some South American Indian tribes.

Q. Like that tribe that Doctor Kidd looked at, the one that has one king and at least three queens.

A. Yes.

Q. Okay.

A. And when you have that small a level of ancestry that creates high levels of background band sharing. I believe there is evidence that there were only a few thousand French Canadians who settled - French people who settled Canada. That's a small number of founders so you have what we call founder effects there as well, and that will generate higher levels of background band sharing than you would expect randomly. Selection can do it.

Q. Selection being what?

A. Natural selection is simply the differential reproduction of individuals. You may have --

Q. I don't understand that Doctor.

A. Differential reproduction?

Q. Differential reproduction.

A. Means one person has ten kids and one person has none.

Q. Okay.

A. Okay? So if a pair have ten their genes are represented more frequently in a population than the pairs that have zero.

Q. Okay, continue.

A. So natural selection generates band sharing frequencies that are different.

Q. Right.

A. Differential mutuation can if you are talking about isolated or semi isolated populations.

Q. Okay, what's mutations?

A. Mutation is where the alleles change.

Q. Okay, but can you get it down to a little bit more basic? Isolated or semi isolated populations.

A. Mutation is very simple. It means that there's a change in the number of VNTR repeats, for example for these kinds, that originates in an individual. Every time there's a new mutation that originates in an individual that new mutation shows up in the progeny of that individual more than it does in other families. Those -- Whoever that family mates with it shows up in those families first so there's always a time lag before mutations become widely distributed throughout a population.

Q. So what do you mean by isolated or semi isolated -- it applies in an isolated or semi isolated population?

A. If there's a higher frequency of mating in a local area or in a particular neighborhood, in a city, or in a particular ethnic group, the mutations that arise there are distributed within that group more quickly than they are distributed to other groups and therefore there's higher levels of band sharing within groups than across groups. By the way --

Q. Like a population in the back woods of some mountain in some State for example that is isolated from everyone else you might expect to find higher mutation rates?

A. Not higher mutation rates. That if there are mutations those mutations will show up there at high frequencies before they begin to show up in the bigger populations.

Q. General population. Okay.

A. There's actually a set of people called "The Blue People" in Kentucky and West Virginia that have a particular mutation that changes their skin color to blue and they are found in essence in two counties.

Q. That's because everybody's just one big happy family, is that right?

A. So to speak, yes.

THE COURT: Whether they're happy is questionable perhaps.

MR. WALSH: What else, Doctor?

A. What else what?

Q. What else could -- You said you could list a whole bunch of them.

A. Oh yes. One of the things is that you mention that this is a high level of band sharing that we found, .197. It's not that high. Alex Jeffries who has done - who originated this whole field has done background band sharing levels on Caucasians from all over the world using their multilocus probes and found that the background level of band sharing is measured at about .15. Okay? So this is not extreme. And Jeffries also points out that you have to take that into account if you are going to come up with match probabilities.

Q. And that was based on a study of population in the Gaza Strip?

A. That was based on a study of 1700 individuals from Europe and North America.

Q. Okay. Just so I understand, can you equate background band sharing with coefficient of inbreeding?

A. You can use -- Yes, you can use both.

Q. You can use both.

A. Coefficient of inbreeding?

Q. Coefficient of inbreeding.

A. Yes, you can use both.

Q. Background band sharing can equate to a coefficient of inbreeding.

A. It's more of a coefficient of relatedness which is related to the coefficient of inbreeding.

Q. Okay. And what if you had a society, Doctor, that was not isolated, that didn't as a norm have incestuous type relationships or marry their brothers or sisters or marry their cousins or marry their uncles or nieces, had lots of migration and immigration into the area, people coming, people going, bringing new people in and they having children, them leaving, bringing others back, in that kind of a community where breeding is presumably random, you don't have this - you have a large population, a reasonably large population, it's not small, not isolated, would you expect to have high levels of background band sharing?

A. No. the expectation is is that you would see no allele differences between any subgroups in that population.

Q. And if you went out empirically into a population and observed on study that this population is not isolated, their marriage patterns are normal, their sexual relationships in terms of who they mate with is normal,

that new people come in, people leave, randomly mate --

A. Sure.

Q. -- you wouldn't expect to find high levels of background band sharing.

A. The theory says you wouldn't.

Q. And if you did, using those statistical tests in a society like that, what would that tell you about your statistical tests?

A. It tells you the statistical test is true. There are frequency differences between the two populations, therefore --

Q. But --

A. Let me finish, please. Therefore --

Q. I haven't stopped you.

A. Okay. Therefore, what it tells you is that your eyes are wrong, that there is non-random mating, that there is differential mutation, that there is some delay in getting alleles between populations because otherwise you would not see a statistically significant difference in allele frequency between Montreal and the R.C.M.P.

Q. Okay. Would it ever just briefly flash through your head, just for the tiniest moment, that maybe I'm not doing it statistically correct?

A. It's the way that it's been done since --

Q. No, no, no, no, I just asked you, if you have a society that I have described where you wouldn't expect high levels of background band sharing yet you are doing a statistical test that demonstrate high levels of background band sharing and you're saying well that means that what you see is not right

in the population but let's do the other side, would it just for the tiniest moment, Doctor, would you think well maybe this statistical test is not correctly done?

A. The statistical test is the standard population genetics as it has been since 1910.

Q. I see. And what you are saying, Doctor, is that all this statistical work that you did yesterday, right, is something that's just completely standard?

A. Yes.

Q. And if - and that there is really no controversy over the fact that you've concluded that there's high levels of background band sharing in this community.

A. .197 is not high levels of background band sharing.

Q. Well tell me, Doctor, then, let's get to it, what does that equate in terms of the coefficient of inbreeding?

A. I have no idea. It's about the equivalent of -- The relatedness of .19 is less than the relatedness of half sibs.

Q. All right.

A. And it's more than the relatedness of first cousins.

Q. Okay. More than first cousin relatedness.

A. That's correct.

Q. So we're talking somewhere between first cousins and uncles?

A. Well we're talking about background band sharing at that level. Let me do one thing so that you will understand, please.

Q. I'm not stopping you Doctor. Continue.

A. Let me just say this, okay. I think that probably people have heard that 99% of the human genome is

fixed. Am I correct? Did they hear about that? There's only one percent that differs. At that 99% of the genome that's .99 band sharing. You are trying to have me say things that have no relationship to what's really going on.

Q. No, Doctor. See, all I'm asking you is questions and I want the answer.

A. Well I'm trying to give you an answer.

Q. Now, the question I have for you Doctor is a very simple question. What is the coefficient of inbreeding that would equate to the level of background band sharing that you saw here?

A. Do I include the entire genome?

Q. Doctor, what is the coefficient of inbreeding that equates to the level of background band sharing that you saw here?

A. I would have to do the calculations.

Q. What was the coefficient of --

A. I told you what the relatedness is.

Q. What was the co --

A. Half of the relatedness.

Q. What was the coefficient of inbreeding that you projected when you were here in the spring for this particular community?

A. Now in the spring I had .275 because it was the five individuals. It goes down to .197 with nine.

Q. And in the spring what was the coefficient of inbreeding in terms of - and I'm only familiar with the .05, .005, that way of expressing it - what was it in the spring that you projected was the coefficient of inbreeding in this community?

A. I didn't project one. Are you talking about Nichols and Balding?

Q. I'm just asking about the coefficient of inbreeding. I'm not asking about Nichols and Balding. I'm asking about the coefficient of inbreeding. What did you project it was when you were here in the spring, Doctor?

A. I don't think I did.

Q. I refer you to page 134 of your transcript Doctor. I have conveniently marked the area and if you wouldn't mind reading, Doctor, from here through to there and then explain to me. I am just a layman, Doctor, I might have misunderstood something.

THE COURT: What was this again Mr. Walsh? Volume what?

MR. WALSH: Volume XIII, My Lord.

A. Could I start on the previous page where it says that we're talking about Nichols and --

Q. Sure. Sure.

A. Thank you.

"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" --

Q. Slow down.

A. I'm sorry.

"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 in-breeding, 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. That's your answer? That was your answer?

A. That was my answer.

Q. Okay, just tell us what the question and then the answer, okay.

A. "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 this is your question --

"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 suggesting that we use a coefficient higher than ever seen in Europe but lower than ever seen in the world, is that right?

A. Yes."

This is all about Nichols and Balding, not about this case as I have testified.

Q. That's about the coefficient of inbreeding Doctor, is it not?

A. It's used by Nichols and Balding.

Q. That still, Doctor, was your testimony back in the spring, Doctor, was it not?

A. Yes, it was. It had to do with Nichols and Balding.

Q. And in fact, Doctor, in the spring you projected a coefficient of inbreeding for the area from where these people came from a little less - a little less than the highest coefficient of inbreeding ever seen in the world according to Cavalli-Sforza and Bodmer, isn't that correct?

A. According to Cavalli-Sforza and Bodmer.

Q. Yes, thank you Doctor.

A. Yes.

Q. What is the Miramichi, Doctor?

A. I have been told it's a river.

Q Okay. And what kind of populations - what kind of towns, villages, people are there, Doctor?

A. I presume mostly Canadian citizens.

Q. How many villages?
A. I have no idea.
Q. How many towns?
A. I have no idea.
Q. Is there any cities?
A. I think Newcastle.
Q. Is a city?
A. Yes.
Q. Okay, thank you. And how big a county is it Doctor?
A. I have no idea.
Q. How many people would be in that county?
A. I have no idea.
Q. How many people would be in the City of Newcastle?
A. I have no idea.
Q. What are their emigration and migration patterns?
A. Don't know.
Q. What are their marriage patterns?
A. Don't know.
Q. Is incestual type relationships a norm in that area?
A. I would hope not.
Q. So, Doctor, you don't know too much about that area that these people came from, do you?
A. Not about the questions you just asked, no.
Q. No. These 9 people, you have taken a data base of 9 people from the Miramichi area, that's what you understand?
A. It's actually 10.
Q. 10. From the Miramichi area, or the City of Newcastle. You're not sure of that.
A. No. I took the 10 people that were presented on these gels under the presumption it came from the same general area.

Q. Same general area. And you concluded high levels of background band sharing?

A. I concluded that there's an empirically observed level of background band sharing.

Q. Okay, fine. That is fine. I just wanted to get the point across, Doctor, that that's what you concluded. So if those people came from - say some of them came from other parts of the province, born in other parts of this province, your conclusions would be the same about this whole province, would it not?

A. There's two ways you could get that. You could get differential migration too. Individuals with certain sets of alleles might migrate into an area more frequently than individuals that migrated out.

Q. Well let's put it in a more basic term Doctor. If, for example, just an example, that the area from which these people came from that is no different. Just assume. You know, just assume that that area is no different than any other place in this province, that they have all the same forces, genetic forces at work, all right? There's nobody blue or anything of that nature, all right? All the same forces. You would have to conclude, Doctor, based on your empirical observations and based on your statistical work that this whole province would be - you would draw the same conclusion about this whole province, would you not?

A. Yes. I would conclude that there are different frequencies of alleles in New Brunswick than there are in the R.C.M.P. data base.

Q. Yes, thank you Doctor. Let's assume, Doctor, that we have the degree of background band sharing that you say we do, that we have the degree of inbreeding that you suggest or say there is either in that community or in this whole province, let's make that as an assumption. You can agree -- You understand that's just an assumption?

A. Fine.

Q. We will accept what you say about that. My understanding is that you corrected because of that. You corrected the R.C.M.P. calculations. Am I right?

A. Corrected is the wrong word. I did not use Nichols and Balding. What I did was did a different calculation using background levels of band sharing.

Q. And you believe that these calculations that you did are statistically valid calculations?

A. The same calculations Jeffries would do.

Q. Scientifically sound calculations?

A. That's correct.

Q. And you arrived at scientifically sound conclusions based on those calculations?

A. That's correct.

Q. So based on those scientifically sound conclusions you have determined that the probability of a five probe match is 1 in 11 million, is that correct?

A. That's correct.

Q. And the point you're simply making with the jury is, look, 310 million and 11 million is a big difference, right?

A. Yes.

Q. You can draw different conclusions or you can draw varying conclusions based on that?

A. That's correct.

Q. Okay. There is one thing they both have in common though, Doctor, in that they are both exceedingly rare figures.

A. They are both small probabilities.

Q. And something like if you had 11 million in the bank, 310 million dollars in the bank, certainly one is richer than the other, would you agree?

A. Yes.

Q. They are both rich, one is richer than the other, but neither one of them is poor, right?

A. Oh yeah, I agree.

Q. So to take it to what we're doing, one in 11 million, one in 310 million, they're both rare, one is more rare than the other, but neither one is common.

A. Neither one is common.

Q. Thank you. So even doing the probability figures based on this level of background band sharing, this level of inbreeding, even taking all that into consideration, you have still come up with a rare pattern?

A. If you're talking about unrelated individuals.

Q. Yes, we'll get to that.

A. Thank you.

Q. Just before we do, you said something and I didn't quite catch it. When you gave the 1 in 11 million and you were comparing it to the 310 showing the jury look at the difference, you said something - you can draw different conclusions about that, now correct

me, you said something about with 1 in 310 million you can exclude everybody.

A. That's the implication of that number because it's bigger than the general population.

Q. And 1 in 11 million you said something like could be 1 or 2 with that pattern.

A. I'm making the assumption that there's about 20 million people in Canada.

Q. Did you also take into consideration, Doctor, what we're dealing with here is semen?

A. You would have to cut it in half.

Q. Cut what in half?

A. If there are 20 million people, if 10 million of them are male, then we're talking about 1.

Q. Sorry, I didn't --

A. If you have 20 million people, if we're talking about semen obviously that has to be a male, so what you end up doing is cutting the total population down to the total number of males.

Q. Total number of males.

A. That's correct.

Q. There's evidence here that the total population of Canada is 25 million, approximately, so half of those would be 12.5 million.

A. Um-hmm.

Q. And that would be different - all age groups, so the potential contributors of semen --

A. 1 or 2.

Q. So you're down to what? What would you give me a guess, Doctor? If we go down to 12.5 million and if you excluded those too young to be sexual mature, what would you think you would get the figure down to?

A. It would still be 1 or 2. The 1 - 1 would be sort of a guarantee in some senses but it's a sampling problem so you may end up with two.

Q. Two what?

A. Two individuals. In fact what you end up doing is there's a thing called the POISSON distribution that would allow you to determine what the likelihood of 0, 1, 2, 3, 4, 5 and so forth and so on.

Q. But what we're dealing with then, Doctor, is whereas 1 in 310 million would exclude everyone, 1 in 11 million you're working on a population of 12.5 million. You're comparing it to 12.

A. Yes. I'm saying there's maybe one other individual.

Q. You're comparing it to 12.5 million people.

A. Yes.

Q. Potential contributors.

A. Right.

Q. And if you excluded those that can't produce semen because they're too young, and I'm hesitant to say those that are at an age where they're not sexually active, then that would even reduce the number even smaller.

A. People produce sperm until very old, but I agree with you. I agree with the implication.

Q. You know what I'm getting at Doctor.

A. Yes.

Q. I don't want to insult anybody here. But you know what I'm getting at. It's going to reduce the total population that you're looking at, would it not?

A. Yes.

Q. So given that, and given that we haven't done that reduction when we got to 12.5 million, you would probably agree with me, Doctor, that probably just as, you know, a good guess, we're probably dealing even very conservatively with 10 million people.

A. Yes.

Q. And you have come up with a probability of 1 in 11 million people.

A. Um-hmm.

Q. Thank you. Now, let's get to this relatedness - relatives. You, after you gave the jury the 1 in 11 million then you threw out two other numbers. One you did on your own, I believe, and that was 1 in three thousand and something.

A. 3,139.

Q. And that was for half sibs.

A. Half sib, nephew, uncle.

Q. Those were potential contributors of the semen?

A. I don't know. I'm just saying that class of relatives has that probability of matching an individual.

Q. Okay. And the other number you came up with was at Mr. Furlotte's request and that was based on full sibs.

A. Full siblings.

Q. A brother.

A. Yes.

Q. For example. With semen it would have to be a brother.

A. Right.

Q. And that was 1 in 37.

A. With that level of background band sharing, yes.

Q. So those numbers came up after 1 in 11 million. If there was no brother, no brother, what relevance would the 1 in 37 have?

A. None.

Q. So the figure that Mr. Furlotte asked you to do has no relevance if there's no brother?

A. That's correct.

Q. Just a number.

A. Yes.

Q. Thank you. If there are no half sibs that could be a potential suspect, no half brothers, no uncles, no cousins, is that what --

A. Nephews.

Q. Nephews. That even though they may exist but that they couldn't be a potential contributor of that semen in the jury's mind then that number would have no relevance to this case?

A. Correct.

Q. So if we're only dealing in the jury's mind with the potential of someone unrelated contributing that semen --

A. How about cousins.

Q. Or cousins.

A. Okay, cousins is 1 in 83,452.

Q. Okay. So if they were dealing with cousins then the probability would be 1 in 83,000 but if in the jury's mind we're really not dealing with cousins that number doesn't mean anything at all.

A. That's not my job. Yes.

Q. And if you're only dealing with unrelated individuals in the jury's minds you're saying look at the one in 11 million.

A. That's the number that I come up with using background band sharing.

Q. The jury would, therefore, Doctor, be dealing with a rare event?

A. If it was only unrelated individuals, yeah, I would call it rare.

Q. It would be rare for the semen to match Mr. Legere's blood and hair unless the semen was from Mr. Legere?

A. Yes.

Q. And if the semen was from Mr. Legere you would expect it to match the DNA patterns in his own hair and blood?

A. Yes.

MR. WALSH: Thank you, Doctor, I have no further questions.

THE COURT: Re-examination Mr. Furlotte.

REDIRECT EXAMINATION BY MR. FURLOTTE:

Q. Doctor Shields I believe you mentioned that Mr. Legere's samples would be shown through the DNA testing that they would be consistent with coming from Mr. -- with the evidence samples.

A. That's correct.

Q. And you mentioned in the absence of laboratory mix-up.

A. Yes.

Q. What would you mean by a laboratory mixup?

A. It has occasionally been the case, and in fact we know of at least two cases from Cellmark, one of the private companies in the U.S., that a test tube with a particular tissue sample or blood sample can be mixed with another sample so that you end up

having the wrong individuals labeled on a gel. It may not be - you know. Could be different individuals. In a lane where it's supposed to be one person it's somebody else and it can be the same individual twice on a gel when they're only supposed to be there once. That sort of thing.

Q. What about the possibility of the spillage of the DNA sample into the different lanes when you're --

A. That's the kind of thing we're talking about is a mix-up where it goes into the wrong lane either because a test tube has been mislabeled or it's 4 o'clock in the morning New Year's Eve and somebody did it when they were drunk. I don't think those sorts of things are likely to be going on very often.

Q. What about the possibility of spillage from -- Besides just mixing up two samples --

A. From one to the other lane.

Q. Across lanes.

A. It's very unlikely.

Q. Now, you mentioned the four or five probe match was rare without developing statistics. Is that also for -- Is that for related or unrelated people?

A. It's for unrelated people. It's a rare event for unrelated people. It is not expected to be rare with related people. A good example is identical twins are expected to match at every locus, period. The probability of 1.

Q. But you said on cross-examination that a four or five probe match would be rare without developing statistics. That's again, only for unrelated people?

A. Yes, it is.

Q. Also, Mr. Walsh brought up the fact that Kenneth Kidd deals with human population genetics and you deal with mostly animal populations rather than human populations, correct?

A. I deal with human populations, and I believe humans are animals, they're not plants. I also --

Q. The fact that you deal mostly with animal populations in the field of population genetics, does that take away from your ability to assess human populations for substructure?

A. No. Can I finish my answer to that other question though because it got cut off in a place I don't want it to be cut off.

Q. Okay.

A. I said that I deal with human populations. I also deal with other animal populations, from beetles to chipmunks, to rattlesnakes, to wolves and so forth and so on. So I deal with all sorts of animals, including humans. The answer to the other question was no, it doesn't make any difference.

Q. Because Doctor Kidd deals with humans would that make him any more qualified to identify substructures within a human population?

A. In my opinion, no.

Q. Mr. Walsh mentioned an affidavit that you prepared in the Vanderbogart case.

A. Um-hmm.

Q. And he mentioned something about you not using upper confidence intervals in that affidavit.

A. That's correct.

Q. And I believe you did mention that there was other parts besides that affidavit went into evidence.

A. The report that I did for the National Academy of Sciences went in as part of the evidence and in there I discuss extensively the use of confidence limits for a variety of reasons, including around frequencies.

Q. And Mr. Walsh also discussed Nichols and Balding with you, and you made the statement that Nichols and Balding is not about this case. Would you --

A. Not about my testimony in this case at this time. Okay. Nichols and Balding offers a different level of correction factor which would result in a smaller number than the number I get using background band sharing. A bigger probability. It's one in 5.9 million in fact.

Q. So that's somebody else proposing a different --

A. It's a different way of doing it.

Q. Again, maybe the last area is Mr. Walsh stated that the way you do it for unrelated people you get a figure of 1 in 11 million and the way the R.C.M.P. did it it was 1 in 310 million, and that both would be rare occasions.

A. Yes.

Q. And this is for unrelated people.

A. Correct.

Q. And there was a discussion that because there wasn't 310 million people --

MR. WALSH: This, I hope, is new My Lord. Mr. Furlotte, I believe, had that opportunity yesterday and the Doctor testified all about 310 versus 1 in 11 and about what it means to him in terms of how many potential contributors there could be and I don't think this is proper redirect.

MR. FURLOTTE: No, I never covered that.

MR. WALSH: Well Mr. Furlotte didn't cover it as he sat through most of yesterday, I appreciate that, but what we're dealing with here is the fact that his own witness covered that area.

THE COURT: Yes. Well, go ahead Mr. Furlotte with your question.

MR. FURLOTTE: Doctor, the fact that there would be say less than the number of people in Canada, than 310 million, or say even less than -- okay, we'll take the 310 million, does that mean that there would have to be 310 million for somebody else out there to have that same match?

A. No. There is a standard statistical treatment to come up with the probability that someone else would match. You use the POISSON distribution and then you can multiply those probabilities taking into account the sample size that you used. It would be unlikely, still, but it would not be a zero probability.

Q. And with related individuals the figure you come up with, I believe, was 1 chance in 3,139.

A. For individuals related at the level of half sibs, nephews or uncles.

Q. Right. Again, would that mean that Mr. Legere would have to have 3,139 relatives in order to find a match?

A. No.

Q. Would that be the same for brothers? Brothers or sisters or full siblings is 1 chance in 1,024.

A. Right. The way of thinking about that is if you went out and sampled a million pairs of brothers, one out of each one thousand and twenty-four would be expected

to match so you'd get that many matches if you sampled a million pairs. It's another way of thinking about how those probabilities operate.

Q. It could be more or it could be less.

A. Absolutely. It's the same as I think was discussed yesterday, sometimes you get eight heads in a row.

Q. So for me to find - or for any of us to find a brother who would match with let's say myself for five probes I wouldn't have to have a thousand brothers.

A. Nope.

MR. FURLOTTE: No further questions.

THE COURT: Thank you very much Doctor Shields. Thank you for coming. Bon voyage. Do you have another witness?

MR. FURLOTTE: That is all the evidence for the Defence, My Lord.

THE COURT: Well now that closes then the case. The next step in the trial will be the addresses of counsel to the jury and then followed by the Judge's charge to the jury. I'm just not certain about the timing on this. This is Wednesday noonhour. I did want to have a --

MR. WALSH: Tuesday, My Lord. You said Wednesday noon-hour. It's Tuesday noonhour.

THE COURT: Oh, Tuesday. I did want to have a session with counsel. I think it was agreed we would have a session where we would discuss --

MR. ALLMAN: If I could make a suggestion, My Lord. It's 11 o'clock. We could take a break, maybe 20 minutes. We could meet with you during that break just to discuss timing. The jury could come back at 20 past and by then hopefully we will have a schedule.

THE COURT: Well, perhaps we will do that. I was going to put up certain things for the jury to consider but perhaps I should discuss it with counsel. Were you suggesting --

MR. ALLMAN: Any schedule that we came up with would, of course, be tentative and if the jury had feelings on the matter we would take that into account, but I just thought it might be nice to have a tentative schedule and we can work that out in the next 20 minutes.

THE COURT: I think perhaps before I put options up to the jury I should discuss it with counsel. What I have in mind is, you know, counsel have got to be given some opportunity to prepare for their addresses and it's just a question of how long and what our timing is between now and the end of the week. So if you people would go out we'll call you back in after the recess, briefly. You will be going home today anyway.

(Jury excused.)

THE COURT: Mr. Allman, was your suggestion that counsel might meet with me in chambers or --

MR. ALLMAN: I said that but I don't mind whether we have a discussion in chambers or right here and now. It really doesn't matter to me.

THE COURT: Well what about right here now. Do you have --

MR. ALLMAN: I have a comment to make.

THE COURT: Let me tell you my thoughts first. May I do that and then you beat me down. Counsel earlier had suggested they would like two or three days, some time ago, a couple of weeks ago when we were trying to plot out the scheduling for the balance of the trial, the timing. I had indicated that I would be quite pre-

pared to give a day between the termination of the evidence and the commencement of the addresses. I think counsel indicated at that time that they'd like perhaps to have a little more than a day. I think two or three days perhaps was suggested, or perhaps three days or something like that, and I said well perhaps two days then would be appropriate depending on how we can fit this within the timing in the week or the timing of days. I did point out then and I point out again now that I don't like the idea of the jury waiting around, sitting around for days and days on end waiting for the termination of the trial. They've been through a lot and I'm sure they want to get down to their main task of deciding what they have to do in considering the case. There is also the disadvantage, of course, that the longer a jury sits around waiting for the termination of a trial the more chance there is of difficulties arising and illnesses and sicknesses and all the other things that can crop up, and be exposed to people who may try to influence them one way or another. That's the sort of thing we want to avoid.

This is Tuesday afternoon. We would run into the weekend. To put this over to next Monday or Tuesday would be too long a break as far as I'm concerned. If we took just one day off, or a day and a half off shall we say, that would mean that counsel would address the jury on Thursday. I think Counsel did indicate before that they might be able to do it in a half day apiece. Hopefully that would be the case which would mean both counsel could address the jury the same day.

and it would mean counsel confining themselves to about three hours or actually something less than three hours when you allow for a break midway through. You're getting down to about two and a half hours really. If that were done say on Thursday and the Judge's charge were on Friday, I've got a lot of ground to cover but if I started first thing in the morning and sometime around noonhour I would be concluded and the jury would retire to consider their verdict. That would be on Friday. Then they would have Friday afternoon and if they take longer, as would very possibly be the case considering the number of exhibits they'll want to look at and so on, they would go into Saturday. If they don't conclude their -- They will, of course, be locked up or incommunicado, is that the word, or is it excommunicado. Anyway, they're confined once they retire and they're not free to separate. If they go into Sunday -- I don't know how long they'd take. Hopefully they would come up with a verdict on Saturday. If they go into Sunday then so be it. There's nothing to prevent court sitting on Sunday or a jury returning a verdict on Sunday, or Monday, or Tuesday, or whatever.

If we took two days now or took two and a half days that would mean we could have the addresses of counsel on Friday and I could deliver my charge to the jury on Saturday. The jury would retire early Saturday afternoon or Saturday morning - Saturday noon, and they would then take as long as they wanted. It creates the difficulty that it would be unlikely that they could before Sunday bring back a verdict or consider the matter as they should consider it and

bring back a verdict. I don't know how the jury would feel about the Sunday business. We run into the problem sometimes of religion and so on and I don't know what impact this has. I rather suspect the jury, who seem to be a keen group, would - and I mean as far as devotion and dedication to the trial is concerned, very possibly they would say well look, let's just treat Sunday as a normal working day and we will go out on Saturday, consider it on Sunday and we come back Sunday, Monday, whatever day.

Do you have anything, Mr. Allman, you would like to comment on?

MR. ALLMAN: Well yes, just a little, and I'm grateful for those indications of Your Lordship, and basically I agree entirely. I certainly don't think that we should set matters off so that nothing else happens between now and next Monday. That's too long for the jury to be away. They will forget things and I'm not in favour of that. I can speak simply for the Crown's position which is this. We would be ready to proceed with our address to the jury but that has to come after Mr. Furlotte's of course. We could be ready on Thursday and then your charge on Friday. That's option number one. That would give Mr. Furlotte one and a half days to prepare his opening for Thursday morning. Purely from a selfish Crown perspective that's what we would prefer I think. I understand, however, of course that Mr. Furlotte's got a problem that we don't have. During the last weeks when the DNA has been dragging on I have obviously been able to use some of my time to prepare

an original closing statement without the DNA, but it's been a big help. Mr. Furlotte hasn't had that benefit so if he feels that he needs two and a half days which would mean counsels' addresses on Friday then my preference, subject to whatever the jury may say, would be counsels' addresses Friday, your summation Saturday, and let the jury come back when they may. I think those are the two options effectively.

THE COURT: Mr. Furlotte, what are your thoughts?

MR. FURLOTTE: Well, My Lord, it's as Mr. Allman has stated. He's in a much position than I am. During the past two weeks he's been able to during the course of the trial read through the transcripts that have been prepared through the trial with different witnesses that had testified. While I have received copies of those transcripts I haven't had time to even open them except for Mr. Allman's opening address. I would definitely need 2½ days, I would definitely need more, but it is what this court is going to tolerate. My position would have been to hold it off until next Monday to give me the rest of this week and the weekend to prepare for final argument but, as the Court has already stated, it does not wish to do that. I can only plead for as much time as this Court will give me.

THE COURT: Yes. Well, I'm in sympathy totally with your position. I will say this, that we did of course have last - we had last Friday, we ended a little -- Although you probably didn't have very much time to devote to it last week.

MR. FURLOTTE: My Lord before you decide on that I have one other matter I would like to put on the record is that this Court, even though at the last motion for the severance of counts this Court held open that it could sever the counts at any time during the trial before it's put to the jury, and I would ask this Court again to sever these counts because of I suppose in one sense the different testimony that has gone into evidence that it's, I believe, too massive for the jury to handle. I believe that the DNA evidence, because of the quality of the evidence that has gone in, it may be very influencial on let's say the Smith case because of testimony by Doctor MacKay that he's of the opinion that all of this occurred at one hand - by one hand. I objected at that time. I didn't think it was proper evidence to be given by an expert witness but the Court allowed it in. But in view of that evidence that it is now in, the jury's already been prejudiced by it, and that I would submit, My Lord, that it is a proper case for a severance of counts at this point.

MR. SLEETH: My Lord if it please the Court, since I argued severance before, I would just make the same comments basically that I did on the last occasion which are that the evidence is so inextricably intertwined it would be virtually impossible to charge the jurors now. They have also heard all of this evidence and they've heard all those factors which would be similar fact evidence. They have now these factors before them. It would be impossible for them to separate features at this stage. It is far too late for this motion now. As for the reference to Doctor

MacKay, you will recall of course, My Lord, that Doctor MacKay subsequently after having made the remark referred to by counsel for the Accused, qualified that somewhat indicating that he was talking about something that could have been done by the same hand or by somebody acting in an identical manner or same fashion. But I would repeat as I urged the Court the last time, the evidence is now before it, and the situation has become even clearer and more severe, all the evidence is before the jurors now and it would be virtually impossible for them to separate the evidence.

THE COURT: Well, on that point I will consider that during the recess that we're about to have and I'll give an answer on that when I come back. But on the other matter, I think what I will do, assuming -- well, if there's a severance of counts or whether there is or whether there isn't, the jury will still be retiring of course, and I think what I will do is when we bring back the jury I will sound them out on this business of following as you suggest, Mr. Furlotte, the Friday for the counsel and Saturday for the judge's charge, and see how this works out with them. They might possibly say well they prefer to do it on Monday if they have religious scrupples. I want to avoid that if I possibly can but at the same time it's difficult for me to tell them they've got to be working on Sunday in a court case. However, we will sound them out and I may even put thoughts to them and send them out to discuss it. I can't and we can't, of course, go into the jury room and discuss

these things with them and say what are your feelings on it.

MR. ALLMAN: There was one other matter, My Lord, and we will again mention this in chambers. There were a number of matters that we want to discuss with Your Lordship. I think these would be matters to be discussed in chambers or at some point. You mentioned the same thing, that you are in the practice of discussing with counsel any particular things, points of law that they want to bring to your attention with regard to your summing up and also with regard to what we can legitimately say in our closing addresses. We have identified a number of issues that we want to bring before you and at some point in time -- That's safe to say, yes --

THE COURT: No, you can't say that. There's no such expression as 'point in time'.

MR. ALLMAN: Right. At some time --

THE COURT: Mr. Walsh has learned that, we've got him trained, and now you're breaking in front of all these -- In front of all these students back here you're breaking this rule.

MR. WALSH: I noted, My Lord, throughout the trial that I seemed to be in the majority in that case.

MR. ALLMAN: And be that as it may, at some moment prior to us making our summations and Your Lordship making your summing up to the jury, we would like to meet with you and go over these matters.

THE COURT: Yes. Well now I'm prepared to do that either in court with the jury excluded, of course, later this morning or to do it in chambers, one or the other. Are counsel prepared now to -- Are you

prepared, Mr. Furlotte, to --

MR. FURLOTTE: I believe the Crown was going to give me a copy of the legal issues that they wanted addressed before we discussed it.

THE COURT: Have you got that?

MR. ALLMAN: What I have got is four cases - headnotes from cases that we want to bring to your attention, and I think perhaps a couple of other issues that there is no direct law on but that we are going to seek your guidance on. What I'll do is this. At the break, hopefully we can get 15 minutes for coffee, I'll give Mr. Furlotte copies of the authorities that we want to refer you to, I'll advise him of what the other matters are, and then when we come back he can tell you when he would be ready to deal with our issues and to raise any issues of his own.

THE COURT: Well, it might be that meeting in chambers would be better than open court to discuss this matter. There will be no decisions made.

MR. ALLMAN: I would leave that up to Mr. Furlotte. Whatever he feels happy with.

MR. FURLOTTE: My Lord I would suggest that we take a fairly lengthy break this morning - or we could bring the jury back and send them -- I guess you still have to make your decision when you are going to want to reconvene, but as far as for the other legal issues that we have to decide --

MR. ALLMAN: Any time between now and Thursday.

MR. FURLOTTE: Yes, that would be fine.

MR. ALLMAN: Why don't we see when the jury want to start again and then we'll see whether we need to --

THE COURT: Let's do that and then we'll thrash out this other problem then. Okay, we'll take 16 minutes.

(RECESS - 11:20 - 11:55 A.M.)

THE COURT: Just before we bring the jury in I will deal with the matter of the application for the severance of counts. This is on the monitor Mr. Pugh?

MR. CLERK: I'll check that My Lord. (Pause.) Yes, My Lord, it's working.

THE COURT: In dealing with the matter of the application for the severance of counts, a similar application was made at an earlier stage of the trial and I refused the application at that time and I gave my reasons for it. It seemed to me at that time that there were rather compelling reasons why perhaps the four counts should be tried together. I did, as Mr. Furlotte has suggested, I did indicate that I would reserve the right to hear a further application through the trial or even on my own account make an order for severance of counts if I felt that the evidence were so voluminous or the matter became so complicated that it would be impossible to either address the jury for counsel or a judge to charge the jury on four counts, and if I felt that it were not in the best interests of justice to let the four counts go to the jury together. But I'm not impressed, really, with the suggestion at this time that it would be that complicated. It will certainly be a difficult job both for counsel and for a judge to address the jury but I don't think it's an impossible task. There is a common thread runs through the whole thing. Mr. Allman in his initial address to the jury

I think took about 2½ hours I believe and covered it, and covered everything rather adequately in that address. I don't see that it's -- At least one thing that he did demonstrate at that time was that one's thoughts can be organized so as to present the thing to a jury in a reasonable fashion so they can consider it. I'm a little concerned about the length of the Judge's address in a situation like this but I don't see that as being an insurmountable thing to do. So I'm ruling against the motion in effect. All four counts will go to the jury.

I think that's all. We'll have the jury back.

(Jury called, all present. Accused viewing from holding cell.)

THE COURT: Well, members of the jury, after you retired just before the recess I discussed here in court with counsel the matter of the timing of the rest of the trial. There are two or three alternatives that are perhaps open as far as timing is concerned. The next day of the trial would be presumably taken up with addresses of counsel. They had earlier indicated to me that probably one-half day, the morning for one and the afternoon for the other, would probably suffice for that. That would be followed the following day by the Judge's charge to the jury and that will take up all the morning and perhaps run into the noonhour a little. It is customary - it's always my practice in any event, to have the Judge's charge follow immediately after counsels' addresses with no gap in between other than the intervening night that is, but not to have any appreciable gap like over a

weekend or anything like that, and it's also desirable, I've always felt, to have counsel address the jury on the same day, that is one after the other. In a case like this where the Defence has called evidence it is the obligation of the Defence counsel to go first and to address the jury first and that's followed by the Crown counsel.

This is a case where I think some appropriate time should be given to counsel and may even be required by the Court to prepare the addresses and we have certain matters, just technical matters, that I will be discussing with counsel probably this afternoon which is going to cut today out of it pretty well, and I feel it would be not inappropriate if counsel had two full days after that to prepare. It has been an involved case. Counsel have been going straight ahead. I'm sure Mr. Furlotte must have felt the pressure a little more perhaps even than Crown counsel inasmuch as he's been alone for most of the trial and hasn't perhaps been able to keep notes of evidence and that sort of thing as well as he might otherwise have done. So I think two days is an appropriate time.

That means that if we took Wednesday and Thursday that would mean the addresses to the jury by counsel would be made on Friday and then the Judge's charge would follow on Saturday. This has the advantage that we don't get into next weekend. I wouldn't like to ask the jury to stand over until next Monday or next Tuesday with addresses on Monday and Tuesday because I think that makes too long a

period. You people are going to be under certain pressures - or at least the risk of pressure from others as jury members and I want to cut that down or eliminate that possibility as much as possible. I don't want to keep you waiting until next Monday and I'm sure, as well, that you people want to get at your job and get it done. So that's why it's a good thing to go ahead this week. The negative thing, of course, is that we run into Sunday. It would mean you would only have Saturday afternoon and evening before the arrival of Sunday to consider your verdict, but you don't have to do that, you can go over. A verdict can be brought in on Sunday or be brought in Monday or Tuesday or however long you people want to take at that stage. But after I have delivered my address to you on Saturday, if we decide on this, you are impounded at that time and you are not permitted to separate. You must stay together. You will be put in the charge of one or two constables who will be guarding you for all their lives are worth to make sure you don't talk to anybody - anybody else. You can talk among yourselves but with nobody else at that stage, and you can't separate. There's one problem about it; you can't even separate to go to church so you may have to resolve your religious obligations in some other way. I'll leave that up to you.

Does the Chairperson see any difficulties about --

JUROR LANCASTER: No. We've talked this over and that will be fine with us. I think God will forgive us if we don't get to church this Sunday.

THE COURT: Well, you will have to straighten that out with God yourselves. I'm not in very close touch with him despite what I said this morning. I shouldn't have said sometimes I'm called God; sometimes people say 'My God' is what I meant to say.

So then the jury will be discharged now until Friday morning at 9:30, and we would see you back. The same arrangements for getting here of course would pertain. On Friday noonhour arrangements would be made the same as in the past for lunch and then on Friday evening you would be separated and going home the same as you normally did. Then on Saturday morning though when you come bring - or in the likelihood that you're going to have to stay overnight, at least one night or perhaps more, bring your overnight bags and whatever you require with you. You will be taken directly from here -- Well, on Saturday what would probably happen is after the charge were over you will probably be taken for lunch and then would be brought back here and put in the jury room. We will try to perhaps arrange even for the other courtroom might be available. It's a larger room and it will be up to you people at that stage, but we I'm sure we could arrange for the courtroom. You could have the run of both rooms. But you would sit on Saturday afternoon, you would sit on -- And then Saturday afternoon we would arrange for you to go back and have dinner the same place and then come back here after in the evening on Saturday

and sit here as long as you want to, to midnight if you want to, or later Saturday evening, or not come back. If you prefer to call it off for Saturday after your dinner is over you can go to the motel where you will be put up. But that's up to you people and you're under no compulsion to bring back a verdict on Saturday. If you have reached a verdict there's no reason why you can't report it, because as long as you people are here in the jury room or on the premises we will be waiting for you to bring back a verdict. But you people take as long as you want to about it. Then on Sunday what we would do is you would be brought down here again to the jury room at 9:30 after breakfast in your rooms and be brought here and you would consider the evidence and so on further, your exhibits, and consider your verdict, and until such time as you do bring your verdict then we'd follow the same procedure. You'd go to lunch and you'd go to dinner in the evening and back to the hotel and so on into December. By Christmas presumably we'd have a verdict.

I think that is about all I can say at the present time. I do want to say before you separate this time, again, please be on your guard as much as you have been I know up until now about talking to anybody about the case or in listening to anybody. And don't even in your own minds be trying to make up your decision or your minds. You have heard all the evidence but you've still got to hear the addresses of counsel and you've got to hear me explain to you what the law is, or what first degree

murder is, second degree murder, and so on, and I will be instructing you about all the things you will have to take into consideration. Counsel will be reviewing the facts of the case and I will be doing the same. So keep an open mind on the matter until you do have a chance to sit down and talk this over together and try to reach your verdict.

Well, that is all I can say now so we will see you on Friday morning.

(Jury excused 12:10 P.M.)

THE COURT: Well, the only other matter is what we did -- Have you got any --

MR. ALLMAN: I have got four authorities that I would like to leave with you and I've given copies to Mr. Furlotte and perhaps you could take some time to have a look at them and then we could all get together after you have had the opportunity to think about them. And also Mr. Furlotte may want a little time to think if he's got some issues he wants to raise. I don't know what time we could have our meeting. Basically I could do it any time but it's more Mr. Furlotte than I.

THE COURT: I don't see why we couldn't do this in chambers as well as in court. I don't think it's necessary to bring in court reporters. If there are any decisions to be -- I will, before you start your addresses, I will in court be advising you what verdicts, for instance, I'm going to leave to the jury. I can advise you tentatively before that but then I will confirm it on the record at that time. Or if there are any other matters to go on the record in relation

to it it can go on when we meet on Friday morning. So we don't have to have the court officials back before Friday morning. Why couldn't we say a meeting in chambers say at 2 o'clock tomorrow afternoon here - or at what other time do you sooner meet? Whatever is convenient.

MR. ALLMAN: It's more up to Mr. Furlotte than me because I'm basically ready to discuss it at any time. It's more Mr. Furlotte's situation. But I would like to give you these just to mull over between now and then if that's acceptable to Mr. Furlotte.

THE COURT: Yes. You've given copies to Mr. Furlotte?

MR. ALLMAN: Yes. There's four cases and one citation.

THE COURT: And what, Mr. Furlotte, would you -- Would you agree that we might set a tentative time to meet in chambers?

MR. FURLOTTE: Sure. It's not going to matter much what time it is. I'll have to take a break from what I'm doing whatever time it is.

THE COURT: Yes. Well what time would be most convenient.

MR. ALLMAN: Is this chambers here or in --

THE COURT: Well, I'm probably going to be here most of the time between now and then.

MR. ALLMAN: Then it really doesn't matter to me what time.

THE COURT: Where are you people, in Fredericton?

MR. ALLMAN: We're in Fredericton but that's no problem.

THE COURT: Oh, well I'll do it in Fredericton. Saves you people coming down here. Let's say 2 o'clock tomorrow afternoon in Fredericton at my chambers in the Justice Building.

MR. ALLMAN: Fine, My Lord.

THE COURT: My office is too small there. We may have to go to one of the courtrooms or somewhere. We'll find a committee room or something there. 2 o'clock tomorrow afternoon. It will be brief, 20 minutes or so.

So the court then is adjourned until 9:30 on Friday morning, November 1st.

Would the Clerk perhaps prepare -- I think he's kept counsel supplied with copies of the exhibit list and could the clerk, I wonder, have that brought up to date and see that counsel get a copy of that as soon as possible.

MR. CLERK: Yes, My Lord.

THE COURT: Counsel were going to prepare a list of the --

MR. ALLMAN: Your Lordship is one step ahead of me. We've got the list but what I was going to do, after Your Lordship rises I'm going to ask Mr. Pugh to just hang around for five minutes, get exhibit P-1 down, he'll have to stay to make sure we don't tamper with it, and we are going to go through our list and make sure that the numbers on there correspond to our list, and then when we have checked that out we will give copies to yourself and Mr. Furlotte.

THE COURT: Mr. Pugh points out that the reporters might like to view some of the exhibits. They did have an opportunity before, of course, to view and even take pictures of some of the charts that were in, and there have been new charts put in but I'm not going to permit the media - I don't think it's necessary to go through the exhibits that are in the boxes and that

sort of thing. Mr. Pugh will you check with the media as soon as we are finished here and if there are charts that they want to look at, even take pictures of, they can do it providing they don't take pictures of anything else in the courtroom, just the charts, the same formula as before. But charts only. Nothing else.

There was some other list or something that --

MR. CLERK: Wanted to speak to the witness list which was corrected -- Mr. Allman has corrected part of the witness list. Do you want to point out your corrections?

MR. ALLMAN: I haven't got it with me, unfortunately.

THE COURT: Well, talk to me tomorrow afternoon about that. And then the list of the pin things tomorrow.

MR. ALLMAN: Yes. Both of those will be resolved by tomorrow.

THE COURT: So, nothing more now.

(ADJOURNED TO FRIDAY, NOV. 1, 1991 @ 9:30 A.M.)

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

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. (Volumes I, II, VII, VIII, XIII, XIV, XVIII, XIX, XXII.)

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 1st day of April,
1992.

BEFORE ME:

Robert L. Jackson,
Being a Solicitor.

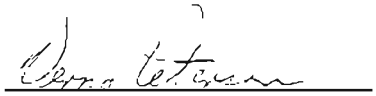
SCHEDULE "A"

RECORDING OF EVIDENCE BY SOUND RECORDING MACHINE ACT

CERTIFICATE

I, Verna Peterson, of Fredericton, New Brunswick, certify that the sound recording tapes labelled R. vs. Allan J. Legere, initialled by me and enclosed in these boxes 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 trial held in the above proceeding on the 26th, 27th. 28th, and 29th days of August, 1991; the 16th, 17th, 18th, and 19th days of September, 1991; the 7th, 8th, 9th, 10th, 21st, 22nd, 23rd and 24th days of October, 1991, and on the 2nd and 3rd days of November, 1991, at Burton, New Brunswick, and that I was the person in charge of the sound recording machine at the time the evidence and proceedings were recorded.

DATED AT FREDERICTON, N.B., the 4th day of November, 1991.



IN THE COURT OF QUEEN'S BENCH OF NEW BRUNSWICK

TRIAL DIVISION

JUDICIAL DISTRICT OF FREDERICTON

B E T W E E N:

HER MAJESTY THE QUEEN

- and -

ALLAN JOSEPH 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, pages 476 to 1003, pages 2332 to 2694, pages 2737 to 2781, pages 2791 to 2884, pages 3938 to 4420, and 4957 to 5364.

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 April, A.D., 1992.

BEFORE ME:

Verna M. Peterson
A COMMISSIONER OF OATHS

Dolores M. Brewer

SCHEDULE "A"

RECORDING OF EVIDENCE BY SOUND RECORDING MACHINE ACT

C E R T I F I C A T E

I, Dolores Brewer, of Fredericton, New Brunswick certify that the sound recording tapes labelled:

HER MAJESTY THE QUEEN

- and -

ALLAN JOSEPH LEGERE

initialled by me and enclosed in these envelopes are the record of the evidence recorded on a sound recording machine pursuant to Section 2 of the Recording of Evidence by Sound Recording Machine Act at the Judge and Jury Trial held in the above proceeding on the 3rd, 4th, 5th, 6th, 23rd, 24th, 25th, 26th days of September, the 15th, 16th, 17th, 18th, 28th and 29th days of October, and the 1st day of November, A.D., 1991 at Burton, New Brunswick, and that I was the person in charge of the sound recording machine at the time the evidence and proceedings were recorded.

DATED at Fredericton, New Brunswick this 4th day of November, A.D., 1991.

Dolores M. Brewer

IN THE COURT OF QUEEN'S BENCH OF NEW BRUNSWICK

TRIAL DIVISION

JUDICIAL DISTRICT OF FREDERICTON

RE: R. v. Allan 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. (Pages 1004 to 1397 inc., and pages 2885 t0 3100 inc.)

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,
Province of New Brunswick,
this 30th day of March 1992.

BEFORE ME:

A COMMISSIONER OF OATHS

Gerald H. Turnbull

MY [illegible]
[illegible] 31, 1994

SCHEDULE "A"

RECORDING OF EVIDENCE BY SOUND RECORDING MACHINE ACT

CERTIFICATE

I, Gerald Turnbull of Fredericton, New Brunswick, certify that the sound recording tapes labelled:

R. v. Allan Legere

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 held in the above proceeding on the 9th, 10th, and 11th days of September 1991; and on the 30th day of September and 1st day of October 1991, at Burton, New Brunswick, and that I was the person in charge of the sound recording machine at the time the evidence and proceedings were recorded.

DATED at Fredericton, New Brunswick, this 30th day of March, A.D. 1992.

Gerald H. Turnbull

IN THE COURT OF QUEEN'S BENCH OF NEW BRUNSWICK

TRIAL DIVISION

JUDICIAL DISTRICT OF FREDERICTON

B E T W E E N :

HER MAJESTY THE QUEEN

- and -

ALLAN JOSEPH 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, pages 1398 to 1688; pages 3101 to 3367; 3374 to 3446.

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 day of March, A.D., 1992.

Marcia L. McLellan

BEFORE ME:

Verna M. Peterson
A COMMISSIONER OF OATHS

MY COMMISSION EXPIRES
DECEMBER 31, 19[illegible]

SCHEDULE "A"

RECORDING OF EVIDENCE BY SOUND RECORDING MACHINE ACT

CERTIFICATE

I, Marcia L. McLellan, of the City of Fredericton, County of York, Province of New Brunswick, certify that the sound recording tapes labelled R. VS. ALLAN LEGERE, initialled by me and enclosed in this envelope is the record or a portion of the evidence recorded on a sound recording machine pursuant to Section 2 of the Recording of Evidence by Sound Recording Machine Act at the trial held in the above proceeding on the 12th and 13th days of September, 1991; and the 2nd, 3rd, and 4th days of October, 1991, at the Sunbury County Courthouse, Burton, New Brunswick, and that I was the person in charge of the sound recording machine at the time the evidence and proceedings were recorded.

D A T E D at the City of Fredericton, Province of New Brunswick, this 30th day of March, A.D., 1992.

Marcia L. McLellan

MARCIA L. MCLELLAN

CANADA
PROVINCE OF NEW BRUNSWICK
PROVINCIAL COURT

BETWEEN:

HER MAJESTY THE QUEEN
on the information of

- vs -

ALLAN LEGERE

AFFIDAVIT SCHEDULED "B"

I, Auréa Rousselle, of the City of Moncton, New Brunswick, make oath and say:

1. THAT I am a stenographer duly appointed under the Recording of Evidence by Sound Recording Machine Act.

2. THAT this transcript being pages 2695 to 2736, 2782 to 2790 inclusively, is a true and correct transcription of the record of these proceedings heard at Burton, New Brunswick, on the 25th & 26th of September, A.D., 1991, 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(a) 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 Moncton, in the County of Westmorland and Province of New Brunswick, this 17th day of December, A.D., 1991,

BEFORE ME:

(A Commissioner of oaths)
BARRISTER & SOLICITOR

Auréa Rousselle
Court Stenographer

CANADA
PROVINCE DU NOUVEAU-BRUNSWICK
COUR PROVINCIALE

ENTRE:

SA MAJESTÉ LA REINE
sur la dénonciation de

- contre -

ALLAN LEGERE

AFFIDAVIT ANNEXE "B"

Je, Auréa Rousselle, de la Cité de Moncton, Nouveau-Brunswick, atteste:

1. QUE je suis sténographe judiciaire nommée en vertu de la loi intitulée loi sur l'enregistrement des témoignages à l'aide d'appareils d'enregistrement sonore.

2. QUE cette transcription, étant pages 2695 à 2736, 2782 à 2790 inclusivement, effectuée en application de l'article 2 et certifiée en vertu de l'article 3 de la loi est bien une transcription complète et fidèle du procès-verbal des procédures entendues à Burton, Nouveau-Brunswick, les 25 et 26 septembre, en l'an de grâce 1991;

3. QU'une copie conforme du certificat établi en application du paragraphe 3(1) de la loi qui accompagnait le procès-verbal lors de la réception des témoignages est annexée et intitulée Annexe "A".

ASSERMENTÉ DEVANT MOI dans la cité de Moncton, comté de Westmorland et province du Nouveau-Brunswick, ce 17 ième jour de décembre, en l'an de grâce 1991.

(Commissaire à l'assermentation)
AVOCAT/AVOCATE

Auréa Rousselle
Sténographe judiciaire

CANADA
PROVINCE OF NEW BRUNSWICK
PROVINCIAL COURT

BETWEEN:

HER MAJESTY THE QUEEN
on the information of

- vs -

ALLAN LEGERE

AFFIDAVIT SCHEDULED "B"

I, Auréa Rousselle, of the City of Moncton, New Brunswick, make oath and say:

1. THAT I am a stenographer duly appointed under the Recording of Evidence by Sound Recording Machine Act.

2. THAT this transcript being pages 3368 to 3373 inclusively, is a true and correct transcription of the record of these proceedings heard at Burton, New Brunswick, on the 4th day of October, A.D., 1991, 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(a) 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 Moncton, in the County of Westmorland and Province of New Brunswick, this 13th day of November, A.D., 1991,

BEFORE ME:

(A Commissioner of oaths)

BEING A LAWYER

Auréa Rousselle
Court Stenographer

CANADA
PROVINCE DU NOUVEAU-BRUNSWICK
COUR PROVINCIALE

ENTRE:

SA MAJESTÉ LA REINE
sur la dénonciation de

- contre -

ALLAN LEGERE

AFFIDAVIT ANNEXE "B"

Je, Auréa Rousselle, de la Cité de Moncton, Nouveau-Brunswick, atteste:

1. QUE je suis sténographe judiciaire nommée en vertu de la loi intitulée loi sur l'enregistrement des témoignages à l'aide d'appareils d'enregistrement sonore.

2. QUE cette transcription, étant pages 3368 à 3373 inclusivement, effectuée en application de l'article 2 et certifiée en vertu de l'article 3 de la loi est bien une transcription complète et fidèle du procès-verbal des procédures entendues à Burton, Nouveau-Brunswick, le 4ième jour de d'octobre, en l'an de grâce 1991 :

3. QU'une copie conforme du certificat établi en application du paragraphe 3(1) de la loi qui accompagnait le procès-verbal lors de la réception des témoignages est annexée et intitulée Annexe "A".

ASSERMENTÉ DEVANT MOI dans la cité de Moncton, comté de Westmorland et province du Nouveau-Brunswick, ce 13 ième jour de novembre, en l'an de grâce 1991.

(Commissaire à l'assermentation)

À TITRE D'AVOCAT

Auréa Rousselle
Sténographe judiciaire